anyin	GDA	gene symbol	bol gene Name	feco	heco	teco	fpr8	hpr8 tpr8		ican	mcan	tcan
V00594_at	V00594	mt2a	Metallothionein isoform 2	1683.1	1698.4	143.4	371.1	414.5	107.8	3.3	261	74.2
X64177_f_at_	X64177	mt1h	Metallothionein	761.9	728.2	93.6	73.7	6.99	27.4	10.4	27.4	14.9
M21121 at	M21121	rantes	SCYA5 Small inducible cytokine A5 (RANTES)	7 807	6617	7 8 8	717	396.6	115.3	1136		7.67
X04500 at	X04500	illb	III 18 Interleukin 1. beta	1993	1	-	10	2000	20.00	2.5.1	5 =	707
M13755 at	M13755	isg15	G1P2 Interferon, alpha-inducible protein (clone IFI.15K)	<u> </u>	545.6	1	253	662	100	3027	10	, 50 44 60 70 70 70 70 70 70 70 70 70 70 70 70 70
J03910_rna1 _at_	J03910	mt1g	(clone 14VS) metallothionein IG (MT1G) gene	602.9		-	1 1	6.1		0		0
X04602_s_at_	X04602	911	IL6 Interleukin 6 (B cell stimulatory factor 2)	408.5	ì	-	70.5	76.5	269.4	14.6		111
U33017_at_	U33017	slam	Signaling lymphocytic activation molecule (SLAM) mRNA	320.7	343.9	685.7	8.4	25.8	т	2.7	24.4	84.5
V00594_s_at_ V00594	V00594	mt2a	Metallothionein isoform 2	167.1	337.3	15	64.9	122.8	34.8	69.4	ļ	4.6
M65290_at_	M65290	i112b/p40	IL12B Natural killer cell stimulatory factor (IL12B)	71.2	261.5	825.7	0	2.3	4.7	32.8	92	412.7
Y00787_s_at_ Y00787	Y00787	811	INTERLEUKIN-8 PRECURSOR	89.1	234.5	40.9	9.8	13.1	8.4	8.2	10.8	10.5
X57579_s_at_ X57579	X57579	activinba	Activin beta-A subunit (exon 2)	166.9	233.7	47.2	22.8	16.8	9.4	14.1	19.3	24.6
X02910_at_	X02910	tnfa	TNF Tumor necrosis factor	144.1	225.5	115.7	73.8	58.6	48.5	27.2	1	43.2
L11329_at_	111329	dusp2	DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1	52.1	177.6	16.1	16.2	14.7	2.4	7.9	1.4	2.9
			MX1 Myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein									
M33882_at_	M33882	mx1	p78)	61.1	1668	84 7	90.3	152.2	868	34	397.3	102
M31165_at_	M31165	tnfaip6	TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR	172.2	163.5	624.1	9.09	100.2	101.8	7.1	5.6	58.6
M59465_at_	M59465	a20	TNFAIP1 Tumor necrosis factor alpha inducible protein A20	e 87	158.7	41.1	65.3	73.5	22.9	7.6	5.9	9.6
L19779_at_	ר19779	h2a	Histone H2A.2 mRNA	53.2	154	83.4	40.2	122.8	1			33.4

Figure 1A

						_			• •			()11	C11, t	u ai	•									
	109.3	604	1	22.8	0.7		0	54.9	53.6	0		9.0	116.5	179.1	0.2	0	56.3	(7	7.5	13.4	43.2	39.3	7
	35.9	212.1		14.6	4.0	0	0.0	4	11.7	6.1		0	17	1. 1	9.0	0	1=	n n		20.8	4.4	39.4	15.8	
	10.6	50	,	51.4	0.4	7		n	13.8	2.6	-	2.3	9.9	4	200	5.2	26.5	4 9		6	2.4	8.6	0.5	
	86.3	498.1	7	49.2	0.4	 	2 7 0	<u> </u>	32.2	33.6	-	0.2	91.6	17.5	0	122.2	83.5	0.7	-	m	8.8	50.4	95.7	
	86.3	192.2	2	72.5	0	73.8	13.8		Δ Σ	8.3		1		35.7	1	27.2	9.69	80.		81.7	1	82.3	22.4 9	
f	143.7	265.8	6	38.8	0.5	52.8	15.3	-	1	6.2	0		_	10.7			23.3	1.2		15.3 8		40.9	39.5	
\mid	204	618.8	644.5	46	147.8	11.4	9.809	703.3	2	333.5	303.7		240.9		ŀ	_	98.2	3.1		- _	,	42.6 4(
-	149.2	143.4	130.6	081	127.2	125	120.8			-		1				- 1		6			_	4	1281.1	
-		- 1		9	- 1			114.4		20/.08	106.5	ĺ	104.1				5./0	84	0	76.5		74.6	71.8	
	233.7	136.8	49.6	42.6	74.3	73.8	110	39.1	1000	100.0	45.8		105.3	50.2		58.7	3	14.6	1.2	57		21	144.3	
SOD-2 gene for manganese superoxide	INTEREST OF THE INDUCED 11.5 KD	Melanara	Interferon regulatory factor 7 (huming)	MMP1 Matrix metalloproteinase 1 (interstitial	MACROPHAGE INFLAMMATORY PROTEIN 1.	ALL TANKOR	Cyclooxygenase-2 (hCox.2) gene	GRO2 GRO2 oncogene	Interfeukin 8 (IL8) gene	Overio dibessi:	Cystic inclusis antigen mRNA	SOD2 Superoxide dismutage 2	Bci.2 related (Bfi.1) mRNA	PTX3 Pentaxin-related gene 135 division	IL-1 beta	CMKBR7 Chemokine (C.C) receptor 7	(Macrophage electron)	one of the second secon	RPS3 Ribosomal protein S3 / wrong name	MX2 Myxovirus (influence)	homolog of murine	116 Interferitin 6 / B and 1	(b cell stiffulatory factor 2)	ì
sod2	ifi27	gro1	irf7	mmp1	mip1a	CAGO	COAC	groz	818	cagb		sod2	bcl2a1 mt1e		ptx3	ccr7	mmp12	ifitmo	dusn5		mx2	91!		
X65965	X67325	X54489	U53830	X54925	M23178	U04636	M57721	10//0	M28130	M26311		XU/834	029680 M10942	M2116K	21504	L31384	L23808	X57351	U15932		M30818			
X65965_s_at_ X65965	X67325_at	X54489_rna1 _at_	U53830_at_	X54925_at	M23178_s_at	U04636_rna1 _at_	M57731_s_at	30_rna1	M26311_s_at	_	X07824	\top		M31166 at	7	1	L23808_at	at		Manore	\top	Y00081_s_at_ Y00081		

89 6	132		r.	20.2	33.8		52.5	35.1 83.6		n	m	79.5	i i		11.6	116.1	6.7		3	2.9	28.7		4 ر ن بر	<u>;</u>	15.7
248.6	34.9		15.6	8	6.5	_	29.3	8.4	-		9.0	23.8	20	1	30.1	43.4	1	31 7	+	4.6	13.9		0.00	1	17.3
18.6	0.2		13.1	12.8	5.4		20.3	1.1	0		1.7	8.4	7 00		4.6	8.8	1.4	116	,	6.6	æ	- C 4	3.8	1	24.6
141.1	20.8		13.7	25.2	7.8		21.7	44.4	0		5.4	47.9	ب ب		10.5	73.3	5.1	47.7	L	6.5	34	C	7.9		13./
266	9.9		97.1	59.5	7.9	1 30	156.1	8.2	5.7		5.2	82.6	3.7		85	15.5	4.4	53.3			3. 1.8	0	18.4	7 01	13./
16	6.1			S	3.3	22	34 5	3.2	4.7	-	7	42.9	5.3		372.7	27.2	4.0	76.1		/0.3	20.0	1.7	16.8	37.8	0.7
77.5	168.3		5.8	32.5	85.6	39.5	37.7	212.3	72.2	70.	7.64	26.3	62.2		19.3	161	78.3	48.3	ľ	107.7	7.4.7	38.5	5.2	17.1	•
71.6	× ()	(280	6.90	4.4	58.9	57.2	55.5	55.4	α,	5	21	48.6		10.4	100	43.6	42.3	7	30.7		39.6	39.5	39.4	
19.8	32.4	(L	110.3	40.4	40.3	23.2	25.8	13	47.3	10.9		51.9	54.1	0 791	34 6		30.7	34.3	φ α	29.6		43.5	22.4	49.2	1.2
CD38 CD38 antigen (p45)	6.16 gene (interferon-inducible peptide	inducible peptide (6.16) gene	TRYPTOPHANYL-TRNA SYNTHETASE	BF B-factor, properdin	Interferon induced leucine zipper protein	(IFF35) mRNA, partial cds	II 15RA laterial protein S3 /wrong name	PI Protease inhibitor 1 (anti-elastase), alpha-1.	antitrypsin	GRO3 GRO3 oncogene	MCP-2 gene	0	SCYA4 Small inducible cytoking Ad	(homologous to mouse Mip-1b)	HEM45 mRNA		TAP1 Transporter 1, ABC (ATP binding	SCYA4 Small inducible cytokine 44	(homologous to mouse Mip.1b)	B94 PROTEIN	Political	TXN Thioredoxin	Mitogen induced nuclear orphan receptor	(MINOR) mRNA	ANIAIN DE LA
cd38		g1p3	wars	pţ	.ff.35	ifi17	il15ra	1	aar	gro3	mcp2		ciape	mip1b	1161143	gadd45	100+	rabi	mip1b	rillaip2	cd155	txn		ifiit4	
D84276		U22970	115700	L13/02	U72882	J04164	U31628	K01396		X53800	9886X	1137546		M69203	10000	M60974	X57522	200	J04130 M92357	HG3415.	HT3598	X77584	737611	U12/0/ U52513	
D84276_at_	U22970_rna1	S at	115702 24	1172882 5 34		J04164_at_	U31628_at_	K01396 at	00000		- 14	U3/546_s_at	M69203_s_at	U88964 at	M60974 s at		X57522 at	, ,	M92357 at	Γ	_	X77584_at	112767 at	,	1

Г		س ا	-	1	6	ा	1	2	lo.i			<u> </u>	(6)		~T			~	<u> </u>	т —	~~ -					_		
		20.1	0	j I					23.2		,	1	65.6		318.2	250.0	0000	ע.	10.4		9.3			15	10.9	30.3	1.3	
		1.5	11 2		10.5	0.2		8.9	11.5	_	C	5	2.1		109.1	30.1	1.50	11.	4.5		9	·	C	87	-	9.6	0	
	1	0.5	10	7	3.6	1.1		22.2	6		α			ľ	2.7	y	2 0	0.0	5.6		y.5	_	-	1	2.	2.6	1.2	
		43.2	r,		0.3	2.1		7.6	15		7	;	16.2		230.5	26.2	-	1		,	4.6		u	0 0	ا بَوَ	7.4	0.7	
	(19.8	6		7.4	m		5.5	13.7		20.7		2.2	- 000	730.1	12.6	67	5	2	;	1		2,70	1.4.2	0.1	7	26.5	
-	•	17.7	10.8		4.5	0	l	5.3	27.5		8.0	-	2.	171	<u>, </u>	13.8	5		1.9	C	07		7.7	10	2 6	777	4.3	
	Ç	124.8	44.9		35.3	8.9	(33	55.8		8.6	1	7.1	127.2	- 1	209.8	20.4		8.5	7	7.0.7		27	25.0	0.00	40.0	3.5	
	00	30.2	38		88	3/.4	-,	3/.1	36.8		35.2	6	34.0	34.2	7.15	34.1	32.5		32.4	200	1,7		32.2	31.6	21:0	27.10	30.9	 -
	23.0	53.9	126.1	į	17	20.	0 7 0	24.0	61.7		1.9	0 00	0.62	14.7		16.9	25.2		2.5	70.6	2		23.7	3.0	43.8	2 0	13.2	
LITTER TITUS DITIONIES (ET ASE 4B) CAMP-Specific	(dunce (Drosophila) homolog phosphodiesterase E4)	G0S2 gene extracted from Human G0S2 gene.	5' flank and cds	AK3 mRNA for adenylate Vince 2	MT1L Metallothionein 11	actor (TRIPIO) monia	end of cds	III.7R Interleukin 7 recentor			Proline-Rich Protein Prb4, Allele	PTGIR Prostaglandin I2 (prostacyclin) receptor (IP)	TNF-related apoptosis inducing ligand TRAII	mRNA	C1NH Complement component 1 inhibitor	(angioedema, hereditary)	L-Kynurenine hydrolase mRNA	P2x purinoceptor mRNA	ICAM1 Intercellular adharias malasis	(CD54), human rhinovirus receptor	NFKB2 Nuclear factor of kappa light	polypeptide gene enhancer in B-cells 2	(p49/p100)	LIMK-2	Ninjurin1 mRNA	FC-epsilon-recentor gamma, chain mBNA	CANADI RESIDENCE DE LA CANADI DEL CANADI DE LA CANADI DEL CANADI DE LA CANADI DEL CANADI DE LA CANADI DEL CANADI DE LA CANADI DEL CANADI DE LA CANAD	NFKB1 Nuclear factor of kappa light
	dpde4		G0S2	ak3	mt11		trip10	il7r			prb4	ptgir		trail		cinh	Myriu	p2x4		icam1			nfkb p52	limk2	ninj1	fcer1g		47,47
	L20971		M/2885	X60673	X76717		L40379	M29696		HG4490.	H148/6	D38128		U37518	0000	M13690	037,721	AF000234		M24283		0000	5/6638	D45906	0/2661	M33195		W58603
	L20971_at_	M72885_rna1	_s_at_ x60672 rn21		X76717_at_			M29696_at_		HG4490.	48/6_T_at_ H148/6	D38128_at_		$\overline{}$	M13690_s_at	157721 at	1:			M24283_at_			5/0038 at	Т	7	M33195_at		M58603 at M58603

Figure 1D

7101017	HG1612.											
HT1612_at_	HT1612	macmarcks	Macmarcks	100	6							
X02875_s_at	X02875	oas1	OIAS (2'.5') olipoardenviate	2.61	8	444.	11.5	30.2	16.9	3.4	11.8	15.6
D28915_at_	D28915	mtan44	Hepatitis Cassociated microtubular aggregate	16./	<u>R</u>	48.7	41.5	58.8	117.7	4.2	20.5	80.4
U48807_at	U48807	dusp4	Dual specific protein phosphataco	8.5	29.6	53.6	10.7	47.1	44.3	13.3	15.5	48
U03891_at	U03891	unknown	Phorbolin I mRNA partial cds	5.6	29.6	7.4	2.4	3.1	9.8	9.7	2.6	217
			GBP1 Guanvlate binding protein 1	43.8	28.9	21.9	189.3	58.3	23.3	4.4	96	30.3
M55542_at_	M55542	gbp1	inducible, 67kD	000					-			
USU648_s_at	U50648	7.	Interferon inducible RNA dependent protein	20.4	4.82	99.4	34.6	20	88	1.5	26.4	75.9
D30755_at_	D30755	NAF1	VIM Vimentia	19.8	28.4	22.3	17.8	6	22.1	40.1	0 70	
U59286 at	U59286	itac	Dot- D1	56.3	28.2	196	100	0	1 0	1 -	0 0	
M34455 at	M34455	ido	Beta-R1 mKNA, partial cds	34.9	27.6	237.9	201	- 1	240.5	14.1	5.3	6.7
U03057 at	U03057		UCU IIIdole 2,3 dioxygenase	273.7	27.5	219.8	279 5	- 1	0.040	0.0	4.4	389.7
			Actili bundling protein mRNA	59.8	27.5	Va		100.5	0	C:1	3.4	901
1109937 2031			Urokinase type plasminogen activator receptor		1		j	10.4	14.1	32	13.4	2.3
_s_at_	1009937	plaur	gene extracted from Human urokinase type			-						
			RTG1 B cell translandi	17	26.9	14.5	12.5	10.7	2.4	~~	C	- 1
X61123_at_	X61123	btg1	Drolliferative	;	-		-		-	7	0.0	, i
U02020_at_	U02020		Pre-B cell enhancing factor (PREE) mona	30.4	26.8	14.4	8.4	4.6	4.4	3.6	7.4	9.7
			מבני (בבני) וווואש	20.9	26.4	37.4	6.9	11.9	14.5	29	7	α
1	X53296		IETRN Interleukin 1 receptor antagonist	Ĺ					-		1	0.0
	M10943	mt1f	Metallothionein-If gene (hMT-If)	0.00 U.U	20.4	6.9	28.7	14.4	4.6	4.3	7.7	4
559049_at	S59049	ier1	RGS1 Regulator of G-protein signalling 1	0 5	26.1	26.6		0	2.7	П	6.0	0
M14660 24	0,000		ISG-54K gene (interferon stimulated gene)	U. T	6.02	15.9	2.2	5.8	9.1	9.9	10.8	34
U66711_rna1		g10p2 e	encoding a 54 kDA protein, exon 2	5.9	25	27.9	100	3127	300	- (ι	
_s_at	U66711	ly6e	Ly-6-related protein (9804) gene	0	- [-	1		3	4	n	33.4
L05072 s at	105072	1		0.0	24./	4.7	6.1	13.6	2.4	2.4	1.7	4
-1			IRF1 Interferon regulatory factor 1	48.2	24.5	63	63.7	0 88	,			
			Prostaglandin endoperoxide synthase 2	-		3	<u></u>	30.05	23.4	3.4	34.5	50.5
L15326_s_at_	L15326	cox2 c	(prostagrafium G/H Synthase and cyclooxygenase)	39.5	23.7	92.4	~	-	u u	,		•
							-	1-1-	0.0	7.7	5	2.4

Figure 1E

139.7 15.8 20.5 50.5 0.4 31.6 0.2 1.4 2.4 0.4 165.6 0.4 3.2 0.2 2.9 2.9 0.4 3.2 0.2 2.9 90.1 0.3 0.3 0.0 0.0 53.5 12.3 23.5 65.7 1.1 41.8 4.2 3.7 9.4 3 5.7 0.4 6.7 0.3 0.8 5.7 0.4 6.7 0.3 0.8 4.3 3.4 3.5 20.3 3.2 4.3 9.3 16.6 11.2 0.6 4.4 6.7 0.3 0.6 6.1 4.4.2 1.7 1.6 1.6 1.6 4.4.3 1.7 1.6 1.7 1.6 4.6.2 1.7 1.6 2.7 1.6 4.6.2 1.7 4.3 1.7 4.3 1.7													
L. M86849 czeb Connewin 26 (GJB2) mRNA 2.9 22.6 13.7 15.8 20.5 50.5 60.6 t. M21005 cage OCLORANULIN A 6.4 22.4 13.6 0.1 1.5 6.0 1.4 5.6 0.8 t. M21005 cage OCLORANULIN A 6.4 22.4 13.6 0.1 1.4 5.6 0.8 t. M28833 dscr1 mRNA TUMPORASSOCIATED ANTIGEN LG 1.7 22.4 2.9 0.4 3.2 0.2 0.9 t. M30657 m3.1 TUMPORASSOCIATED ANTIGEN LG 2.87 2.18 4.9 3.2 0.2 0.9 0.0	U19523_at	U19523		dystonia) (alternative products)	0 0 1	0	000						
M21005 Cage	M86849_at_	M86849	cx26	Connexin 26 (GIR2) mRNA	10.0	27.8	139./	15.8	20.5	50.5	0.4	22.4	132.8
L. U28833 decrit movement of the properties o	M21005 at	M21005	Сара	CALGRANIIIN A	2.3	77.0	31.6	0.2	1.4		0.4	0.1	4.5
t. U98833 dscr1 mina decret method by the modern (DSCR) 1 1 22.4 2.9 0.4 3.2 0.2 2.9 0.0 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3				Down synchron orition	6.4	22.4	165.6	0	1.4	5.6	0.8	0	60
t, M90657 m3s1 TUMORASSOCIATED ANTIGEN L6 18.5 22.1 53.5 12.3 23.5 6.5 7 1.1 M16750 pim1 PIM1 Pim-1 oncogene 28.7 21.8 41.8 42.3 7 9.4 3.5 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2	U28833_at		dscr1	mRNA	,		(,		-			
Mid-550 pim.1 PiM.1 Pim.1 oncogene 28.7 21.8 41.8 42.3 23.5 65.7 1.1	M90657_at		m3s1	TUMOR-ASSOCIATED ANTIGEN I 6	/	22.4	2.9	4.0	3.2	0.2		1.3	1.2
Micheso pimi	U66838_at	_		Cyclin A1 mRNA	18.5	77.7	90.1	0.3	0.3	0	0	0	0
M16750 pim1 PIM1 Pim-1 oncogene 28.7 21.8 41.8 42.3 34 35 20.3 32	M16750_s_at				2.3	22.1	53.5		23.5		1.1	1.9	23.6
X66486 adora2a ADENOSINE AZA ŘECEPTOR Co. N. (21.0) 4.1.8 4.2. 3.7.9 9.4.3 3.2. L13391 g0s8 RRGULATOR OF G-PROTEIN SIGNALLING 2 6.1 21.1 7.3 0.4 6.7 0.3 0.8 L13391 g0s8 REGULATOR OF G-PROTEIN SIGNALLING 2 6.1 21.1 7.3 0.7 4.2 1.2.8 0.7 L13391 g0s8 REGULATOR OF G-PROTEIN SIGNALLING 2 6.1 21.1 7.3 0.7 4.2 1.2.8 0.7 Intraction of Control o		$\overline{}$	pim1	PIM1 Pim-1 oncogene	7 00	5	;						
D86967 KIAAO212 gene	X68486_at_	X68486	adora2a	ADENOSINE A2A RECEPTOR	70.7	21.8	41.8	4.2	3.7	9.4	3	5.9	8.2
Light Goss REGULATOR OF G PROTEIN SIGNALLING 2 6.1 21.1 7.3 0.7 4.2 12.8 0.7	D86967_at	D86967		KIAA0212 pene	80.0	21.8	49.3	3.4	3.5	20.3		1.6	8.6
M32315 thriz C75kD thriz C7					23.9		5.7	0.4	6.7	0.3		2.1	4.9
The National Continuer The Residence The	L13391_at_	L13391	g0s8	REGULATOR OF G. PROTEIN SIGNALLING 2	7		,	1		-			
Mag Mag				TNFR2 Tumor necrosis factor recentor 2	5	1.12	<u>ن</u>	5		12.8	0.7	0.5	2.1
X66401 tap2	M32315_at	M32315	tnfr2	(75kD)	70 6	7							
X66401 tap2 TAP1, TAP2, LMP2 address TAP2, LMP2 address TAP1, TAP2, LMP2, LMP3 address 30.6 20.6 32.4 12.9 9.6 6.3 6.1 U64197 rmip3a/larc CC chemokine LARC precursor 10.8 20.2 164.2 17 12.2 16.1 0.6 D14874 adm ADM Adrenomedullin 18 20.1 46.2 3.4 4.5 10.4 2.5 AM56284 ge GYPC Glycophorin C (Gerbich blood group) 9.4 19.9 7.1 7 6.5 1.7 1.6 L19871 atf3 ATF3 Activating transcription factor 3 10.6 19.7 9.6 28.1 39 12.4 5.4 X78710 mtf1 factor MADOR HISTOCOMPATIBILITY COMPLEX 8.7 19.6 11 14.8 9.5 1.7 1.6 M69043 ikba ENHANCER-BINDING PROTEIN MAD3 23.9 19.6 11.7 0.3 0.9 0 0 L13210 mac2bp Mac.2 binding protein mRNA	X66401_cds1			LMP2 gene extracted from Hisabiens manage	1,00	7.07	78.5	0.3		0.6		-	2.5
M62831 etr101 Transcription factor ETR101 mRNA 4.6 20.4 4.3 4.5 11.2 0.6 10.4	_at_	X66401	tap2	TAP1, TAP2, LMP2, LMP7 and DOB	308	30.0		- (- ((-	
U64197 mip3a/larc CC chemokine LARC precursor 10.8 20.2 164.2 1.7 12.2 16.1 1.1 M36284 ge GYPC Glycophorin C (Gerbich blood group) 9.4 19.9 7.1 7 6.5 1.7 1.1 L19871 atf3 ATF3 Activating transcription factor 3 10.6 19.7 9.6 28.1 39 12.4 5. X78710 mtf1 factor MAJOR HISTOCOMPATIBILITY COMPLEX 19.5 19.6 1.1 14.8 9.5 4.7 4. M69043 ikba Nicotinamide N·methyltransferase (NNMT) 3.7 19.6 1.7 0.3 0.9 0.0 L13210 mac2bp Mac.2 binding protein mRNA ROBABLE G PROTEIN COUPLED RECEPTOR 12.7 19.5 21 5.6 3.5 11.5 27. L13210 cxcr4 LCR1 HOMOLOG LCR1 HOMOLOG 29.4 18.8 10.8 0.2 0.9 7.3 5.6 D17357 actbA 5 upstream region 29.4 18.8 10.8 0.2 0.9 7.3 5.6 D17357 actbA 5 upstream region 29.4 18.8 10.8 0.2 0.9 7.3 5.6 D17357 actbA 5 upstream region 29.4 18.8 10.8 0.2 0.9 7.3 5.6 D17357 actbA 5 upstream region 29.4 18.8 10.8 0.2 0.9 7.3 5.6 D17357 actbA 5 upstream region 29.4 18.8 10.8 0.2 0.9 7.3 5.6 D17357 actbA 5 upstream region 29.4 20.4 20.4 20.4 20.5 2	M62831_at_	M62831	etr101	Transcription factor FTR101 mBNA	0.00	20.0	32.4	12.9	9.6	6.3	6.1	23.6	31.9
D14874 adm ADM Adrenomedulin 10.8 20.2 164.2 1.7 12.2 16.1 M36284 ge	U64197_at_	U64197	mip3a/larc	CC chemokine I ABC predictor	4.0	20.4	4.3	9.3	16.6	11.2	9.0	0.5	1.2
M36284 ge GYPC Glycophorin C (Gerbich blood group) 9.4 19.9 7.1 7 6.5 1.7 L19871 atf3 ATF3 Activating transcription factor 3.7 10.6 19.7 9.6 28.1 39 12.4 L19871 atf3 ATF3 Activating transcription factor 8.7 10.6 19.7 9.6 28.1 39 12.4 X78710 mtf1 factor MAJOR HISTOCOMPATIBILITY COMPLEX 8.7 19.7 8.9 2.9 5 1.1 M69043 ikba	D14874 at	D14874	adm	ADM Adresomed tilling	10.8	20.2	164.2	1.7	12.2	16.1	0	3.9	6.4
M36284 ge GYPC Glycophorin C (Gerbich blood group) 9.4 19.9 7.1 7 6.5 1.7 L19871 atf3 ATF3 Activating transcription factor 10.6 19.7 9.6 28.1 39 12.4 X78710 mtf1 factor MTF-1 mRNA for metal-regulatory transcription 8.7 19.7 8.9 2.9 5 1.1 M69043 ikba ENHANCER-BINDING PROTEIN MAD3 23.9 19.6 11 14.8 9.5 4.7 U08021 nnmt MAJOR HISTOCOMPATIBILITY COMPLEX 3.7 19.6 11 14.8 9.5 4.7 L13210 mac2bp Mac-2 binding protein mRNA 6 19.5 21 5.6 3.5 11.5 2 AL L06797 cxcr4 LCR1 HOMOLOG LCR1 HOMOLOG 12.7 19.2 30.6 8.8 7.9 19 1.4 D17357 actbA 5 upstream region 29.4 18.8 10.8 0.9 0.9 0.9 0.9 0.9 </td <td>M36284_s_at</td> <td></td> <td></td> <td></td> <td>18</td> <td>20.1</td> <td>46.2</td> <td>3.4</td> <td>4.5</td> <td>10.4</td> <td></td> <td>5.2</td> <td>16.1</td>	M36284_s_at				18	20.1	46.2	3.4	4.5	10.4		5.2	16.1
L19871 atf3 ATF3 Activating transcription factor S.78710 mtf1 factor MAJOR HISTOCOMPATIBILITY COMPLEX S.78710 Major Major	1	_	ge	GYPC Glycophorin C (Gerbich blood group)	Č	(1			_	-		
MTF-1 mRNA for metal-regulatory transcription MTF-1 mRNA for metal-regulatory transcription MAJOR HISTOCOMPATIBILITY COMPLEX MAJOR HISTOCOMPATIBILITY MAJOR	L19871_at_	L19871	atf3	ATF3 Activating transcription factor 3	10.4	7.0	1.0	h	6.5	1.7	1.6	6.0	2.3
M69043 Ikba	X78710 at	 Y78710	194	MTF-1 mRNA for metal-regulatory transcription	201	13.7	0.0	7.87	<u>65</u>	12.4		1.5	3.9
M69043 ikba ENHANCER-BINDING PROTEIN MAD3 23.9 19.6 11 14.8 9.5 4.7 U08021 nnmt mRNA 3.7 19.6 1.7 0.3 0.9 0 L13210 mac2bp Mac.2 binding protein mRNA 6 19.5 21 5.6 3.5 11.5 2 At LO6797 cxcr4 LCR1 HOMOLOG LCR1 HOMOLOG 12.7 19.2 30.6 8.8 7.9 19 1 D17357 actbA 5 upstream region 29.4 18.8 10.8 0.2 0.9 7 3		27.07.70	711111	ractor	8.7	19.7			ŭ	-	C		(
Micotinamide N-methyltransferase (NNMT) 3.7 19.6 11 14.8 9.5 4.7 1.3210 mac2bp Mac.2 binding protein mRNA 6 19.5 21 5.6 3.5 11.5 2.1 2.05 2.1 2.05 2.1 2.05 2.1 2.05 2.1 2.05 2.1 2.05 2.1 2.05 2.1 2.05 2	M69043 at	M69043		MAJOR HISTOCOMPATIBILITY COMPLEX	-	-			,	7:7	1	0.1	6.3
U08021 nnmt mRNA 3.7 19.6 1.7 0.3 0.9 0 0.5		2	BOWL	EINTAINCER-BINDING PROTEIN MAD3	23.9	19.6	11	14.8			4.3	7	0
L13210 mac2bp Mac-2 binding protein mRNA 3.7 19.6 1.7 0.3 0.9 0	U08021 at	U08021	nnmt	INICOLINAMIDE N-methyltransferase (NNMT)		-	-	-			-		0
Maccop	113210 at	113210	macohn	CANADA COM	3.7	19.6	1.7	0.3	60	Ĉ	α		
It L06797 cxcr4 LCR1 HOMOLOG Activin beta-A gene, regulatory sequence of actbA 5 upstream region 29.4 18.8 10.8 0.2 0.9 7.3 5	1,5-2,1-2,1-3	2777	יוומרכווו	iviac. 2 binding protein mRNA	9	19.5	21	9	27	110	27.5	5 0	† [c
Coccept	106797			PROBABLE G PROTEIN COUPLED RECEPTOR						21	6./3	0.11	34.5
D17357 actbA 5 upstream region 29.4 18.8 10.8 0.2 0.9 7.3 5	E00/3/ -3 al		cxcr4	LCR1 HOMOLOG	12.7	19.2	30.6			0	14 0	-	۲ ۵۵
29.4 18.8 10.8 0.2 0.9 7.3 5.	D17357 at	D17357	, t	Activin beta-A gene, regulatory sequence of		-				-	14:0	1 1	30.7
	- A- / CC / - A-	01/33/	action	o upstream region	29.4	18.8	10.8	0.2	6.0	7.3	ņ	C	-

Figure 1F

	AF005775	41:2	3 11333 6 533 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5			_		_	_	_		
10 7 7	0.000	2	(clarp) mRNA, alternatively spliced	7.8	20	27.0	7	L		-(1	-
579630 at	C70C20	rcn]	Reticulocalbin	5.7	18.4	613	5 -	7.7	13.4	700	9,7	18.4
DE0663 at	57 5039	exti	EX 1 Exostoses (multiple) 1	4.9	183	47	γ α	10.	13.7	7.6	1.7	41.5
20003	030663	tctel1	CW.1 mRNA	23.1	17.0	33 6	1 0		0 .	3.5	5.5	5.3
AF008445 at	008090	sema4d	Semaphorin (CD100) mRNA	1.3	17.6	3.7	4.3	13.5	2.0	1.0	13.5	30.8 20.8
	AF008445	plscr1	Phospholinid scramblase mBNA	6							+	3
D45248_at_	D45248	pa28b	Proteasome activator hPA28 subunit heta	72.9	17.3	127.1	2	7.6	38.3	1.2	6.3	88.5
J15460_at_	U15460	batf	BZip protein B.ATF mRNA	13.1	7/1	6.2	17.1	8.2	5.7	34.3	17.3	5.5
X65724_at_	X65724	dpu	Compilator	19.8	17.1	26	1.5	0.4	6.0	m	3.3	
8440 at		ctat/	STAT4 Signal transducer and activator of	33.4	17.1	39.4	0	1.2	0	3.5	0.5	2.5
U50527_s_at		tipic	danscription 4	6.4	16.4	40.6	0	1.4	6.5	3.1	2.4	7
	U50527		BRCA2 region, mRNA sequence CG018	9.0	16.4	76.11		0	g	,		
M87503_at_	M87503	isgf3	I RANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT		-			0.0	10.4	20.00	13.9	20.7
M55543 at	MARAA	6000	INTERFERON-INDUCED GUANYLATE.BINDING	9.6	16.3	20	5.9	27.5	8.5	8.1	1.8	5.5
L06633_at	106633	pscdbn	Transcription factor monit	30.7	16.1	47.1	11.4	3.5	6.1	7.5	191	23.5
8277_at_	X68277	dusp1	Alpha-tubulin mRNA	3.9	16	15.4	0.7	1.3	9	5.4	2.2	13.6
D21261_at_	D21261	tagIn2	SM22-ALPHA HOMOI OG	10.5	15.9	12.7		7.3	9.8	2		1.6
M31724_at_	M31724	ptp1b	PTPN1 Tyrosine phosphatase 1	4.1	15.8		6.0	7.4	2.4	3.3	0.5	2.3
X85116_rna1				14./	15.8	16.2	6.7	8.1	4.1	4.6	3.5	7.3
s_at_	١	epb72	Epb72 gene exon 1		ı,	1	,	_			_	
248481_at	248481	mmp14	MT-MMP protein	100.	13.6	67.7	5.1	9.1	13.8	0.8	6.5	12.7
U19261_at_	U19261	traf1	Epstein Barr virus induced protein mRNA	25.7	0.01	10.7	. I	8.8	2.7		0	2.4
HG544.	HG544.			7.07	13.4	72.7	χ N	12.7	9	5.8	9.5	8.1
H1544_at	HT544	ecgi	Endothelial Cell Growth Factor 1	0.00	15.2	α			,	1		
0040_al_	D10040	taci2	FACL1 Long chain fatty acid acyl coA ligase	24.7	15.0		1 0 0		7.7		16.5	7
X03656_rna1			G-CSF protein gene extracted from Human	,;;	7.61	7.07	13.5	ر ن	12.4	2.2	4.4	24.1
- 1	10	gcsf	gene for granulocyte colony-stimulating factor (G-CSF)	Š	(
X59417_at_	X59417	psma6	PROTEASOME IOTA CHAIN	19.4		37.6		1.2	0.5	1	0	1.5
				8./	15.2	10.8	6.5	7.2	8.1	2	8 9	7

			HYPOTHETICAL MYELOID CELL LINE PROTFIN		-	-						ſ
D29642_at_	D29642		8	9	7.	10.2	,				(ı.
X52541_at_	X52541	egrl	EGR1 Early growth response protein 1	000	15.1	200	2.7		7 1	4.0	χ	ي ن ت
-			WNT5A Wingless-type MMTV integration site		1.51		1	0.1	\ 	5	5	0.8
L20861_at_	L20861	wnt5a	5A, human homolog	11	15	11	C	1	C	-		-
X74039 at	X74039	njaur	asmir					-	,	1	-	0.1
M13792 at	M13792	ada	ADA Adenosine deaminase	1.6	15	7.3	1.6	4.2	2.8	1.5	5.4	5.1
M83667_rna1				13.5	2.4	108.1	0.0	1:0	9.9	3.6	2.1	12.3
_s_at_	M83667	cebbd	NF-1L6-beta protein mRNA	00	1/1/2	10.0	C	7	,	i c		-
X05232_at_	X05232	mmp3	MMP3 Stromelysin	20.4	14.7	ο α	0 0	7,0	, c	200	-1 c	<u>.</u>
X12451_at_	X12451	ctsl	CTSL Cathepsin L	α	1 2	2 0	2 0	7 0	. i.	5	5	
١,	D87953	rta	RTP	170	† c	0 0	0.01	ر: د	5.1	=	2.8	10.9
	D42043	KIAA0084	KIAAOO84 gans partial ada	17.0	14.2	50.6	0	6.0	0.5	1.2	0.8	വ
	M80244	d16s469e	1	24.8	14.1	27.1	7.1	3.1	4.5	8.3	9.8	19
1	1100672	11000	II JOB STATE THE IN EIN EIN	25.2	14.1	24.5	14.5	10	2.7	1.5	1.6	7.8
M5/015 5 2+	2,000	11010	ILIUR Interieukin 10 receptor	9.5	14.1	9.1	10.6	15	9.5	4.2	5.9	5
10-5-010+014)	M54915	i.i.					-			-		
	2010	111111	CINIT FILL 1 OF CORENE	11	13.7	37.2	2.1	2.1	6.2	6.0	0.7	50
D13146 cdc1			2,3.cyclic nucleotide 3 phosphodiesterase									;
013140_cus1	013146	i c	gene extracted from Human 2',3' cyclic.									
	2	1	incredude o pinospinodiesterase gene	15.9	13.4	25.3	6.2	4.4	10.1	5.6	3.8	11.2
U83461_at_	U83461	copt2	Putative copper uptake protein (hCTR2) mBN4	9 6	0							
AB000115_at				0.5	13.4	13.1	5.3	101	12	2	4.7	22.6
1	AB000115	unknown	mRNA	σ	13.1	0	α	0 90	000	,	,	ŗ
17.00	, , ,	<u> </u>	AMPD3 Adenosine monophosphate deaminase				j.	20.3	7.07	3.4	1.0	9/.6
D12//3_S_dL_D12//3	012//5	ampd3	(isotorm E)	14.7	13.1	18.9	0.1	2.7	6	ď	1.0	
D04110_d1	004110	Digs	lob family	1.7	13.1	122	9	196		0 0	1 -	1 0
00339/_s_at	1000							?	;	0,4		0.0
i	003397	4100	Receptor protein 4-1BB mRNA	4.6	13.1	90.4	3	20.1	26.2	0	0	ς,
	00.00		INP10 Interferon (gamma) induced cell line;		-			+		,		2
M68840 at	M69940	Up10	protein 10 from	12.5	13.1	442.2	137.9	290.4	501.4	5.4	205.9	4514
al al	MI00040	11404	IMACA Monoamine oxidase A	11.2	13	11.7	8.0	3.4	0	0.7	1	0
M35999 at	M35999	itgb3	11GB3 Integrin, beta 3 (platelet glycoprotein	C		3		,	 	-	1	
				Ø.3	12.8	21.8	0.0	-	0	1.7	4.0	C

Figure 1H

M37435_at	M37435	mcsf	CSF1 Colony stimulating factor 1 (M-CSF)	7	0 0 1	ļ	100		-			
U83171_at_	U83171	· udc	Macrophage derived chemokine precursor (MDC) mRNA	14.3		0 -	0./5	177.1	9 0	4 r	9.6	6.3
X06256_at_	X06256	itga5	ITGAS Integrin, alpha 5 (fibronectin receptor, alpha polypentide)		0.00	1 0	0.1	1		o.	n	0.5
J04080 at	104080) 1.0 0.10	C1S Complement component 1, s	7.0	17.8	χ, γ	11.6	13.2	2:9	6.0	2.9	0.8
M55067 at	M5E067	2	NCF1 47 kD autosomal chronic granulomatous	4.2	12.6	61.6	5.6	8.9	31.4	3.7	6.4	18.9
Z11697_at_	Z11697	cd83	CD83 ANTIGEN PRECURSOR	2.5	12.6	24.2	19.1	28.5	22.1	4.4	9.8	17.2
L37936 at	L37936		MITOCHONDRIAL ELONGATION FACTOR TS	ò	17.0	χ.	19.6	3.5	9	4.1	10.4	7.2
U52682_at_	U52682	irf4	IRF4 Interferon regulatory factor 4	9 6	12.5	19.6	9.0		0.4	9.0	2.6	5.1
U91616_at	U91616	ikbe	l kappa B epsilon (IkBe) mRNA	16.3	12.4	3,3	12.5	д. Р. П	2.2	1.3	3.2	7
Seesse at	266896	sccal	SCCA1 Squamous cell carcinoma antigen 1	28	12.3	47.6			2 6	10	000	1.0
X66363_at_	X66363	pctk1	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1	71.	-	32.3					7	
U20647_at	U20647	znf151	ZNF151 Zinc finger protein 151 (pHZ-67)	2.9	1 2	26.3	5 0	\ \ \ \ \	1.0) c		5.2
V00535_rna2 _s_at_		ifnb1	Interferon beta 1 gene extracted from Gene for human fibroblast interferon beta 1	a c		101		1 (4	<u>x</u>	80
D86968_at_	D86968	map3k4	KIAA0213 gene, partial cds	α α	11.0	10/.4	93.4		165.4	1.2	0	ा
M97936_at_	M97936	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.41 PHA/BETA			7.,	7.8	2	-	3.6	8	7.4
U15174_at_	U15174	nip3	Nip3 (NIP3) mRNA	1 C	11.4	16.9	13.4	7.7	11.4	48.3	40	28.5
X90858_at_	X90858	dn	Uridine phosphorylase	12 2	11.4	2/.3	0.0	2.1	0.8		1.7	11.1
U44975 at	U44975	bcd1	DNA-binding protein CPBP (CPBP) mRNA,			01	4:4	×.	5	4.5	6:1	80
M27436_s_at			F3 Coagulation factor III (thromboplastin	2.4	11.3	6.8	3.7	7.1	7.8	1.5	4.2	5.3
109060	M27436	f3	tissue factor)	1.5	11.2	32.6			٦.	'n	-	ū
LOSOOD_al	Loones	nspr4	DNAJ PROTEIN HOMOLOG 2	12.8	11.1	12.7	10.9	20.7	9.7	1.7	3.9	2 8
M37766_at_	M37766	bcm1	CD48 CD48 antigen (B.cell membrane protein)	13.2	10.9	20.8	8.2	13.4	13.1		6.4	29.8
1103105 21	1103105	2 14	DA 2 section sense	7.1	10.7	24.3	23.4	33.6	11.7	1.5	18	6.7
000100-01	0001000	7-+0	B4-2 protein mkina	29.4	10.7	8.2	11.4	5.7	T.	6.4	26	7

+6 2 /4/4/	_	_										
0.00	U76764	76bo	CD97 CD97 antigen (leucocyte antigen)	14.8	10 7	3.4	14.5	2.8	23	17	6	7 7
M64929_at_	M64929	ppp2r2a	PPP2R2A Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Cr.	, c	1	C	L				
U67171_at_	U67171		Selenoprotein W (selW) mRNA	2.5	10.6	2.0	7.0	15.7	χ 4 π	7	<u> </u>	7.7
D10923_at_	D10923	hm74	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74	u						 		0
D50840_at	1-1	gcs	Ceramide glucosyltransferase	0 4	10.5	2.6	6.6	9.8	1.7	4.0	2.5	1.2
M16364_s_at	M16364	ckp	CXB Creatine kings B.	1			2	1				70
			ANPEP Alany (membrane) aminopoputidano	20.5	10.4	11.1	109.5	18.8	7.4	5.5	2	4
			(aminopeptidase N, aminopeptidase M,									
M22324_at	M22324	anpep	microsomal aminopeptidase, CD13)	5.4	10.4	7.5	1.9	1.9	0	2.2	3.1	7
	182979	בומם	Cytokine receptor (EBI3) mRNA	17.4	10.2	54.9	0	9.0	m	0	2.1	125
X69910 at	X69910		iffilmunoglobulin-like transcript-3 mRNA	11.2	10.1	14.5	6.7	15.1	9	1.2	43	17.4
X52425 at	X52425	ואני	Fos mkiva for transmembrane protein	5.8	10.1	26.4	4.1	2.3	9.7	3.9	6.4	29.3
75-03-100	V35453	Ī	IL4K Interleukin 4 receptor	9.8	10	10	2.9	3.1	4.4		2	0 7
X77366_at_	X77366	nfe211	ICF11 Transcription factor 11 (basic leucine zipper type)	2.3	10	16.4	κ. τ.	4	2 4			1
D79206_s_at_	D79206	sdc4	SDC4 Synderan 4 (amphialycan pundocan)				-				ĵ.	
D38583_at_	D38583	s100al1	Calgizzarin	5.0	2) 0	71.7	15.2	11.2	10.2	2.7	2.7	9
HG2981.				٥	ρ	7	5.8	17	3.1	1.2	0.4	2.1
HT3125_s_at			-									
	HT3125	cd44	Epican, Alt. Splice 1	13.1	0	α	- (,	(-
L22342_at_	L22342	unknown	Nuclear phosphoprotein mRNA	8 %	7.0	1 2	7 6	1 0	2 [7.7	2.3	
J04102 at	104102	etc2	ETS2 V-ets avian erythroblastosis virus E26			1	1	100	+	C	12.2	21.7
L08177 at	108177	ehi2	CMKBB7 Chemoking (C C)	23.3		53.3	0.7	4.7	0	0	0.5	3.3
			Chicago Calendonie (C.C.) receptor /	3.6	9.6	6.2	2.2	2.1	4.1	5.1	2	2.1
1	U49835		CHIT1 Chitinase 1	17	σ	O C		C	-		,	
			COT Proto-oncogene c-cot (protein.				-		<u>v.</u>	20	0	8.0
D1449/ at	U1449/ M69066	cot	Serine/threonine kinase)	4.1	9.5	27	0	9.0	4.4	0.5	0	1.2
מססססם שר	00060101	trisn	MSN Moesin	7.3	9.5	3.7	2.4	5	=	000	-	0 21

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	3.4 2.2	0.4 9.4	100	2 1		3.5 2.8		010				0	7		8/7		1,	3.1 4.6			1							
	2.3	4.4 (, ,	0 0		3.7								7 0	<u>n</u>		, (~	2/4	2 7 %	2 Z Z Z	W W W W	7 Z M 2 Z	3278	302 3576	20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
_	1.2	2.1				0.1	u u	5 6	;			α	0	149	11.0			\perp	0		y u	100	1994	1997	112101	1000		1 0000 1200
	2.4	4.8	7			0	ų					α	Š	σ	L	7	, 0		6.7		102	10.2	10.2 2.6 2.9	10.2 2.6 2.9	10.2 2.9 2.9 3.6 5.1	10.2 2.6 2.9 3.6 5.1	10.2 2.96 3.6 5.1 0.55	2.6 2.9 3.6 5.1 0.5
	5.6	2.1	- 0	0.1		3.4	2	;				4			:	4	16.7	2	27		17	0.3	0.3	7.100.1	1.2	1.2	1.2 1.3 1.6 0.2 0.2	1.7 0.3 1.2 1.6 0.2 0
	5.1	10.1	2 7	24.2		6.3	36.3	27.9				9	-	12.9		120	15.7	1	6.2		4.0	13.7	3.4 13.7 4.9	3.4 13.7 4.9	13.7	13.7	13.7 13.7 27.5 6.7 6.7	3.4 13.7 4.9 27.5 6.7 63.7
-		9.4	9 6	9.3		9.3	0	9.2				6		9.1		σ	σ	1	6.0	σα			8.9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0	0 0 0 8 0 0	0 0 0 8 8 8 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
		χ.	2.4	7.1		9.9	9	3.3				3.6		2		13.4	4.4		3.1	3.5		26.3	26.3	26.3	2.9	26.3	26.3	26.3 2.9 2.7 2.7 9.9
COMINIA Cyclin dependent kinase inhibitor 1A	(pz1, cip1)	GI YOVI DEPTINE N	TETRADECANOYLTRANSFERASE	Glutamate transporter	U30999 Homo sapiens MV3 melanoma Homo	sapiera corre merra, mara sequence	Chemokine receptor X (CKRX) mRNA	Receptor 4-1BB ligand mRNA	MHC encoded proteasome subunit gene LAMP7	from Hisaniens gene for major	histocompatibility complex encoded	proteasome subunit LMP7	BONE MARROW STROMAL ANTIGEN 2 (BST.	2)	GGTB2 Glycoprotein-4-beta-	galactosyltransferase 2	X BOX BINDING PROTEIN 1	PML Probable transcription factor PML	{alternative products}	Tat interactive protein mRNA	TFRC Transferrin recentor (ng0 CD71)	(1) (20) (2)	Kynurenine 3-monooxygenase	Kynurenine 3-monooxygenase EXCITATORY AMINO ACID TRANSPORTER 1	Kynurenine 3-monooxygenase EXCITATORY AMINO ACID TRANSPORTER 1 CYBA Cytochrome b. 245, alpha polypeptide	Kynurenine 3-monooxygenase EXCITATORY AMINO ACID TRANSPORTER 1 CYBA Cytochrome b. 245, alpha polypeptide PGM1 Phosphoglucomulase 1	Kynurenine 3-monooxygenase EXCITATORY AMINO ACID TRANSPORTER 1 O'YBA Cytochrome b. 245, alpha polypeptide PGM1 Phosphoglucomutase 1	Kynurenine 3-monooxygenase EXCITATORY AMINO ACID TRANSPORTER 1 CYBA Cytochrome b. 245, alpha polypeptide PGM1 Phosphoglucomutase 1 MATRILYSIN PRECURSOR
	caudo			glt1	rd166	2012	ccr6	41bbL				lmp7	9	bst2		b4galt1	xbp1		myl		cd71			eaat1	eaat1 cyba	eaat1 cyba pgm1	eaat1 cyba pgm1	eaat1 cyba pgm1 mmp7
0.5001	D64142		M86707	U01824	6660871		AF014958	U03398				Z14982		D28137		D29805	M31627		M79462	0/466/	X01060	113153		D26443	D26443 M21186	D26443 M21186 M83088	D26443 M21186 M83088	D26443 M21186 M83088 L22524
1100570 24	D64142 at			U01824_at_	U30999 at	1		U03398_at_			Z14982_rna1	at		D2813/_at		7	M31627_at		1	1	1	113153_at_						

M87434_at_	M87434	oas2	69/71 KD	11.8	8.6	21.2	15.4	33.1	16.5	2.5	5.3	17.5
S54005_s_at_	S54005	thymosinb10	THYMOSIN BETA-10	4.2	8.6	1.7	m	4	27	4 4	200	0
X01677_f_at_ X01677	X01677	g3pdh	GAPD Glyceraldehyde-3-phosphate dehydrogenase	r.	α	000	-			i d	7 ,	
			MMP10 Matrix metalloproteinase 10	3.5	o o	2.0	7		۷.۵	6.0	1	7.1
X07820_at_	X07820	mmp10	(stromelysin 2)	13.3	8.6	98.8	0.2	0	1.5	1.3	2.2	4
U43185_s_at			STAT5A Signal transducer and activator of				-					
	043185	statba	transcription 5A	7.6	8.5	14.5	1.2	0.8	1.1	15.9	10.5	7
×17003 24	×17003	1	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,									T
A1/093_at_	A1/093	nia-cda12	F ALPHA CHAIN PRECURSOR	12.7	8.4	5.2	5.3	1.8	4.3	21.8	12.4	2
U03100_at_	U03100	catenin-a1	CTNNA1 Catenin (cadherin-associated protein), alpha 1 (102kD)	o c	0	,		((,		
Г	U72649	btg2	BTG2 (RTG2) mRNA	2.7	0 0			ν, α	5	7.7	0.2	2.5
1119557 c at		-9.5	Caromono coll constitution	3.1	χ.	4./	1.5	0.9	9.0	3.2	9.0	1.4
5 1	U19557	scca2	Squaritous cell carcinoma antigen Z (SCCAZ)	17.5	α	24.2	-	0	ر. در			
			Clone rasi-1 matrix metalloproteinase RASI-1				5	5			7	
X92521_at_	X92521	mmp19	mRNA	5.8	8.2	21	6.0	10.1	2.7	23	0.7	r.
Y00451_s_at_	Y00451	alas1	ALAS1 Aminolevulinate. delta: svnthase 1	17.8	α	1 4 6	S	C		-		1
			INTERFERON CAMMA ID DECLE ATEN 1 2111	2)	0.2	14.0	70	23	23.9	1.4	12.2	/:/
3_at_	L07633	pa28a	PROTEIN PRECURSOR	5.1	8.1	13.1	ıc	4	9	0	~	00
at_	L40377	cap2	Cytoplasmic antiproteinase 2 (CAP2) mRNA	7.4	ω	-	27	r úr	5	5.0		107
d	S81914	iex-1	IEX.1	7.9	8	10	, -	0	5 0	2 7 7	0.0	1 2
J	M30894	tcrg	TCRG T cell receptor gamma chain	8.9	α	40.3	-	2	0 6	Ω i		1
	M93056	ei	LEUKOCYTE ELASTASE INHIBITOR	23.4	α	30.8	37	ά	0	9 4	2 0	1 0
L27476_at_	L27476	zo-2	X104 mRNA	33	7 9	٣	, r	200	200	2 0	0 0	2 0
M97935_s_at			SIGNAL TRANSDUCER AND ACTIVATOR OF		?	,	;	1	2		0.0	7:7
	M97935	stat1	TRANSCRIPTION 1-ALPHA/BETA	4.1	7.9	10.5	0	r.	100	σ	17.0	7 75
U43522_at_	U43522	fak2	Protein tyrosine kinase PYK2 mRNA	5.2	7.9	16.3	-		7 2	0,0	1001	20.7
X91504 at	X91504		TFCOUP2 Transcription factor COUP 2 (a.k.a.									43.3
Ţ	MOADED	9000	MART 1	2.4	7.9	9.9	0	1.1	0	1.2	0	3.7
Т	W124009	csua	DINA-BINDING PROTEIN A	14	7.8	12.1	0	0.8	0	0.3	0	0.1
U20158_at_	U20158	lcp2	76 kDa tyrosine phosphoprotein SLP-76 mRNA	3.7	2	00	α	126	3.4	,,	,	2
					12.	;	5	j	ŗ	5		ົງ ວ

egr4 EGR4 Early growth response 4 1.4 7.8	1.4 7.	7.			2.4	1.5	2	0.1	0	0	6.3
cd44 Epican, Alt. Splice 11 13.5	13	13.5	1	7.7	25.6	۰ ۲	4 4	-	C	0	
EIF5 Eukaryotic translation initiation factor 5 eif5 (eIF5)	5	5.6	4	7.7	16.1	12	5 5	-	2 -	0.0	ν. Σ
Major Histocompatibility Complex, Class I, E (Gb:M21533)		5.7		7 6	0		r c	0	C	0	
PML Probable transcription factor PML (alternative products)		α		7 6	1 6			1	2 1		7.0
		8	1	7.6	7.2	6.5	1 6		1.7	0.0	11.1
PRE-MRNA SPLICING FACTOR SRP75 2.5		2.5	1	7.5	4	1.4	6.1	m	1 4	, r	10
	ceptor interactor (TRIP14) gene, 3'	4.6	1	7.5	43	105.3	185.2	124 5	-	2	1361
il2r IL2RA Interleukin 2 receptor, alpha 9.3		9.3		7.4	1	1	1			1 6	13.0
Phosphoribosypyrophosphate synthetase. prpsap1 associated protein 39 2 1	osphate synthetase.	2 1		7.3	6.4			3	0 0	† 0	7. 0
Nuclear orphan receptor LXR-alpha mRNA		1.5		7.3	9.6	34.8	11.7	0 0	ο α	5 -	2 2 2
actor, alpha	actor, alpha	2	1 1	7.3	11	0	0	0	3.3	4.4	0.0
CYCTATIN A	4	4.8	ı	7.2	5.4	2.3	3.9	5.2		2	1.8
4 Golgin 245 mDNA		12.8	- [7.1	6.5		1	1	2.2	0.5	0.5
BNA binding protein Ft. 3 BNA		3.3	-	7.1	17.2	5.9	2.5	6.7	0.3	1.7	6.3
rpa2 RPA2 Replication protein 42 (32km)		2.5	- 1	7.1	6.4	3.1	2.1	5.1	2.1	4.1	9.5
Myleoid differentiation primary response		0.2		+	27.3	0.2	1.6	m		2.2	5.6
		2.2		7	α	<u>ب</u>	17.0	,	-	,	ŗ
		0.1		1	13.0	2 α	17.7	16.7	0 -	4:4	7.
DUAL SPECIFICITY MITOGEN.ACTIVATED			1	+	1:01))	 	10./	7.7	3.1	18
JAKA PROTEIN KINASE KINASE 3 13.5	13.5	2		6.9	18	12.2	2.1	2.9	5.6	1	7.3
nuscle) 8.6	nuscle) 8.6	9	1	6.9	4.1	C	0		2 -	2 0	5 0
	2',3'-cyclic nucleotide 3'	-	1				5		-	5.5	7.7
		21.4		6.9	9.7	5.5	8.5	18	0	-	ď
Iglrx Glutaredoxin (thioltransferase) 7	XX Glutaredoxin (thioltransferase) 7	1	l	6.9	3.5	6.7		200) (7	0 0

Figure 1M

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						m	v CI	RΟ	15.	111	r macoi	ıCl	u, er	141.					
60	89	9	†	2.3	2.1	ı,	000	193		7 7	u u			0.1	2 1	0 4		2.7	5.2
000	m	,	J. 1	3.6	1.6	,	2 -	26	6.0	7 0	o m	α	0 -	1 (χ	7		0.22	E.0
-	6.5		1	1.2	9.0	9	1 4	2	1 2	0	2	7	5		7.7	0.0		9	0.2
1.4	2.6		,	1.9	0.5	C	1	4.2		21.0	8 %			5	5 0	0		24.	2 0
3.6		α		2.1	6.4	0	4 2		6.0	- -	4 2	α ς			0 0	ο α			80 0
6.0	0.3	0 m		8.6	2.6	4 0	α	0.3	4.0					5	0 0				7.0
15.8	5.6	9		7.8	2.1	2.1	7	3.5	23.6	147.9	80,	3.7	α /	0 6	7.7	m		0.25	30.6
6.8	6.7	6.7	-	6.7	9.9	9.9	99	6.5	6.5	47.9		6.3) m	0 0	200	0 0		70	0 0
	2.7	7.7		10.7	2.6	3.8	4.8	5.5	3.7	28.6	6.1	3.8	2 6		0 0	18.9	17.	1771	7.7
CORTICOSTEROID 11-BETA DEHYDROGENASE, ISOZYME 1	KIAA0082 gene, partial cds	ADAR Double-stranded RNA adenosine deaminase		MOP1 mRNA	PRKCD Protein kinase C, delta	PTPRA Protein tyrosine phosphatase, receptor type, alpha polypeptide	Spermine synthase	Transmembrane protein	Metallothionein-I-A gene, complete coding sequence	Cyclooxygenase-2 (hCox 2) gene	Major Histocompatibility Complex, Class I, E (Gb:M20022)	Nrf2	DsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA	mRNA fragment encoding beta-tubulin. (from clone Dibeta.)	IL13 receptor alpha-1 chain	MDU1 Antigen identified by monoclonal antibodies 4F2, TRA1.10, TROP4, and T43	Interleukin 10 (11 10) gene	815A9.1 gene (myosin heavy chain) extracted from Homo sapiens chromosome 16 BAC clone	UBIQUITIN.CONJUGATING ENZYME E2.CDC34
hsd11		adar		hif1a	pkcd	lrp	sms	adam8	mtla	cox2	hla	nrf2	adarb1	tubulinB like	il13ra1	86pa	1110	7. C. T.	cdc34
M76665	D43949	U10439		U22431	D10495	M34668	249099	D26579	K01383	D28235		S74017	U76421	66500		M21904	U16720	AF001548	L22005
1	D43949_at_	U10439_at_	U22431_s_at	ヿ゙	D10495_at_	الد		D26579_at_	K01383_at_	D28235_s_at_	f at	S74017_at_	U76421_at_	V00599 s at V00599	Y10659_at_		U16720_rna1 s at	548_rn	at

Inventors:

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735278 at	735278	am12	PERPOSE 1 serute miveloid leubagmis month	C V.		. 00	1	000				
		1	ייים במתר מתחבר וואכוסות ובתישבווווש ווועוא	14.0	0	77.77	22.0	3.3	23.4	9.	4.2	19.6
	M87507	casp1	ILIBC Interleukin 1, beta, convertase	1.7	9	50	_	4 4	27	c	۲,	19.7
U32849_at_	U32849	nmi	Hou mRNA	5.2	9		10.4		20.0	7 0	2 0	7.000
D78156_at_	D78156	gap1m	RasGTPase activating protein, partial cds	7.2	5 6	3.6		2	1 0) -	210	10.53
D87434_at_	D87434		KIAA0247 gene	12.4	5.9	~	17	8		7	0	0.0
		-	S100A10 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide	ļ								
M38591_at_	M38591	call!	(p11))	4.1	5.9	5.6	m	7 3	4 6	۲.	7 0	1
M73780_at_	M73780	itgb8	ITGB8 Integrin, beta 8	4.3		20.8			7.4	200	0	0 0
M91670_at_	M91670	psma2	Ubiquitin carrier protein (E2.EPF) mRNA	5.4		m		25	5.2	20		
U11732_at	U11732	etv6	ETV6 Ets variant gene 6 (TEL oncogene)	4.4	5.9	6.4	1.9			c	1 4	
U42408_at_	U42408	lad1	Ladinin (LAD) mRNA	6.3	5.9	67.8	0.3		Δ	0	0	-
			GRANULOCYTE:MACROPHAGE COLONY. STIMULATING FACTOR RECEPTOR A! PHA									
X17648_at_	X17648	gmcsfR	CHAIN PRECURSOR	9	5.9	12.9	0	1.9	0	0.5	6.0	8
HG3597.	HG3597.		Major Histocompatibility Complex, Class I									
HT3800_f_at_	HT3800	hla	(Gb:X12432)	7	5.8	3.3	6.5	2.3	3.6	4	4.3	1.6
x15949_at	X15949	irf2	IRF2 Interferon regulatory factor 2	6.1	5.8	6.1	5.3	102		-		σ
X60592_at	X60592	cd40	CD40 CD40 antigen	6.3	5.8	21			0 00	0	7	
HG987.	HG987.									1		1
HT987_at_	HT987	igfbp7	Mac25	2.3	5.7	2.8	4,8	4.9	2 7	1.0	C	2
J33821_at_	U33821	tax1bp1	Tax1-binding protein TXBP151 mRNA	2.4	5.7	10.3		2	12		0	156
X65644 at	X65644	hiven2	IMMUNODEFICIENCY VIRUS TYPE I ENHANCER	ć	1		,					
D38551_at	D38551	unknown		7.1		12.3	0 0	n <	4 0	7.7		5.4
HG2167.	HG2167.			?						7	0.0	2.8
HT2237_at_	HT2237	pkht31	Protein Kinase Ht31, Camp-Dependent	8.6	5.6	4	7	Λ.	~	0	C	0
			INDUCED MYELOID LEUKEMIA CELL									t.
08246_at	L08246	mcl1	DIFFERENTIATION PROTEIN MCL1	3.3	5.6	4.6	4.1	2.4	7.6	1.4	1.5	σ,
_40393_at_	L40393	numb	(clone S171) mRNA	1.5	5.6	9	9.0		0		000	2 5
M16038 at	M16038	u <u>v</u>	LYN V.yes.1 Yamaguchi sarcoma viral related	7	U	-	:	,	,	,		
Y58521 at	VE9621	250.00	ALIOL FAD DODE OF VOODBOTTING	6.7	0.0	7.7	0.11	٥: /		9.1	4./	7.1
A30321_a1_	A300041	Illupoz	NOCLEAR FORE GLYCOPROLEIN P62	8.3	9.6	15	10.8	7.2	15.3	1.7	0.3	6.8

Inventors:	Nir Hacohen, et al.
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	104.6	1	1286	α -	0	C		-	σ	0 0		3	4.	٠ -	7 4	-1 L		9.	=	-			σα		ς <u>Γ</u>	2	0.8		1:/	10.7	13.2	0.8
	9.1	-	77 5	0		C		2 4				1 .	2	0		200			0.8	0		o	7 5	α	0.0	1	0.5		7	1.7	6.3	9.0
	8.9		19	10	;	С	1		4 1	0			۲.۶	4		0.0	7 6	<u>1</u>	1.1	-		4	1	0	7	;	1.2		=	1.1	3.1	2.2
	37.9	5.6	58.6	200		С	,	0		-	1 0		0.1	4		2 0	? -		8.0	-	?	C	0 0		0 00		3.7	(5	27.3	6.1	1.4
-	17.5	2.4		40		~	+	2	7 1	5.2				œ	α	0.7	5 0	0 0	3.7	000		0	90	26	0		3.8	(2.3	4.7	2.8	0
	61.8	0	59.4	C	,	0		2.5	2.5	25.1	,) -	?	r.		0,0		1	1.4	- m	+	-	6.0	0.3	3 6		2		2.0		3.5	0.4
-	32.7	15	683		?	94.7	-	33			9	1 0	1.7	7.3		7.6	2 0	?	1.4	4 4	-	4		K. K.			2	٦	1	6.71	12.2	10.1
	5.2	5.2	5.2			5.1	L	5.1	5.1	2	ıc) u	,	77	2	0 4			4.8	4.8	-	4.8	4.8	4.8	4.7		4./	7	1 1	7	4.7	4.7
	15.9	3.6	3.2	4.8		1.3	-	8.4	2.8	7.1	3.6			8.2		89	αV		2.3	12.8		10.8	4.3	2.8	2.9		٩	u		χ.		6.9
_					-		L		 	-	_	H	7)	_	-	-	+	4		Ē			_	-		+		+	1		4
IGFBP4 Insulin-like growth factor binding	protein 4	Xq28 mRNA	Humig mRNA	Mitogen inducible gene mig.2	PAI2 Plasminogen activator inhibitor, type II	(arginine-serpin)	PTPN12 Protein tyrosine phosphatase, non-	receptor type 12	Platelet alpha SNAP mRNA	Unknown product	MUC1 Mucin 1, transmembrane	FTH1 Ferritin heavy chain	Sodium/potassium-transporting ATPace heta. 3	subunit mRNA	PGK1 Phosphoglycerate kinase 1	TRANSCRIPTION FACTOR RELB	LDHA Lactate dehydrogenase A	Profilin mBNA		DUAL SPECIFICITY MITOGEN.ACTIVATED PROTEIN KINASE KINASE 1	Platelet-derived growth factor (PDGFA) A chain	gene	MAP4 Microtubule associated protein 4	Sec7p-like protein mRNA, partial cds	Randomly sequenced mRNA	VIVO - 010110 1100 Q V 11		HOK Hemopoletic cell kinase	IAP homolog B (MILID) mbyla	Mobb information (Millip) illiniva	MET 51 SOIOTH SIDNA (MCN3) MRINA	IN 5.5 nucleotidase (CD73)
7	1gtbp4	cxorf6	mig			pai2		ptpgl	snapa	d1s1733e	muc1	fth1		atp1b3	pgk1	nfkb reIB	ldh1	nfn]	1	mapkk1		pdgfa	map4	sec7p-like	rac1	ار د واط		hck	cian1	7420	casp/	Cliff
2000	M62403	U46023	X72755	Z24725		M31551		M93425	U39412	D28124	J05582	L20941		U51478	V00572	M83221	X02152	103191		L11284		M19989	M64571	U59752	D25274	D49824		M16591	1137547	1167319	CTC (00	A33740
M62403_s_at		U46023_at_	X72755_at	Z24725_at_	M31551_s_at			M93425_at_	U39412_at_	D28124_at_	J05582_s_at_ J05582	L20941_at_		U51478_at_	V00572_at	M83221_at_	X02152_at_	J03191 at		L11284_at_	M19989_cds2		M64571_at_	U59/52_at_	D25274_at_	D49824 s at	M16591 s at)	U37547 at	Т	T	1001/40_dL

Figure 1Q

			PML Probable transcription factor PML		-	-	-		-		-	
X63131_s_at_ X63131	X63131	myl	{alternative products}	9	4 7		_	C			((
X75593_at_	X75593	rab13	Rab 13	000	1	Ŧ.	1 0	0.0	ο.α	2.3	10.3	9.9
HG2825.	HG2825.			3.2	7	4	2.2	1.2	0	1.1	5.9	1.9
HT2949_at_	HT2949		Ret Transforming Gene	2.6	4	r		0		C	-	:
							7	0.1		7.0	-	
U77396_at_	U77396	litaf	LPS-Induced TNF-Alpha Factor (LITAF) mRNA	6.1	4 6	σ	۳.		Ċ	Č		(
X89750_at_	X89750	hpe4	TGIF protein	57	7	2 4		7	2 0	7.1	4	٦
			GAPD Glyceraldehyde-3-phosphate);	7	0.0		S	ر ان	8:1	2.7	5.9
D00763_at_	D00763	psma4	dehydrogenase	9	4 5	'n	C C	,			;	1
M60721_at_	M60721	hlx1	Homeobox gene	100			0.01	ψ. υ. α	ام		11.2	3.7
J04173_at	J04173	pgam1	PGAM1 Phosphoglycerate mutace 1 (basis)	6.5	4.0	5.4	-1	9	0.7	2.2	2.4	2.4
ĺ	125081	arho	APMO Aphysia and applicate Illutase 1 (Utalli)	3.7	4.4	4.4	4.3	3.2	4.3	<u></u>	4.8	2.2
	MRR33R		SCBLIM DESTRICT	5.3	4.4	9.1	2.5	0.3	8.0	1.1	0.3	0
1			SENCIN PROTEIN MSESS	ω	4.4	5.6	1.4	4	5.9	4	2.2	7
M94250 at	M94250	E G	MDK Midkine (neurite growth-promoting factor					-			?	
U05681 s at				2.7	4.4	20.2	1.7	0.2	4.5	0	0.1	14.1
	U05681	bc13	Proto-oncogene BCL3 gene		-	1, 7,0	-		(
U28014_at_	U28014	casp4	ICH.2 PROTFASF PRECIIRSOR			7.77	- - - -	4.1	9.0	-	1.7	5.2
M37583 at	M37583	h2a7	H2A7 H2A7 histore	13.5	4.4		9.7	1.5	3.5	7.2	7.2	8.9
				5.1	4.3	2.9	5.2	6.1	1.7	13	70	Q
			CLU Clusterin (complement lysis inhibitor;					-	-			
M63379_at_	M63379	ī	restosterone-repressed prostate message 2;			-			***			
			H A.A MHC class protein 1 % % !!! % %	6.4	6.4	84.1	0.4	2	12.1	1.1	1.6	19.6
M94880_f_at_	M94880	hla-a	B40, .Cw3)	0	0	C	,					
7,000	000				t i		0	1.1	2.4	1.3	1.7	5.9
1	032944	dlc]	Cytoplasmic dynein light chain 1 (hdic1) mRNA	2.9	4	2 6	7	'n		_	(•
┪	09/000	hc3	PSMA3 Proteasome component C3	9.4	4.2	200	r 0	2	1 1	+	7.0	4
M22976_at_	M22976	cyb5	CYB5 Cytochrome b.5	000	10	0 0		4 0	7,7	4	4.6	12.4
	M28983	113	III 1A Interleukin 1 slubs	7.1	1.5			30.2		1.7	2.1	5.6
1			CATD1 Choose AT 12-1	5.1	4.2	17.4	0.9	0.4	5.3	6.0	0	3.6
			profein 1 (hinds to michael material)						-		-	
	M97287	satbl	associating DNA's)	Г	-	r	(•	,			
U09825_at_	U09825	znf173	ZNF173 Acid finger protein 7NF173	0.00	1 0	0.0	0.2	7.7	8.1		9.0	4.7
			The state of the s	2.3	4.2	4./	6	8 0.0	14.3	0.8	1.4	4.2
											1	

					II	We	nto	ors	:		INI	r Ha	ico	ne	n,	eī	ai.											
O		10	000	, c	ŝ	3.2		0,4	ט ע	0.0	6.0	-	1	0	0	ď		4.4	0	10.3		0	7.0	1	4.0	7.7	7.4	6 9
0	-	0.7	6	, C		5,	7 0	0.1	0 0	0.		-	1	r.	7.7	C	7.7	7	Ċ	4.7		ď	0 0	0	5 -	7	4.1	2.3
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4.2			-	1.5	,	5 0	0 0	0.7	2.2		1.6		3.5	r,	,	24.7	, , ,	<u>}</u>	-	,		٦.	11.5	1	2 0	2	5	14.7
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8.0	α	11.2	1 7	0	-	5 0	1	ک د	α	2	1.5	C		6	1	ιĊ	V (α			0	100	2		1	1	2.8
2.4	2	3.8	2 3	900	;	7.11	1 6	10	י ע		1.9	10.2		10.5		σ	2 4	5	13.4	5		m	67	0	1	, ,	+	14
4.2	4.2	4.2	4	4 1		1 C	7 0 %	000	5 0		3.9	σ «	3	8		œ	α ~	2	3.7	;		3.7	37	3.7	2 7	, (<u></u>	3.7
1.9	3.7	7.2	4.4	2.4	0	5.0	1 9	1 5	280		5	2		4.5		5.9		+	6			3.3	4 4	2	43	u c	7	2.4
Ubiquitin gene	TNNT2 gene exon 11 troponin	HISTONE H3.3	KIAA0162 gene	(clone cc44) senilin 1 (PS1; S182) mRNA	Heparan N-deacetylase/N-sulfotransferase-2	Tetratricopeptide repeat protein (thr2) mBNA	KIAA0005 gene	C4A Complement component 4A	RagA protein		Calcium ATPase isoform 3x/a mRNA	Pim-2 protooncogene homolog pim-2h mRNA	ATF4 CAMP dependent transcription factor ATF.	4 (CREB2)		MHC class I molecule (MICB) gene	PolyA site DNA		Ras-Related C3 Botulinum Toxin Substrate		Nuclear Mitotic Apparatus Protein 1, Alt. Splice	Form 2	EDN1 Endothelin 1 (alternative products)	INTESTINAL MEMBRANE A4 PROTEIN	UBE1 Ubiquitin activating enzyme F1	Biliverdin-IXalpha reductase mRNA	Protein tyrosine phosphatase PTPCAAX1	(hPTPCAAXI) mRNA
	tnnt2	h3f3b	supt6h	ad3	ncst2	tpr2		c4a			atp2b3	pim2		atf4		micb			ras-related			nmap1	edn1		alst	blvra		ptp4a1
U49869		248950	D79984	L76517	U36601	U46571	D13630	M59815	U41654		U57971	U77735		D90209		U65416	224724	HG1102.	HT1102		HG2238.	HT2321	105008	L09604	M58028	U34877		U48296
U49869_rna1 _at_	آيد	Z48950_at_	at_	L76517_at_	U36601 at		D13630_at_	ļ ,	U41654_at_	U57971_s_at		U77735_at_		D90209_at_	U65416_rna1	_s_at_			HT1102_at_	HG2238	HT2321_s_at HG2238				M58028_at_	U34877_at_		U48296_at

Figure 1S

				11110	entors:	IN	ır Ha	ico	men,	era	11.								
17.3	32.7	,	2.9	m		N .	1.7	2.5	4.8	9.1	2.7	m		0.0	7	1.5	7.1	1	1
3.1	20.7	o c	<u> </u>	4.0			j j	1.9	6.0	2.2	0.1	0		4.1	1.6		1.4	2	10
9	0.5	-	0.8	4.4	1	5 .	× ×	8:1		0.5	0.3	9.0	C		1	5.7	2.7	(r)	000
2.6	30.8	rt.		6.0			7.7		6.1	1.6	18.1	0		7.7	7	5	8.9	1.7	0
2.8	0	2.2		1.2	-		0	2.1	9.7	0.5	9.0	0.7			5	4	3.7	1.2	6.2
0	9.0	īC	5.2	0.3	7		7.0	O 0	4.5	2.4	1.7	0.4	C		200	3.2	13.3	3.1	0.5
16.6	233.2	3.8	2.5	2.1	<u>v</u>		j (0, c	4 (υ 1	13.5	36.8	3.2	000	7 -	0.1	4 0	2.0	3.7	2.3
3.7	3.7	3.6	3.6	3.6	4	000		3.0		ກ ດ	3.5	3.5	2 6		0, W	j ;	4.0	3.4	3.3
2	12.5	5.7	2.2	2.4	^	α		7.7	0.7	200	4.3	2.6	α		7 7	ا أ	0	9:1	1.9
Lysophospholipase homolog (HU·K5) mRNA	EDIT-IIgand chemokine	BETA-2-MICROGLOBULIN PRECURSOR	HNRPA2B1 Heterogeneous nuclear ribonucleoprotein A2/B1	DTR Diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)	Protein phosphatase.2A catalytic subunit alpha gene extracted from Human protein phosphatase 2A catalytic subunit alpha gene	Annexin V (ANX5) gene. 5'-untranslated region	Uridine diphosphoglucose pyrophosphorylase	HNRNP C2 protein mRNA	Translational initiation factor 2 beta subunit	CSPG2 Chondroitin sulfate proteoglycan 2	(versican)	Lipiu-activated protein kinase PRK1 mRNA	L43579 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 110298, mRNA sequence	ENO1 Enolase 1. (alpha)	NADH-CYTOCHROME B5 REDUCTASF	C5R1 Complement component 5 receptor 1 (C5a lipand)		CRFB4 Cytokine receptor family II, member 4	HSPA4 Heat shock 70kD protein 4
huk5 min3h/elc	DIA/OCCIO	b2m	hnrpa2b1	dtr	ppp2ca_	annexinV	ugp2	i			CSpg2	havi		eno1	dia1	c5ar		il10rb	hspa4
U67963	001/100	J00105	M29064	M60278	M60483	U01691	U27460	M16342	M29536	000	016306	20000	L43579		M28713	M62505			12/23
U67963_at	277,100	J00105_s_at_	M29064_at_	M60278_at_	M60483_rna1 _s_at_	U01691_s_at 	U27460_at_	M16342_at_	M29536_at_	11 0000	1	1		+	M28713_at_	M62505_at_			L12/23_at_

Figure 1T

						11	ive	H	OIS	٠.		14	11 11	ac	One	711,	et al.									
6	2 4	90	2	0 -	1	7.	;	C		2 2		57			2	i o		7	-	10	27	ά -		4	ري 0	2.4
0.3	-	3.1	-	0	0.0	2	1	0	0.00	0		3.6	,	7.7	0			0	-	0	-	,		2,	2.7	1.3
0 7	4	90	-	1.1	7.0	23		0	-	174		0.4	C	0.7	1.8	1.4		0	0.7	80	-	-	1	7.7	1.1	0.5
9	0.0	8		0	1	5.9		0 6	20.1	114		1.6	-		3.7	4.4		4.6		4.7	0 4	ē		7	0	0
	1.5	2.5			21	1		0.1	10.5			4.8	<u> </u>		4.1	3.5		9.0	26	60		4	5	12.7	2.2	14.8
0.7	2.2	F	С С			4.7		0	9.2		-	S)	,		1.6	2.5		0.3	40	0	6.0			7:	1.5	7
3.7	3.4	1.7	,	1 2		10.3		3.1	2.7	35.9		2.2	,	;	2.4	8.9		91.6	2 4	20	9	3.7	0	0.7	12.3	4
3.3	3.3	3,3		0 00		3.2		3.2	3.2	3.2		3.2	۲.	1	3.1	3.1		3.1	3.1	3.1	3.1	3.1	,	7.7	m	3
2.3	2	3.9	~	100		4		<u>N</u>	4.6	e		2.7	α	2	7	5.6		2.3	2.6	2.1	6.4	3.7	2	5	1.9	8.5
MIC2 Antigen identified by monoclonal antibodies 12E7, F21 and 013	Arginine-rich nuclear protein mRNA	Uridine nucleotide receptor (UNR) gene	Myelodysplasia/myeloid leukemia factor 2 (MLF2) mRNA	ALDOA Aldolase A	MACS Myristoylated alanine-rich Cikinase	substrate		Triosephosphate Isomerase	Hbc647 mRNA sequence	K12 protein precursor mRNA	Nuclear chloride ion channel protein (NCC27)	mRNA	Proteasome subunit p44.5	EIF4A2 Eukaryotic translation initiation factor	4A (eIF-4A) isoform 2	NP Nucleoside phosphorylase	SCYA1 gene (secreted protein I-309) extracted	from Human secreted protein (I-309) gene	PEPTIDYL.PROLYL CIS.TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR	B12 protein mRNA	PGD Phosphogluconate dehydrogenase	ATP6E ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD	Galectin	PROTEIN TRANSPORT PROTEIN SECRI BETA	SUBUNIT	FACTOR VIII INTRON 22 PROTEIN
66po			mlf2	aldoa		macs		tpi		k12		ncc27	psmd11		eif4a2	. du	Ç Ç	1309		tnfaip1	pgd	atp6e	lgals9			dxs522e
M16279	M74002	U40223	U57342	X12447		D10522	HG2279.	HT2375	U68494	U77643	000	093205	AB003102		D30655	K02574		M5/506	M80254	M80783	U30255	X76228	249107		125085	M34677
M16279_at_	M74002_at	U40223_at_	U57342_at_	X12447_at_		D10522_at_	HG2279.	HT2375_at	U68494_at_	U77643_at		093205_at_	AB003102_at		D30655_at_	K02574_at_	M57506_rna1	_at	M80254_at_	M80783_at_	U30255_at_	X76228_at_	Z49107_s_at			M34677_at_

Title. Lesponse of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

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	2.3	0.5	rt.	3	7	4.6		7.2		α	1 4	1 2	7 4	5	α ις	12.4	2 7	ì	7.0	i u		1.0	0	1	0.0	3.6	1.3
-		3.2	ď	7	0	3.9		4.2	60	7	60	9.0	-	1	0	-	2	>	0		-	1	-		C		0.2
 	-	1.6	0	1	1.1	1.8		1.2	29	60	0.7	4.1	,	1	200		20	<u> </u>	C	200	-	+		+	C	2.8	4.2
	5.5		C		m	0		7.4	4 4	0.7	2.5	2.1	-	+	7.7	c	0 %	;	C	5 7			C	1	4.6	5.2	2.4
		5.2	σ		5.2	60		5.9		2.5	m	3.7	-	1	33	6	6	2	α	α 4		1	23		0.1	5.6	7.3
-	4.7	2.3	7	;	5,5			12	4.2	80	2.4	3.5	г С		1.2	6.1	1 4	+	~	1 4		1	2.2		0	7.5	0
	5.0	2.9	- C	-	2	3.7	-	5.4	3.4	2.2	2.6	1.6	0	3	9.5	41.5	7.1	!	ر. بر	17.1	, ,	j	3.6	-	5.3	6.4	8.2
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	ກ .	-	-		6	1.7		æ		8	1.9	2	_		2				0				m		7	2	<u></u>
,	-	2.1	7.1		2.9	4.1		3.3	6.1	2.8	-	2	4			∞	4		ന്	2.1	σ		5.			5.	8.
TYROSINE-PROTEIN KINASE RÉCEPTOR ECK	APE1 ADD riboniation footen 1	ARE LADE-TIDOSYIATION TACTOR 1	Na, K-ATPase beta-1 subunit mRNA	Chromatin structural protein homolog	(SUPT5H) mRNA	Glutathione-S-transferase homolog mRNA	Sin3 associated polypeptide p18 (SAP18)	mRNA	PRG1 Proteoglycan 1, secretory granule	KINESIN HEAVY CHAIN	COATOMER DELTA SUBUNIT	VIM Vimentin	Integrin associated protein mRNA.		PKU alpha, partial cds	ETS-like 30 kDa protein	Heat shock transcription factor 4		Tumor Necrosis Factor Receptor 2 Associated Protein Trap3	(clone EST02946) mRNA	FCGR2A Fc fragment of IgG, low affinity IIa, receptor for (CD32)		GRB2 Growth factor receptor-bound protein 2	CAB3b mRNA for calcium channel beta3	subunit	ANX1 Annexin (lipocortin I)	Cytochrome P450 db1 variant b
- <u>-</u> -	arf1	alli	atplbl		spt5h			sin3	prg	kif5b	arcn1	vim	cd47		pkua		hsf4		traf2		fcgr2a		grb2			anxa1	cyp450db1
M59371	M84332	14104332	016799		U56402	U90313		U96915	X17042	X65873	X81198	219554	225521			D63134	D87673		HG4683. HT5108	L43576	M31932		M96995		U07139	X05908	X07619
M59371 at	M84332 at	116799 c 2+	010/33_3_41	U56402_s_at	ı	U90313_at_		_ J		1	X81198_at_	Z19554_s_at_	Z25521_s_at_	AB004884_at		D63134_at_	D87673_at_	HG4683.	HT5108_s_at HG4683.	L43576_at_	M31932_at_	M96995_s_at			U07139_at	X05908_at_	X07619_s_at_ X07619

Figure 1V

Title: sponse of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

						Inve	me	ors:	Nir i	Hace	oh	en,	ei	al.										
۲	0 7		Ū.	1	0		7.7	80	0	5	11.8	(٥	σ			m	ď	,	0		131	4 9	0.4
-	4 4			1	9	-	-		7		0.4	,	1.3	2 0	1		4.2	7		4 2		7 1	c	1.9
	6		-	1	7	-	0		7	ì	2.4	(6.3	0	-		9.0	0	2	1 3		-6	00	0.3
α	4		,	7.7	C		5	2.2	α	3	0	-	5	4.2	6		0	7	2	0.7		10.9	10	0.7
40	<u> </u>		0	7.7		-	?	7.1	-		0	-	=	2.5	2 8		0.1	4 5	?	6.0		0.4	0.5	0.2
0	7.3		-		00		2	1.5	7 4		0	-	5	1.3	22	,	9.	6 4		2.3		0	0	0.7
12.5	7.5		α	7	3.1	2 0	0.7	21.5	, ,		11.4	7	20.0	11.1	49		2.9	Α		11.1		19.1	9.7	3.3
2 9	2.9		α,		2.8	000	0.7	2.8	α		2.8	0		2.8	2.7		7:7	2.7		2.7	\mid	2.7	2.7	2.7
2.3	4.9		π.	,	11.4	-	7.7	6.4	21.8		3.1	ō	0	5.4	4.2		4:1	2.6		11.6		5.6	4.4	1.2
GUANYLATE CYCLASE SOLUBLE, ALPHA:3 CHAIN	EWSR1 Ewing sarcoma breakpoint region 1		Sridaii Nuclear Kibonucleoprotein, Polypeptide IC, Ait. Splice 2		Nuclear Factor Nf.116	VDR Vitamin D (1,25- dihydroxyvitamin D3)		STAT3 Signal transducer and activator of transcription 3 (acute-phase response factor)	DAF Decay accelerating factor for complement (CD55, Cromer blood group system)	PAM Peptidylglycine alpha amidating	monooxygenase	NE.H gene exon 1 (and ioined COO)	DON Dootin (Doot String)	Now Result (Reed Stellberg cell expressed intermediate filament associated protein)	Proteasome subunit HsC7.1	EVEOR Dinding Drotoin Att California	According Freeze, Air. Spiles 2	Transcriptional Coactivator Pc4	Thyroid receptor interactor (TRIP7) mRNA, 3'	end of cds		Inhibitor of apoptosis protein 1 mRNA	Osteoclast stimulating factor mRNA	PGF Placental growth factor, vascular endothelial growth factor-related protein
guc1a3	ews				nfil6	vdr		stat3	daf	-	Darii	nefh		rsn	psmb2			TCPC4		trip7		ciap2	ostf1	pgf
X66534	66899X	1000	HG1322. HT5143	HG3494.	HT3688	103258		129277	M31516	107751	17//51	X15306		X64838	D26599	HG1139. HT4910	HG4297.	HT4567		L40357		U45878	U63717	X54936
X66534_at_	X66899_at_	HG1322.	H15143_5_4(H15143	HG3494.	HT3688_at_	J03258 at	i i	L29277_at_	M31516_s_at _	+c 10775M	W3//21_dL	X15306_rna1 at		X64838_at_	D26599_at_	HG1139. HT4910 at	HG4297.	HT4567_at		L40357_at	JU45878_s_at		U63717_at_	X54936_at_

Figure 1W

1 itle: Esponse of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

				111	vento	315		Mir	Ha	ico	he	en, <i>et</i>	ai.							
1.6	6.2	0	α	2	13.8	0	3.1	3.6	9	5.5		0		7.8	0		9	16.2	2.5	1.1
1.8	1	1.7	=	1.7	1.2	0.1	4.1	C	2.4	0	0.5	1 9		1.6	10.7	90	C	4		0.3
6.0	1.4	1.7	_	1.5	9.0	0.7	0	6 6	6.0	1.4	60			4.7	~	C	0 3	2 6	1.3	6.5
0.2	0	0.5	6	0.5	8.2	21.6	1.9	10.2	4.5	1.0	0 3	77	1	Σ.	10.3	7.2	0	11 4	2.4	3.4
6.0	0	1.1	Ľ.	2.3	5.6	11.3	2.3	6.3	8.7	2.1	1 4	4 2	,	2.5	16.9	3.55	1.6	4.6	4.1	0.1
2.2	0.4	1.7	6	0.2	6.0	6.4	4.2	0	6.4	4.4	0.5	2.2	;	4	38.4	0	6.0	11.1	2.8	1.4
7.6	12.2	7.2	2.5	5.7	13.7	2.2	4.8	4	5.5	12.8	0	9.9	1	4	8	0	2.9	10.6	2.5	1.8
2.7	2.7	2.7	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6		5.3	2.5			2.5	2.5	2.5
3.3	0.7	37.7	83	5	4.4	0	3.4	6.0	1.7	5.5	0.2	3.6	,	7	2.9	0	1.9	20.5	1.9	2.6
ARHG Ras homolog gene family, member G (rho G)	SERYL-TRNA SYNTHETASE	DNA-BINDING PROTEIN A	Single-Stranded Dna-Binding Protein Mssp-1	ANX7 Annexin VII (synexin)	FACL1 Long chain fatty acid acyl-coA ligase	ERF.2 mRNA	TOP1 DNA topoisomerase (Cytochrome P450 (CYP2A13) gene	YMP mRNA	Grb2-related adaptor protein (Grap) mRNA	Elongation factor-1-beta	REL V.rel avian reticuloendotheliosis viral oncogene homolog	Eac. hinding protein (DAXX) mDNA	ימי בווימוול אינינון (ביניגי) ווויאין, אמן נומן כתי	Monocyte Chemotactic Protein 1	Bactericidal Bpi'Gene	PP2A B56-beta mRNA	NATURAL KILLER CELLS PROTEIN 4 PRECURSOR	Scaffold protein Pbp1 mRNA	HSPA6 Heat shock 70kD protein 6 (HSP70B')
rhoG		csda		anxa7	facl1	erf2	top1		emp3	grb2-rel	eef1b2	nfkb crel	Axe		mcp1		ppp2r5b	nk4	pbp1	hspa6
X61587	X91257	X95325	НG2639. HT2735	J04543	L09229	U07802	007806	U22028	U52101	U52518	X60489	X75042	AF006041		HG4069. HT4339	HG4336- HT4606	L42374	M59807	U83463	X51757
	X91257_at_	s_at_	HG2639. HT2735_s_at HG2639 HT2735	J04543_at_	L09229_s_at_ L09229	_	U07806_s_at _	_r_at_	H		X60489_at	X75042_at_	AF006041_at	090701	s_at	HG4336. HT4606_at_	L42374_s_at_	1	U83463_at	X51757_at_

Figure 1X

7	1	Palitac	PRUTEASOME COMPONENT C8	2.8	2.4	4.2	8.2	6	52	29	17	0 7
	D26600	psmb4	PROTEASOME BETA CHAIN PRECURSOR	3.4	2.4						, ,	1 1
D8/446_atD8/	D87446		KIAA0257 gene, partial cds	5.2	24	3	4 4	1 0	-	5	0 0	10
13972 at 113	(13972		SIAT4A Sialyltransferase 4A (beta-							1	7	/-
1	L26247	sui1	RPI 3 Ribosomal protein 13	3.1	2.4	4.1	-	1.9	2.3	0.4	0.7	4.4
17				'n	4.7	4.5	2.3	2.7	2.1	1.7	5.6	2.2
\neg	M55998	collagen-a1	Alpha-1 collagen type I gene, 3' end	σ «	2 4	7	<u></u>	-	7 7	C	-	
M63180_atM63	M63180	tars	TARS Threonyl-tRNA synthetase	m	2.4	σ		ά	101	2 4	5 0	5
M96843 at M96	M96843	d2bi	ID2 Inhibitor of DNA binding 2, dominant	:	i	5	2		2	2	5	
1		2	BCH1 PAG (recombination cotinution	14.6	2.4	1.6	3.9	0.5	1.9	2.4	3.1	3.8
	U28386		cohort 1	2.8	2.4	15.4	2	-	σα	2 7	۲, د	0
J28963_atU28	U28963		Gps2 (GPS2) mRNA		2.4	333		25		, ,	,,,	0 -
_			ERBB2 Verb.b2 avian endhrohlastic laukamia					i			;	
X03363 c at X03	6988UX	, ,	viral oncogene homolog 2 (neuro/gliobiastoma		•••							—
	202	erobz	derived oncogene homolog)	2.6	2.4	3.9	0	1.4	0.5	0	1.2	c
	107909	emp1	848	6.1	2.4	1.8	4.2	1.6	1.4	1.4	0	1
Ţ	103	ursp	Spot14 gene	4.6	2.4	4.5	2.9	2.5	0	c	70	α
Z49835_s_at_ Z49835	835	grp58	PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR	60	2.4		0	0				9
AF001294_at						2		3.6		0	ς υ	4
\top	AF001294	ldi	IPL (IPL) mRNA	2.6	2.3	9	4.5	0	0	o	ď	
1	042087		KIAA0118 gene, partial cds	7.1		10.9		19			, c	ή α
U20232_at_ U20	U5U532	HML2	Macrophage lectin 2	0	2.3	0	C		c	1/2	5 0	
L00352 at L00;	100352	1	LOW-DENSITY LIPOPROTEIN RECEPTOR							3	5	3
,			200000	21.4	2.3	9.5	5.5	2.8	6.0	1.9	7.7	4.6
	343	pi3	P13 Protease inhibitor 3, skin-derived (SKALP)	4 1	0	200	Ċ	1	0	Č		
	M23254	capn2	CAPN2 Calpain, large polypeptide L2	2.2	2 0	7 7	5 6	7 4		4 1	5	<u>ا</u> . بازد
U47634_atU47	U47634	b-tub4	TUBB Beta-tubulin	100	5 0	100	100	2 0	2,4	\ \ \ \	7.0	0,4
			TNF receptor associated factor 6 (TRAF6)		53	7	0.7	6.2	2.4	-	6.0	0.6
	798	traf6	mRNA	4.4	2.3	5.1	0.2	2.5	0.5	0.2	C.	4
10/00 at 15/06	90/	10512	I-OS-RELATED ANTIGEN 2	∞	2.3	30.2	5.3					

X84709 at	x84709	fadd	Mediator of receptor induced toxicity	1.7	2.3	2.5	C1	2.1	0	0.3	F	3.4
	Y04754	27.6	Yeast methionyl-18NA synthetase homologue	1.5	2.3	4.5	0	0.7	6	0	9.0	2.2
014812 at	D14812)	KIAA0026 gene	1.7	2.2	5.2	3.5	2.5	6.3	0.7	1.4	2.7
,	106132	vdac1	VDAC1 Voltage-dependent anion channel 1	4.4	2.2	3.2	1.7	2.5	0	1.3	9.0	3.4
M27533_s_at	M27533	cd28lg	lg rearranged B7 protein mRNA VC1-region	2.6	2.2	36.8	0.4	3.8	5.5		4.7	19.8
		0	SPONSE		- 6		1	,	- -	c	· ·	7
X60003_s_at_ X60003	X60003		PROTEIN	N. 1	2.2	2.5			1		7.0	0
X70811_at_	X70811	adrb3	ADRB3 Adrenergic, beta 3., receptor	2.7	2.2	2.3	4.0	1	3.1	1.5	0.0	ρ., γ
HG3417. HT3600_s_at HG3417. HT3600	HG3417. HT3600		Gtp Cyclohydrolase I, Alt. Splice 1	4.9	2.1	12.8	c.i 8.	12.1	3.2	0.8	9.0	7.5
M11717_rna1	71711M	hsnala	Heat shock protein (hsp 70) gene	83	2.1	m	9.6	3.5	2.7	1.2	2.3	٦
M85169 at	M85169	d17s811e	Homologue of yeast sec7 mRNA	4.1	2.1	3.7	4.4	0.8	1.6	4.6	5.5	2.3
1114969 at	U14969	rpl28	Ribosomal protein L28 mRNA	1.6	2.1	1.5	2.1	2.5	2.7	0.7	0.5	-
			MEF2A gene (myocyte specific enhancer factor 2A C9 form) extracted from Human myocyte.					_				
U49020 cds2			specific enhancer factor 2A (MEF2A) gene, first									
sat	U49020	mef2a	coding	1.7	2.1	2.5	2.8	17	0.7	2.4	8.0	3.5
1158970 at	U58970	tom34	Putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA	2.9	2.1	7.4		0	7.6	5.6	2.7	7.7
X07743 at	X07743	plek	PLECKSTRIN	6.7	2.1	5.7	13.9	10.7	2.7	3.6	1.6	5.6
YB0230 at	X80230	cdc2 4	mRNA (clone C.2k) mRNA for serine/threonine protein kinase	1.6	2.1	9	6.0	0.7	0	1.3	0.8	5.9
X89985 at	X89985	bcl7b	BCL7 B cell lymphoma protein 7B	3.2	2.1	3.2	5.7	6.5	4.3	1.9	0.3	0.9
725884 at	225884	clcn1	CIC-1 muscle chloride channel protein	3.2	2.1	1.9	0	1.4	2.7	1.6	0.1	0.5
Z47727 at	247727	rbp7	RNA polymerase II subunit	2.7	2.1	3.3	1.2	4.8	1.9	0.4	9.0	1.8
		crem	CREM CAMP responsive element modulator	3.4	7	6.3	13.7	7.8	50.6	5.1	1.6	7.4
D31887 at			KIAA0062 gene, partial cds	3.2	2	45.2	0.4	9.0	6.8	1.2	0	0.1
	D86961		KIAA0206 gene, partial cds	15.1	2	6.6	19.5	4.8	1.1	1.2	2.4	3.7
	,,,,,,,		Effector cell protease receptor 1 (EPR-1) gene,	6.0	с.	(·	C C	· .	C.	0	9.0	1.9
L32866_at_	L32866	epri	partial cos	17:-3	1	1,71	5	1				

	9	GRL GIUCOCORTICOID receptor	1.9	7	3.9	4.2	4.7	11.5	1.2	1.5	1 4
U73824	dap5	P97 mRNA	4.3	C1	C1	3.5	3.4	3.2	13	0.8	000
		Epidermoid carcinoma mRNA for ubiquitin-									
D83004		bendless gene product	'n	0	77	C	C	Ċ	u	-	Ċ
		0						7			7:7
M10277	actb	ACTB Actin, beta	2.1	0	2.4	0.7	-	9			-
										1	
M27749		Immunoglobulin-related 14.1 protein mRNA	5.6	6.1	4.2	C	С	7	C	Ċ	7.0
629	ell2	RNA polymerase II elongation factor ELL2	2	1.9		0				0	17
X53416	аррх	FLN1 Filamin 1 (actin-binding protein-280)	1.6	1.9	2.6	- 3	12	C	90		
0226X	11172	INTERLEUKIN.1 RECEPTOR, TYPE II PRECURSOR	и С	-	-				5 6	;	• 0
		PPP1CB Protein phosphatase 1, catalytic	2		7.7	5	0.0	7.	6.3	7.	7.7
X80910	ppp1cb	subunit, beta isoform	5.9	1	27	4	-	-	C	0	1
		CTINNB1 Catenin (cadherin associated protein),						?			2
X8/838	ctnnb1	beta 1 (88kD)	4.9	1.9	1.4	3.8	0.5	2	2.8	1.6	0.6
708265_s_at_ Y08265		DAN26 protein, partial	6.4	1.9	1.6	1.7	1.7	-	1 1	0 3	0
L38951		Importin beta subunit mRNA	1.9	1.8	17	2	0.5	2.5	1 9	σ	0
U28015	casp5	TY protease	2.6	1.8	16.2	3.4	0	23.2	c C	عاد	1 -
U44799		U1-snRNP binding protein homolog mRNA	2.2	1 8	3.6		-	2 4			, ,
		Mitochondrial NADH dehydrogenase									
		ubiquinone Fe-S protein 8, 23 kDa subunit									_
065579	ndufs8	mitochondrial protein	C	-0	((-		- i		
U71364	cap3	Cytoplasmic antiproteinase 3 (CAP3) mRNA	3 7	<u>ο</u> α	28.4	5 0	2 4	2 0	<u>∩</u> C	0	
U03644		Recepin mRNA	1.6	17	3.4	10	4 1	0 9	o o	5.0	ο α ο α
U22897	ndp52	Nuclear domain 10 protein (ndp52) mRNA	3.4	1.7	8.3	6.5	3.4	8.6	-	1.6	6.2
J04617_s_at J04617	efla	EEF1A1 Translation elongation factor 1-alpha-1	1.8	1.6	1.7	80	2.3	88		0	=
M23114	atp2a2	ATP2A2 ATPase, Ca++ transporting, cardiac muscle. slow twitch. 2	3.4	-	-	-	3 6		0		
S82297	b2m			9 9	- C	100	0 <	2 6	1 2	40	ν. Σ

Figure 1AA

U89505_at U89505	rbm4. lark	Hlark mRNA	1.3	1.6	4.2	α	ō	17		- -	lu lu
		DNA binding protein from Human DNA			!	?			-		4.
		sequence from PAC 339A18 on chromosome Xp11.1.Xp11.4. Contains KIAA0178 gene,									
		similar to mitosis specific chromosome				-					
797054 xnt2		segregation protein SMC1 of S.cerevisiae, DNA									
797054		Uniding protein similar to URE-B1, ESTs and STS. Intyne≡DNA /annot=CDs			1						
at U29171	csnk1d	CSNK1D Casein kinase 1 delta	4 4	9 -	7.7	1.5		2.3	2.8	0.7	2.3
U58087_at_ U58087		Hs·cul·1 mRNA	5.0	0 4	2.7	7.7	2.4	0	0.1	0.3	1.4
U66464 at U66464		Hemathonoite in a standard of the condition of the condit	0, 1	0	10.2	5	2.5	8.	6.0	0.2	3.9
	hcg.v	HCG V mRNA	0	1.5	0	1.3	1.7	0	0.5	0.5	0.1
Г			2.9	1.5	m	2.4	3	0	2.1	0	1.8
	anxa6	ANX6 Annexin VI (p68)	10.2	r.	v	0	,	,		,	
D86976_atD86976		KIAA0223 gene, partial cds	iα	0 0	7		-		200	5	4.7
		Guanine Nucleotide Binding Protein Ral Ras.	0.1	-		5	7.0	5	2.3	0.7	6.0
HT1103_at_ HT1103		Oncogene Related	C.	1	27.0	,	Ç	Ċ			
M20867_s_at	:				C: /4	1 7	7	4.7	7.0	2.1	12.5
M2086/	glud1	GLUD1 Glutamate dehydrogenase	0.6	1.4	0	2.8	1.5	-0	0.5	0	0
Ţ		14-3-3 epsilon mRNA	2.7	1.4	1.6	1.4	0.5	0		7	- 0
		CD116 (C) marronhare antices of CD116 (C)						-			
J03925_at J03925	cd11b	polypeptide)	-	,	Ĺ	((,			
M14199_s_at			0.0	7:7) ()))	0.8	0	2.2	1.4	1.2
M14199	lambr	LAMR1 Laminin receptor (2H5 epitope)	0.7	1	Ċ	-	Ľ	-	Ċ		(
M26/30_s_at M26/30_s_at	Q Q	Mitochondrial ubiquinone-binding protein (QP)				31,		+		5	5
at M29877	4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EliChi Elicopidate	9.0	1.2	1.5	9.0	1	1.6	1.5	6.0	1.1
1	1000	COM Lucosidase, alpha-L- 1, tissue	0	1.2	0.3	0.1	1	0	8.0	0.7	0.8
M55409		EEF1G Translation elongation factor 1 gamma		-	C	,	ı	(-		
		2	17.7	7.1	ر ن	7.1		0	7	0	Δ.

Figure 1BB

07510			Matk=megakaryocyte associated tyrosine					-	-			Γ
3/3100_filld1 _at_	875168	ctk	kinase [numan, Genomic, 261 / nt 13 segments]	Ċ	1	C	C					
U50196_at_	U50196	adk	ADK Adenosine kinase		7.7	200	0.0) -	5 0	1.7	1.0	7.7
					7:-	0:1	7.0	11	2	;	1.5	٦
J03592_at_	103592	ant3	ANT3 Adenine nucleotide translocator 3 (liver)	0.5	1.1	-0	0.3	6.0	C	7	-	α
M11119_at_	M11119	PL1	Endogenous retrovirus envelope region mRNA (PL1)	C	=	C	-	-	5			3
			ERCC1 Excision repair cross complementing					?		5	7-7	7
			rodent repair deficiency, complementation group 1 (includes overlapping antisense									
M13194_at_	M13194	ercc1	sednence)	-	1.1	0	0	0.7	0	0		(°
U80040_at	U80040	aco2	ACO2 Aconitase 2, mitochondrial	0.7	1.1	0	0.7	0.7	0		1 9	
XU6956_at_	X06956		TUBULIN ALPHA-4 CHAIN	1.1	1.1	0	m	1.4	0	0	0.8	0
X59543_at	X59543	rrm1	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE MI CHAIN	1.1		6	C	- C		, C		
X67247_rna1					+			7	3	3	5	
- 1	X67247	rps8	RpS8 gene for ribosomal protein S8	0.5	1.1	0.6	0.5	-	- L	α		7
D14662_at_	D14662	aop2	KIAA0106 gene	1.1	-	0		0.7		0.0		5
- 1	D25538	adcy7	KIAA0037 gene	0	-	0	Ö	90	c	0.5	0 2	C
D26308_at_	D26308	blvrb	NADPH-flavin reductase	0	-	0	0	0.8	0		0	
D/9990_at_	0/8860		KIAA0168 gene	0.7	7	0.3	2.2	1.3	0	1.3		0.8
L13939_s_at_		ap1b1	Beta adaptin protein mRNA	0	-	C	C	7			L C	
M23197_at	M23197	cd33	CD33 CD33 antigen (differentiation antigen)	0		C	0.5	1 2	c	0	ς α	5
D82348_at_	D82348		5-aminoimidazole-4-carboxamide-1-beta-D. ribonucleoti de transformylase/inosinicase		C		C	-	,		9 !	
D87433 at	D87433	kiaa0246	KIAA0246 gene partial ods	5 0	0.0	5 0	0.0	1	5	5	5	5
			יייי ליייי איייי אייייי אייייי איייייייי	5	0.9	٥	5	0.3	0	0	9.0	0
M22632 at	M22632	C+05	GOT2 Glutamic-oxaloacetic transaminase 2,									
W22032_at	W122032	Role	mitochondriai (aspartate aminotransferase 2)	0.1	6.0	0	0	-	0	0	0	0
	M58285	hem1	Membrane associated protein (HEM-1) mRNA	0	0.9	0	0	0.5	0	2.5	0.3	0
IM33221_at_	M93221	mmr	M6PR Mannose receptor	0	6.0	0.3	0	0.8	C	-	C	70

Figure 1CC

-				-							
ncor2 horn	Sile.	Silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA	0.2	6.0	0	0.1	0	-	3.2	0.6	0.4
hrg4 Retir	Retir	Retinal protein (HRG4) mRNA	6.0	6.0	0	0		0	0.7	0	0
PUT ISON	PUT	PUTATIVE GLUCOSAMINE.6-PHOSPHATE ISOMERASE	0	8.0	0	0	9.0	0	8.0	0.1	1.2
High hmgiy exon	High	High mobility group protein (HMG·I(Y)) gene exons 1.8	0	0.8	0	3.6	2.2	2.1	80	0.1	1.2
cmd1a LMN	Σ Σ	LMNA Lamin A	1.9	8.0	2.1	3.8	2	1.6	0.7	-	60
309	809	60S RIBOSOMAL PROTEIN L10A (CSA·19).	8.0	8.0	0	2.6			C	0	90
fbp1 FBP1	FBP1	FBP1 Fructose bisphosphatase 1	0	0.8	0	4.0	0	0	0	9.0	0
Tumor	Tumor	Tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds	0	0.7	0	0	60	0		1 7	C
aif1 Allogra	Allogra	Allograft inflammatory factor-1 (AIF 1) mRNA	0.2	0.7	0.7	0.4	0.5	<u>15</u>	0	0.7	0.4
8 744F	144L 8	L44L gene (L44-like ribosomal protein)									
extrac	extrac	extracted from Human Bruton's tyrosine kinase				-					
riboso	ribosc	ribosomal protein (L44L) and FTP3 (FTP3)									
agmx1 genes	genes	-	Ö	0.7	0.3	1.4	1.1	6.0	0	9.0	0.4
KH ty	KH ty	KH type splicing regulatory protein KSRP				-					
mRNA	mRN/		0	0.7	0	1.5	0.9	0	0.3	0.5	0.1
	Gene	Gene encoding prepro form of corticotropin									
	releas	releasing factor	1.1	0.7	0	0.5	1.1	0	0.3	0	0.5
rps26 RPS26	RPS26	RPS26 Ribosomal protein S26	0	0.7	0	0	1.1	0.4	0	0.4	0
	Transf	Transforming growth factor beta induced gene									
3	produc	product (BiGH3) mRNA	0	9.0	0	9.0	9.0	0	6.0	0.7	9.0
	LST1	LST1 mRNA, cLST1/E splice variant	6.0	9.0	0	3.3	1.1	0	0	0.1	0
rp123 RPL1	RPL1	RPL17 Ribosomal protein L17	0.4	9.0	0.7	1.7	0.8	7	0.4	9.0	6.0
CLASS	CLASS ALPHA	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR	C	0	0	0	-		0	5	
	TGFBF	TGFBR2 Transforming growth factor, beta		5	7:0		1		9		
hnpcc6 recep	recep	receptor II (70.80kD)	0	0.5	0	0.5	0	0	2.1	0.3	0

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			PPP3CA Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A									
L14778_s_at_	L14778	calna	alpha){alternative products}	П	0.5	0	г	1	0.3	9.0	1.9	0
M28825_at_	M28825	cdla	CD1A CD1a antigen (thymocyte antigen)	0	0.5	0.1	0	1.4	0	8.0	1.5	0
M61827_rna1 s_at	M61827	cd43	Leukosialin (CD43) pene	C	0.5	0.5	1.5	0 4	0.3	0.1	0.5	4 0
U51587_at_	U51587		Golgi complex autoantigen golgin 97 mRNA	0	0.5	0	0	0	0	0.8	1.2	0.5
J04430_s_at_	J04430	acp5	ACP5 Acid phosphatase 5, tartrate resistant	0	4.0	1.2	0.5	9.0	0	6.0	9.0	8.8
			PTGS1 Prostaglandin-endoperoxide synthase 1 Corostaglandin G/H synthase and									
M59979_at_	M59979	cox1	cyclooxygenase)	0	0.4	0	0.7	9.0	0	0	0	0
U47927 at	U47927	isot	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T	0	0.4	-	1.4	0.7	0	1.4	0	0
			Nain gene (neuronal apontosis inhibitory	-						-		
			protein) extracted from Human basic								-	
			transcription factor 2 p44 (btf2p44) gene,				_					
			partial cds, neuronal apoptosis inhibitory									
U80017_rna2			protein (naip) and survival motor neuron					_	_			
at	U80017	gtf2h2	protein (smn) genes	0	0.4	0	0.7	0.2	0	0.4	0.7	9.0
228407_at_	Z28407	rp18	RPL8 Ribosomal protein L8	1.2	0.4	8.0	2.1	0.4	2.7	1.5	9.0	1.3
M11313_s_at	M11313	a2m	A2M Alpha-2-macroplobulin	- 2	С	c	~	ur C	C	0	0	C
			Pyrroline-5-carboxylate dehydrogenase						-	\mid		T
U24266_at_	U24266	aldh4	(P5CDh) mRNA, long form	0	0.3	0.5	Ö	0.3	0	0.1	0	0
			Chromosome 16p11.2 BAC Clone CIT987SK.					-	-	-		
U46025_at_	U46025		234F9 complete sequence	0	0.3	0	0.3	0.2	0	П	0.3	0
X55733_at_	X55733		EUKARYOTIC INITIATION FACTOR 4B	0.2	0.3	0	0.3	0.3	0	0.1	8.0	6.0
Z97074_at_	297074		Rab9 effector p40	0.2	0.3	0	1.6	9.0	0	2	1.5	0.5
D87466_at_	D87466		KIAA0276 gene, partial cds	0	0.2	0	1	0.5	1.2	0.4	0.2	0
U09578_at_	009578	3pk	MAPKAP kinase (3pK) mRNA	0	0.2	0	1.1	0.4	0	0	0	0
x63422 at	X63422	a+n+d	ATP5D ATP synthase, H+ transporting, mitochondrial E1 complex delta subunit				-	, C		9 0	-	
V03#52_at	72455	athou	יייונטכווטווחוומן ד כטוווטופא, חפונס אחטוווו	5	0.1		1	5	5	0	5	7
X78817_at_	X/881/	RhoGAP4	[KIAA0131 gene, partial cds	0	0.1	0	0.0	1.1	0	0	0.1	0

Figure 1EE

							citto	э.		1 111	11	ucc	,,,,	υl1 ,	C1													
	0	0.5	0.8		2.2			0.1	•		2.0	5 0	5 0	ी	C	o C	0 0			C		olc			ţ.	C	1 (0.3
	E 0	0.0		5	1.6	(4.0	6.0	α		- c	7.1	710	\ - -	C	c				0	C	2 6	2	2 0		C	0.7	0.3
		5	1.5) !	X.		5	4.0		1 4	0.0	n	5 0	5	C	0		,		0.4	17	0 0	C	0 0	>	1.7	0	0.4
-		5	5 0		4			0			7.7	5 0	5 0	5	C	0) (7		7.9	0	90		0 0	+	0	0	0
-	7.7	J. 0	2000	7	4.0	1).)	0.2		3) -) -	- L	200		60) C	}		1.4	0.7		c	C	,	1.3	0	0.7
-	5 0		4.0		5		0.7		0.4		5 0		> 0		0	0	C	1		0.5	0	0	C		+	0	0	1.4
	5 0	3	5 0		>	-		9.0			5 0		0		0	0	C	-		0	0	0	C	C	-	0	0	0
	5 0	5 0	0 0				5	5			0	0			0	0	0	-		0	0	0	0	0		0	0	0
	٥١٥					C		٦	0.4						0	0	0			0	0	0	0	0		0	0	0
N H	PUTATIVE PROTEIN PHOSPHATASE OF	KIAA0179 gene partial cds	Stac	Cancellous bone osteoblast mBNA to 003005		Tyrosine Kinase Svk	Tariched Day (110)	ore children Dia, Ciolle 319	Zinc Finger Protein Hzf4	LBR Lamin B receptor	Frizzled gene product mRNA	Phosphomevalonate kinase mRNA	ADORA3 Adenosine receptor A3	FCER2 Fc fragment of IgE, low affinity II,	receptor for (CD23A)	LYL·1 protein gene	GO-RICH SEQUENCE DNA-BINDING FACTOR	TCF3 Transcription factor 3 (E2A	immunoglobulin enhancer binding factors	E12/E47)	VCL Vinculin	Br140 mRNA	PLCB2 Phospholipase C, beta 2	Chromosome 17q21 mRNA clone LF113	Clone CIITA-8 MHC class II transactivator CIITA	MKNA	P21-activated protein kinase (Pak1) gene	DU I DUTP pyrophosphatase
denn	pp2c-like	kiaa0179	stac			syk	Cna.Furiched	200		lbr	fzd2	pmvk	adora3		cd23	lyl1	tcf9		(eZa	vcl	br140	picb2		71:1	ciita		dut
AB002356	D13640	D80001	D86640	D87119	HG3730.	HT4000	HG3995- HT4265	HG4126	HT4396	L25931	L37882	L77213	ل277730 ا		M15059	M22638	M29204		0	M31523	M33308	M91585	M956/8	U18009	0300	010239	75157	031930
AB002356_s_ at	D13640_at	D80001_at	D86640_at_	D87119_at	HG3730. HT4000 s at HG3730		HG3995. HT4265 at	HG4126.	HT4396_at_	L25931_s_at_	L37882_at_	L77213_at_	L77730_at_			M22638_at_	M29204_at_		001101	1	7	1	M956/8_at_	U18009_at_	110250 24	U10239_dl_	127152 at	U31930_at_

Figure 1FF

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1- 505361	707.7611	9	Putative holocytochrome c-type synthetase				-	-		-		C
U30/0/_al_	/0/050	IICCS	C)	5		5	5	>		1	1.5	7
U41767_s_at	U41767	adam15	Metargidin precursor mRNA	0	0	0.5	1.5	0	0	0	0	0.3
U51269_at	U51269	arvcf	Armadillo repeat protein mRNA	0.1	0	0	0	0	0	1	0.8	0.1
U51336 at	U51336	itrpk1	Inositol 1,3,4-trisphosphate 5/6-kinase mRNA	0	- 0		0.5	0	0	-	1.1	0.2
U53446_at_	U53446	dab2	Mitogen responsive phosphoprotein (DOC.2) mRNA	0	0	0	0	0	0	0	0.2	0
U62739 at	U62739	bcat2	Branched-chain amino acid aminotransferase (ECA40) mRNA	0	0	4.0	0	0	9.0	0.5	0	0
U63825 at	U63825	DIPA	Hepatitis delta antigen interacting protein A (dipA) mRNA	0	0	0	6:0	1.1	0	0	4.0	0
U68142_at_	U68142		RalGDS like 2 (RGL2) mRNA, partial cds	0	0	0	1	0	0.8	0.4	0	0
U70439_s_at	U70439	ssp29	PHAPI2b protein	0	0	0	0.7	0.7	0	0	6.0	0.4
U78525 at	U78525		Eukaryotic translation initiation factor (eIF3) mRNA	0	0	0	1.9	0	0	0.1	0.5	0
U79285_at	U79285		GLYCYLPEPTIDE N. TETRADECANOYLTRANSFERASE	0	0	0	G.3	0	3.5	2.2	2.7	П
U79288 at	U79288		Clone 23682 mRNA sequence	0	0	0	9.0	0	5.1	0	0	0.8
U93049_at	U93049	slap-130	SLP 76 associated protein mRNA	0	0	0	0.4	0.1	0	0	0.2	0.5
			FES Feline sarcoma (Snyder Theilen) viral (v. fes)/Fujinami avian sarcoma (PRCII) viral (v.									
X52192_at_	X52192	fes	fps) oncogene homolog	0	0	0	0	4.0	0	0.2	0	0
X69978_at_	82669X	ercc5	ERCC5 DNA excision repair protein ERCC5	6.0	0	0	1.4	0	0	0	1.2	0.3
X79204_at_	X79204		SCA1 Ataxin 1	0	0	0	0	9.0	0	0.3	6.0	0
X90824_s_at_ X90824	X90824	usf2	USF2a & USF2b, clone P2	0	0	0	6.0	0.3	0	0	0.5	1.1
X97074_at_	X97074	claps2	CLATHRIN COAT ASSEMBLY PROTEIN AP17	0	0	0	0.1	0	0	0.1	0.3	0
Y13247_at_	Y13247		Fb19 mRNA	0	0	1.4	0	1.7	0	0	0	0
Z34897_at_	234897	hrh1	HRH1 Histamine receptor H1	0	0	0	0	0.3	0	0	9.0	0.1
Z50749_at_	[250749	ppp1r7	Sds22-like mRNA	0	0	0	0.3	9.0	0	0.1	0.1	0

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affyID	GBA	gene symbol	gene Name	faco	hoco	1000	0.01	1	1	Γ	- 1	
			0100		Ì	1		npro	tprs	ıcan	mcan	tcan
M13755 at	M13755	isa15	סוסים ותנפוסום alpha-inducible protein (clone let ז אבן ובון		i i							
VODEO/	VODEON	12613	M-t-ll-th	214.1	545.6		- 1	662	100.2	302.7	208.8	34.3
V00394_di	v00394	mıtza	Metallothionein isotorm 2	1683.1	1698.4	143.4	371.1	414.5	107.8	3.3	261	74.2
M21121_at_	M21121	rantes	SCYA5 Small inducible cytokine A5 (RANTES)	728.7	661.7	83.4	717	396.6	115.3	113.6	87.4	437
			ISG-54K gene (interferon stimulated gene)						1			
M14660_at_	M14660	g10p2	encoding a 54 kDA protein, exon 2	5.9	25	27.9	109	312.4	206	0	Ľ	33.0
			INP10 Interferon (gamma) induced cell line;				Ī	1		1	,	5
X02530_at_	X02530	inp10	protein 10 from	12.5	13.1	442 2	137.9	290 4	501.1	r.	205.0	15: 4
M24594_at_	M24594	g10p1	IFI56 Interferon induced protein 56	19.8		77.5	1		141 1	1 9 8 1	7 870	100
			TNF-related apoptosis inducing ligand TRAIL			2	Ţ		11	2.0	2.0.0	00.0
U37518_at_	U37518	trail	MRNA	14.7	34.2	1343	1719	230 1	5000	n L	100	010
U59286_at_	U59286	itac	Beta-R1 mRNA, partial cds	20.00	276	ľ	ł	-	2000	2 0	102.1	2000
			INTERFERON ALPHA INDITIOED 11 5 KD		27.7			0./02	240.0	0.0	7,4,4	389.7
X67325_at_	X67325	ifi27	PROTEIN	136.8	143.4	618.8	265.8	1922	498	ŗ	21.01.0	600
			Thyroid receptor interactor (TRIP14) pene 3'				2	1	1	3	2177	7.400
L40387_at_	L40387	oasl		4.6	7.5	43	105.3	185.2	124.5	1 7	0 4	13.6
M33882 at	M33882	mx1	MX1 Myxovirus (influenza) resistance 1, homolog of murine (interferon, includible protein 578)		0 0	7	0	L	0	i		
119779 24	19779	h23	History LOAD TOWN	1.10	100.0	04.7	-	- 1	å	34	397.3	102
-17//J_at	-13//2	115.0	TISCOILE TIZA, Z MIRINA	53.2	154	83.4	40.2	122.8	65.8	7.9	10.8	33.4
V00594_s_at_	V00594	mt2a	Metallothionein isoform 2	167.1	337.3	ŗ	64 9	1228	348	69.4	52.2	ō
			TUMOR NECROSIS FACTOR INDUCIBLE				1	1]		75.7	Ť.
M31165_at_	M31165	tnfaip6	PROTEIN TSG-6 PRECURSOR	172.2	163.5	624.1	9.09	100.2	101.8	7 1	75	28
			6-16 gene (interferon-inducible peptide									
U22970_rna1			precursor) extracted from Human interferon-									
s_at_	U22970	g1p3	inducible peptide (6.16) gene	115.3	68.2	28	70.6	97.1	13.7	13.1	7 6	r,
X07834_at_	X07834	sod2	SOD2 Superoxide dismutase 2, mitochondrial	57.7	104.1	240.9		1	916	00	17.0	116.5
M34455_at_	M34455	ido	IDO Indole 2,3 dioxygenase	273.7	27.5	2198	1	80.0	α 20		100	106
			SOD-2 gene for manganese superoxide				i		5	?		
낡		sod2	dismutase	233.7	149.2	204	143.7	86.3	86.3	10.6	35.9	1093
U52513_at_	U52513	ifit4	RIG-G mRNA	25.1	39.3	96.2	92.1	84.6	86	13.2	39.1	94.7
X99886 s at X99886	9886X	mcn2	MCP.2 gene	i.	i		1	1				
			T Paris	51.9	10	26.3	42.9	82.6	6.74	4 8	23.8	79.5

Figure 2A

Figure 2B

			Honatitie Caccaciated misself L.									
D28915_at_	D28915	mtap44	protein p44	00	29.6	73	107	47.1	7		r.	0
J04164_at	J04164	ifi17	RPS3 Ribosomal protein S3 /wrong name	25.8	57.2	37.7	34.5	45.6	70.3	11.0		35 1
L19871_at_	L19871	atf3	ATF3 Activating transcription factor 3	10.6	197	9	200	200	10.0	2 4	2 4	1.00
					-	2	1:07	5	1,6.7	1.	7	ر د
L05072_s_at_ L05072	L05072	irf1	IRF1 Interferon regulatory factor 1	48.2	24.5	63	63.7	38.0	200	(1	27	и С
U29680_at_	U29680	bcl2a1	Bcl.2 related (Bfl.1) mRNA	105.3	97.0	678	70.7	20.2	117 5	1 6	0.4.0	170.3
D14661_at_	D14661		KIAA0105 gene	7 1	10.7	1	22.7	33.6	117.5	+ u	0 0	1/9.1
V00535_rna2	_		Interferon beta 1 gene extracted from Gene for			5:	t.07	2	, <u> </u>	-	0.1	0.
_s_at	V00535	ifnb1	human fibroblast interferon beta 1	0	2	187.4	68.1	0 66	165 /	,	Č	C
M87434_at_	_	oas2	69/71 KD	1 8	8	010	- 1 - 1 - 1 - 1	33.1	1 200.1	7 0	ט כ	1750
M92357_at_	M92357	tnfaip2	B94 PROTEIN	29.6	39.7		20.1	γ (γ (γ	20.5	3 0	13.0	7 90
J05037_at_	J05037	sps	L-SERINE DEHYDRATASE	C		200	10.0	21.0	2 4	7	2.51	707
HG1612 HT1612 at	HG1612. HT1612	macmarcks	Macmarcke		, ,				0.01			10
** 37000M	2700011	200		19.4	30	44./	11.5	30.2	16.9	ж. 4	11.8	15.6
W62370 at	M229/6	cg(c)	CYB5 Cytochrome b-5	2.9	4.2	2	5.5	30.2	4.6	1.7	2.1	5.6
M58603_at_	M58603	nfkbp50	NFKB1 Nuclear factor of kappa light polypeptide gene enhancer in B·cells 1 (p105)	26.1	30	000	ď	1 08	7	ď	7	,
			Exon 1b; used only in type 2 transcripts from		2	5.53	1.0.1	7.00	2.7	5))	10.1
X94563_xpt2			H.sapiens dbi/acbp gene exon 1 &							-		
_r_at	X94563		2./ntype=DNA /annot=exon	14.2	m	m	4.6	29	œ	00	5.	
1000	0	;	NCF1 47 kD autosomal chronic granulomatous									
MOSUO/ at	/anccivi	ncti	disease protein	25	12.6	24.2	19.1	28.5	22.1	4.4	8	17.5
X60592_at_	X60592	cd40	CD40 CD40 antigen	6.3	5.8	21	8.9	27.6	5.3	6	3.5	114
M87503_at_	M87503	isgf3	TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT	4	16.3	σ	n O	27.5	α	α -		u u
			PTX3 Pentaxin-related gene, rapidly induced by		?			2	2.5		2.1	
M31166_at_	M31166	ptx3	IL·1 beta	82.7	88.9	807.3	21	27.0	1000	r.	2	20.0
AB000115_at	4R000115	amoundari	V NO					1			i	20.5
1770007	2100000	TIMO MILE	WINIT.	y. 8	13.1	24.9	8.4	56.9	28.7	3.4	6.1	37.6
072882_s_at	U72882	ifi35	Interferon induced leucine zipper protein (IFP35) mRNA, partial cds	23.2	58.9	39.5	22	26.7	212	20.3	29.3	52 5
U33017_at_	U33017	slam	Signaling lymphocytic activation molecule (SLAM) mRNA	320.7	343 9		α	ς. α	~	,	2. 1.0	4.2
					5.2		5	0.07	7	4, 19	4.4.4	0.4.0

L22343_at	L22343	ifi175	Nuclear phosphoprotein mRNA	0.5	2.1	7	4.5	25.4	36.7	0.1	2.6	11.9
D90070_s_at_	020060	pmaip1	LRP1 ATL-derived PMA-responsive (APR) peptide	1.3	31	125.8	16.9	24.1	249.1	0	0.4	11.1
S76638_at_	S76638	nfkb p52	NFKB2 Nuclear factor of kappa light polypeptide gene enhancer in B.cells 2 (p49/p100)	23.7	32.2	27	14	24.1	5.6	1.1	2.8	15
U66838_at_	N66838		Cyclin A1 mRNA	2.3	22.1	53.5	12.3	23.5	65.7	1.1	1.9	23.6
Y00081_s_at_ Y00081	Y00081	91	IL6 Interleukin 6 (B cell stimulatory factor 2)	144.3	71.8	1281.1	39.5	22.4	95.7	0.5	15.8	39.3
U80073_at_	U80073	tap	Tip associating protein (TAP) mRNA	2.3	1.5	6.1	19.7	21.8	31.1	0.1	2.6	7.6
			PRG2 Proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major									
Z26248_s_at_	226248	prg2	basic protein)	0	1.2	1.1	2.3	21.3	9.7	0	0	0
L08069_at_	690801	hspf4	DNAJ PROTEIN HOMOLOG 2	12.8	11.1	12.7	10.9	20.7	9.7	1.7	3.9	8.8
M31627_at_	M31627	xbp1	X BOX BINDING PROTEIN:1	4.4	6	15.4	16.7	20.6	27.1	3.2	3.1	4.6
J04056_at_	J04056	cbr1	CBR Carbonyl reductase	0.1	3.9	9.0	3.7	20.5	7.4	4.2	7.3	Ξ
U19523_at_	U19523		GCH1 GTP cyclohydrolase 1 (dopa-responsive dystonia) (alternative products)	18.8	22.8	139.7	15.8	20.5	50.5	4.0	22.4	137.8
U03397_s_at												
	U03397	41bb	Receptor protein 4.1BB mRNA	4.6	13.1	4.06	m	20.1	26.2	C1	2.3	13.8
			PDE4B Phosphodiesterase 4B, cAMP specific									
L20971_at_	120971	dpde4	(dunce (Drosophila)-homolog phosphodiesterase E4)	23.9	38.2	124.8	1,51	00	43.2	C rc	<u>.</u>	20.1
			Mitogen induced nuclear orphan receptor					?	2		1	
U12767_at_	U12767	minor	(MINOR) mRNA	49.2	39.4	17.1	37.8	19.7	13.7	24.6	17.3	15.7
at	D64110	btg3	Tob family	1.7	13.1	12.2	1.6	19.6	9.1	2.6	1	9.9
at	879639	ext1	EXT1 Exostoses (multiple) 1	4.9	18.3	47	8.1	19.4	6.8	3.5	6.0	5.3
	HG2724.										T	
HT2820_at	HT2820		Oncogene TIs/Chop, Fusion Activated	0	0	20	18.8	19.3	9.68	0	9.0	101.1
M16364_s_at												
1	M16364	ckb	CKB Creatine kinase B	50.5	10.4	11.1	109.5	18.8	7.4	5.5	7	4
X77584_at_	X77584	txn	TXN Thioredoxin	22.4	39.5	5.2	16.8	18.4	7.9	3.8	8	2.5
U09278_at	U09278	fap	Fibroblast activation protein mRNA	0	O	0	14.8	17.9	67.4	0	0	0
M62403_s_at	MEDAND	i A P	GFBP4 Insulin-like growth factor-binding protein	i i	ı					,		
	INIO2403	Iginp4	t	15.9	5.2	32.7	61.8	17.5	37.9	6.8	9.1	104.6

Figure 2D

[;	7.	20.2		9.2	24.6	1.2		1161	181	2	17.4	1 4	7 0			t t	4.0	54.9	23.2	0	-	20.5	000	5
,	4.7	0 0		10.7	19.3		σ	43.4			4	0.0	-		2 7	` .	1.5	4.7	11.5	0	1 7	14.5	2	
1	0.1	2.1		2	14.1	9.0	-	88	2.1	-		4.2	1 0	4		7 0	5	S	6	0.5	2 4	0.6	-	
7 ;	1.7	7.4		10.3	9.6		α 4	73.3	16.7	6	9	9.5			9 7			87.4	15	34.5	2 4		13.1	
17.0	7,7	17		16.9	16.8	16.6	15.7	15.5	15.4	15.2	15.1	15	14.7	14.5	1 4 4	143		13.8	13.7	13.7	13.6	13.5	13.4	•
2		2.0		38.4	22.8	9.3	9.5	27.2	7.8	14.2	6.7	10.6	16.2	6.9	787	2 5		15.3	27.5	9.9	6.1	4.3	8.2)
α ς	2.7	48.8	(7.8	47.2	4.3	5.7	191	13.1	4.1	14.5	9.1	161	0	9	1.2		9.809	55.8	9.0	4.7	3.7	20.8	
7	σ	31.1		4.5	233.7	20.4	10.6	43.7	7	0.1	10.1	14.1	177.6	3.4	26.4	6.0		120.8	36.8	0	24.7	17.6	10.9	
00	1 4	43.8		۲.۶	166.9	4.6	m	34.6	10	8.2	11.2	9.5	52.1	1.9	65.5	0		110	61.7	0	8.6	1.3	13.2	
Myleoid differentiation primary response protein MyD88 mRNA	Calgizzarin	Ninjurin1 mRNA	Monocyte Chemotactic Protein 1			I ranscription factor ETR101 mRNA	PPP2R2A Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	HEM45 mRNA		Annexin II, 5'U'R (sequence from the 5'cap to the start codon)	Immunoglobulin-like transcript-3 mRNA	IL10R Interleukin 10 receptor	DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1	KIAA0069 gene, partial cds	LIRN Interleukin 1 receptor antagonist	Cysteine protease	(c) (c) (d) (c) (c) (d) (d) (d) (d) (d) (d) (d) (d) (d) (d	11 7D Intelliging 3	ZNET82 2000	Tal Too Reite	Ly-6-related protein (9804) gene	Semaphorin (CD100) mRNA	CD48 CD48 antigen (B·cell membrane protein)	
myd88	s100a11	ninj1	mco1		activinba	etr101	ppp2r2a	hem45	stat50		lir5	IIIOra	dusp2		illrn	prsc1	CX02	1175			ly6e	sema4d	bcm1	
U70451	D38583	U72661	HG4069. HT4339		X57579	M62831	M64929	U88964	Y8ZZOO	D28364	082979	2/9000	111329	D31885	X53296	D55696	1104636	M29696	X98253	0000	U66711	008090	M37766	
U70451_at_	D38583_at_	U72661_at_	HG4069. HT4339_s_at		X57579 s_at_ X57579	1VIDZ631_at_	M64929_at_	U88964_at_	782200_at_	D28364_at_	U829/9_at	UUUb/2_at_	L11329_at_	D31885_at	X53296_s_at_ X53296	D55696_at_		9696 at	1	U66711 rna1	s_at_	Ubusuu_at_	M37766_at_	

Figure 2E

itga5 ITGA5 Integrin, alpha 5 (fibronectin receptor, alpha polypeptide) ITGA5 Integrin, alpha 5 (fibronectin receptor, alpha polypeptide) INTERLEUKIN:8 PRECURSOR traf1 Epstein-Barr virus-induced protein mRNA C1NH Complement component 1 inhibitor c1nh (angioedema, hereditary) ICp2 76 kDa tyrosine phosphoprotein SLP-76 mRNA IL18 Interleukin 1, beta IL18 Interleukin 1, beta G4p Cyclohydrolase I, Alt Splice 1 G5p Cyclohydrolase I, Alt Splice I G5p Cyclohydrolase	MHC class I molecule (MICB) gene ITGA5 Integrin, alpha 5 (fibronectin re alpha polypeptide) INTERLEUKIN-8 PRECURSOR Epstein-Barr virus-induced protein mR C1NH Complement component 1 inhit (angioedema, hereditary) 76 kDa tyrosine phosphoprotein SLP-7 IL1B Interleukin 1, beta Galectin KIAA0207 gene Pre-B cell enhancing factor (PBEF) mF ERF-2 mRNA Nuclear orphan receptor LXR-alpha mi ERF-2 mRNA SDC4 Syndecan 4 (amphiglycan, ryudi ICAM1 Intercellular adhesion molecule human chinoming receptor	Ceptor, NA Ditor Sitor Situa RNA	889.1 89.1 1.6.9 1	3.8 234.5 15.4 15.4 15.4 10.9 10.9 10.9 10.9 10.9 10.9 10.9 10.9	9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	11.6 9.9 8 8 8 8 8 8 6 5.1 1.7 1.1 1.3 8 8 8 8 8 8 6 5.1 1.7 1.1 1.3 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5	13.2 13.2 13.2 12.7 12.7 12.7 12.7 12.7 12.7 12.7 12	2. 24.7 2. 29.7 2. 20.3 3. 2. 20.3 3. 3. 4 2. 20.3 3. 4. 4 3. 4. 5 3. 6. 4 3. 6. 6 3. 7 3. 7 3. 8 3. 8	4.1 0.0 8.8 8.2 8.0 0.0 1.1.4 6.0 8.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0		8.0 0 0 8 8 1 10.5 1 10
U15932	gdsnp	Protein tyrosine phosphatase mRNA	57	76.5	44.5	0 0.0	11.1	0 0 0 0 0	0 4	4	13.4
HG3884. HT4154	hpx42	Homentic Protein Hox.42	<u> </u>		2 0	0 0	7 7	0 0			4.0
X97324		Adipophilin	- C	200	n &	1 0 0	108	5.7	5 0	5 0	0 4
		Urokinase type plasminogen activator receptor gene extracted from Human urokinase type									
009937	plaur	plasminogen receptor	17	26.9	14.5	12.5	10.7	2.4	m	3.5	3.7
X07743	plek	PLECKSTRIN	9.7	2.1	5.7	13.9	10.7	2.7	3.6		5.6
U32849	imi	Hou many	C		- 5-	. 0.	,		ļ		

Figure 2F

	4.6 3.2	7	.2	2	1	Ш	9
Actin bundling	Actin bundling protein mRNA 59.8 27.5 8.	4	4.1 10	10.4 14.	1.	32 13.4	2.3
CLC Charot Ley	CLC Charot-Leyden crystal protein 0.5 2.7 0.	00	2.6 10	10.2	5.8 0.3	3 0.8	1.6
SSA1 Sjogren sy	SSA1 Sjogren syndrome antigen A1 (52kD, 15 A2 15	1 2	7	01		0 0 0	100
IRF2 Interferon	6.1 5.8		m	1	2		0 0
APT1 Apoptosis	1 1 8 5	2	m	10.2 24.			17.2
Putative copper	Putative copper uptake protein (hCTR2) mRNA 3.6 13.4 19	9.1	2.9	10.1	12	5 4.7	22.6
d16s469e INTEGRAL MEM	25.2 14.1	24.5 14	4.5	10	-	5 1.6	7.8
TY protease	2.6 1.8	16.2	3.4	10 23	23.2 0.	3 6	1.5
RPS3 Ribosomal protein S3	protein S3 0.8 3 26.	2	8.2	10	43 1.	1.4 5	72.9
HISTIDYL TRNA SYNTHETASE	0.5	10.4	6.3	10	8.1	1 0.5	7.2
Zinc finger transcr mRNA	Zinc finger transcription factor hEZF (EZF) mRNA 0	0	0.0	9 9	7 5	0	C
ABLE G		, ,		-		<u></u>	
HM74	5 10.5 2	9	8.9	9.8	1.7 0.	2.5	1.2
Calmodulin Type I	1.5 6.9 1	Ε.	5.8	9.7	3.9	3 0.5	9.0
Msgl·related gene 1	0 0.7	0.4	7.2	9.6	0.4	2 0	0.4
LMP2 gene extracted from H.sapien TAP1, TAP2, LMP2, LMP7 and DOB	LMP2 gene extracted from H.sapiens genes 30.6 20.6 32.	2.4 12.	6	9.6	6.3 6.1	1 23.6	31.9
MAJOR HISTOCO	PLEX 23.0 10.6	-	0 5	4	-	, c	0
CD83 ANTIGEN PRECURSOR	18.7 12.6				و ا	, -	7.0
Mitochondrial 16S	Mitochondrial 16S rRNA gene (partial) 2.7 4 0	0.7	3.2	9.4	3.8	1 1.2	0.5
FUT4 Fucosyltran	.3)	_	_	-			
fucosyltransferase, myeloid specific)	2.8 5.4	5.3	3.7	9.3 10	10.4 0.	3.3	11.4
Interferon-inducib			_		L		
kinase (Pkr) gene	19.8	3	7.8	9.3	22.1 40.1	.1 24.8	19.1
14-3-3 PROTEIN TAU	1.1 1.9	4.9	5.5	9.3	m	1.9 1.8	5.2
PROTEASOME (4.2	03 C1	9.2	5.2 2.	9 1.7	4.2
Epb72 gene exon 1	0	0 10	-	-	2 %	α 0	127

	•
Inveors:	Nir Hacohen, et al.

27.8	18.9	4.2	42.8		6.4	2.4	4		13.9	3.8	3.2		6.2	<u> </u>	3.2	5.5	1.3	83.6	7.3		3.3	9.7	30.7	33.8	
6.2	6.4	1.4	0	ļ.,	2.3	0	2.4		2.9	0	2.6		1.9	_	0.3	17.3	1	8.4	3.5		0.5	7.4	4		
7.9	3.7	0.8	0.5	-	_	2	6.0		5.1	0	0	-	5.6		1.6	34.3	0.3	1.1	4.6	_	0.1	2	14.9	5.4	-
14.9	31.4	14.3	9.9		2	2.7	4.5		9	1.8	7.7	-	33.6		2.5	5.7	4.7	44.4	4.1		16.7	61 61	19	7.8	
0	6.8	8.9	6.8	- 0	8.8	8.8	8.7	:	8.7	8.5	8.5		8.3		8.3	8.2	8.2	8.2	8.1		8.1	8.1	7.9	7.9	-
11	5.6	6	14.9		3.9	1.3	4.9		4.2	5.5	28.5	-	6.2		2.7	17.1	7.6	3.2	6.7		3.1	6.7	80		
12.9	61.6	4.7	51.9		6.5	10.1	5.5		9.4	7.6	ō	-	333.5		0.3	6.2	1.3	212.3	16.2		0.2	3.5	30.6	85.6	
9.1	12.6	4.2	0	;	6.7	15.6	2.6		9.5	6.9	2.2		107.8		1.3	17.2	6.0	55.5	15.8		1.3	6.9	19.2	64.4	
2	4.2	2.3	6.0	ļ -	7.7	12.2	1.7		3.6	21.4	9.0		109.8		0	13.1	2	13	14.7			7	12.7	46.3	
BONE MARROW STROMAL ANTIGEN 2 (BST-2)	C1S Complement component 1, s subcomponent	ZNF173 Acid finger protein ZNF173	SODIUM. AND CHLORIDE DEPENDENT BETAINE TRANSPORTER	ADAR Double stranded RNA adenosine	deaminase	MT-MMP protein	YMP mRNA	MHC.encoded proteasome subunit gene LAMP7. E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility	complex encoded proteasome subunit LMP7	CNP 2',3'-cyclic nucleotide 3' phosphodiesterase	HARS Histidyl tRNA synthetase		Interleukin 8 (IL8) gene	ANX4 Annexin IV (placental anticoagulant	protein II)	Proteasome activator hPA28 subunit beta	ACHE Acetylcholinesterase (YT blood group)	IL15RA interleukin 15 receptor alpha chain	PTPN1 Tyrosine phosphatase 1	BASIC TRANSCRIPTION FACTOR 62 KD	SUBUNIT	GLRX Glutaredoxin (thioltransferase)	PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG	BF B-factor, properdin	
bst2	c1s	znf173	slc6a12		adar	mmp14	emp3		lmp7	duo	hars		81		anx4	pa28b	ache	il15ra	ptp1b		gtf2h1	glrv	cxcr4	bf	
D28137	J04080	U09825	U27699	0.00	010439	248481	U52101		Z14982	M19650	X05345		M28130		M82809	D45248	M55040	U31628	M31724		M95809	×76648	262907	L15702	
D28137_at_	J04080_at_	Т.			at	Z48481_at	U52101_at_	Z14982_rna1	_at	M19650_s_at _		M28130_rna1	_s_at_						1		M95809_at	X76648_at_	L06797_s_at_	L15702_at_	

28.5	1		10.9		10.4		ivein		1.8			1.6	8 1	1.6	8.9	5.4	Τ-	π. Έ	L		1	00		1.7	0	L
40			2.8		4.3		-		6.0			0.7	0.1	0.5	0.3	6.8		4.2	4.9			Ċ		0	C	
48.3	1.2	9.2			1.7	C			1.7			1.3	0	2	1.7	2		1.5	2.1	0		0.6	3	0.4	0.7	
11.4	38.3	13.7	5.1		8.7	C	7 9		3			4.6	24.5	8.6	15.3	8.1		7.8	7.7	m		2.8	ì	2.8	86	
7.7	7.6	7.5	7.5	,	7.4	7 0	7		7.3			7.3	7.3	7.3	7.2	7.2		7.1	7.1	1		7		7	89	
13.4	C1	10	10.6	,	3.7	7.7	6 9		2.4			3.8	5.4	4	10.8	6.5		3.7	4.7	7.3		4.7		4.8	8	
16.9	127.1	61.3	8.8	;	0.4	0			5.3			5.6	2.4	12.7	15	10.8		8.9	4.5	c		4.3		1.4	0.3	
11.4	17.3	18.4	14.4	(2.2	Ç	2 -		3.7			5.9	0	15.9	5.6	15.2		11.3	5.5	3.4		6.0		0.8	5.1	
7.4	28.9	5.7	10.8	,	5	<u>.</u> π			1.6	-		4.1	9.0	10.5	8.3	8.7		2.4	1.3	2.5		6.3		0.3	0.2	
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.ALPHA/BETA	Phospholipid scramblase mRNA	Reticulocalbin	CTSL Cathepsin L	MNDA Myeloid cell nuclear differentiation	anugen	TCEB1L Transcription elongation factor B (SIII), polypeptide 1-like	JUP Junction plakoglobin		Centractin, Alpha	S100A10 S100 calcium binding protein A10	(annexin II ligand, calpactin I, light polypeptide	((p11))	Desert hedgehog (hDHH) mRNA, partial cds	Alpha-tubulin mRNA	NUCLEAR PORE GLYCOPROTEIN P62	PROTEASOME IOTA CHAIN	DNA binding protein CPBP (CPBP) mRNA,	partial cds	TRAF interacting protein I-TRAF mRNA	Tropomyosin Tm30nm, Cytoskeletal		Ras-Related Protein Rap1b		Histone H4 gene, clone F0108	TINUR.	LYN V.yes-1 Yamaguchi sarcoma viral related
stat1	plscr1	rcn1	ctsl	7	rilliga	skola	db3				11	calll	dhh	dusp1	nup62	psma6		bcd1	itraf	tm30nm		raplb			nurr1	
M97936	AF008445	D42073	X12451	032101	06/100	247087	268228	HG4606-	HT5011		1030604	M38591	U59748	X68277		X59417		U44975	U59863	HG3514. HT3708	HG3521.	HT3715		M16707	S77154	
M97936_at_	AF008445_at	D42073_at	X12451_at		MO1/30_dl	Z47087 at	±	-	HT5011_at_			7	at	X68277_at_	at	X59417_at_		_	at	HG3514. HT3708_at_	Γ		al	_s_at_	S77154_s_at_ S77154	

Figure 21

M79462_at_	M79462	lmyl	r with right and transcription factor PML (alternative products)	3.1	σ α	2	7 0	6.7	ď	,,	o C	0
			Brain expressed HHCPA78 homolog fhuman. HL.							0.0	0.0	0.0
, (((1		60 acute promyelocytic leukemia cells, mRNA,	,								
5/3591_at_	5/3591		2704 nt]	0.2	1.6	0	5.1	6.7	3.2	0.3	0.4	8
X14684 s at X14684	X14684	do.h	SSB Sjogren syndrome antigen B (autoantigen		,	,	,				-	
D84276 at	D84276	cd38	CD38 CD38 antigen (n45)	22.7	7.4.	J 0	ρί	ر ا ه	12.1	4.	9.4	9
M12174_at	M12174	arh6	ARH6 Abivsia ras-related homolog 6	1 2	000	153.3	1.0	9.0	3.02	210	34.9	132
U16811_s_at				1			5	0	7.7	ر ن		7
	U16811	bak1	Bak protein mRNA	6 0	3.7	0	σ «	v	2.7	α c	Ľ.	1
HG2167.	HG2167.				-			2		2.7	7	
HT2237_at_	HT2237	pkht31	Protein Kinase Ht31, Camp Dependent	8.6	5.6	4.3	7.8	6.5	~	0	ir C	2
X89985_at_	X89985	bcl7b	BCL7 B cell lymphoma protein 7B	3.2	2.1	3.2	5.7		4 3	0	0	0
Z48950_at_	248950	h3f3b	HISTONE H3.3		4.2	i α m	12	5 2	2	1	200	0.0
X61970_at_	X61970	psc5	PROTEASOME ZETA CHAIN	4.3	5.5	000	26	0.0	27	1 -	ά	7 9
			IMMUNODEFICIENCY VIRUS TYPE I ENHANCER	-				5	1	-	2)	5
X65644_at_	X65644	hivep2	BINDING PROTEIN 2	9.1	5.7	12.3	œ m		4.7	2.2	C	η.
M72885_rna1			GOS2 gene extracted from Human GOS2 gene 51					?		1	3	ţ
_s_at	M72885	G0S2	flank and cds	126.1	38	44 9	10.8	6	n V	10.4	17	10 7
L22342_at_	L22342	unknown	Nuclear phosphoprotein mRNA	3.8	9.7	11 4	4	9 1 9		1 -	1001	21.7
			Modulator recognition factor I (MRF-1) mRNA, 3'						+	?	17:17	
M62324_at_	M62324	mrf-1	end	4.8	8.6	10.2	7.9	٠ <u>-</u>	14.3	α	2	0
U01691_s_at											<u>-</u>	7
	U01691	annexinV	Annexin V (ANX5) gene, 5' untranslated region	8	3.6	4.3	6.2	φ	2.2	00	0	1 7
D10040_at_	D10040	fac12	FACL1 Long chain fatty acid acyl coA ligase	24.7	15.2	26.2	13.5	5.9	12.4	2.2	4.4	24.1
U96915_at	U96915	sin3	Sin3 associated polypeptide p18 (SAP18) mRNA	33	~	4.7	- 2	o u	7		-	,
X96719_at_	X96719	aicl	AICL (activation induced C-type lectin)	0	1.7		0 4			1 5	70	ν ο
S59049_at_	S59049	ier1	RGS1 Regulator of G-protein signalling 1	4.5	25.9	150	000	a u	-	2 4	100	2 5
			ACTIN, AORTIC SMOOTH MUSCLE (ALPHA.				1,1		7.7	5	0.51	4
X13839_at_	X13839	acta2	ACTIN 2)	0.1	0.7	1.2	7.5	ري 00	5.6	o	5.4	2
X54304_at_	X54304	mlcb	Myosin regulatory light chain mRNA	3.6	5.9	1.3	6.4		4.8	1.6	=	
K01396 at	K01396	, n	PI Protease inhibitor 1 (anti-elastase), alpha-1-	,		1			-	;	+	
5 0000	2220	aar	January positi	47.3	55.4	72.2	4.7	5.7	5.9	6.0	4.7	m

-			mRNA in the region near the btk gene involved in			-	_	-		-	F	Γ
L20773_at_	L20773		a-gamma-globulinemia	2.8	1.8	1.2	3.2	5.7	3.9	1.3	6.0	2.6
L37360_s_at_	137360	efna3	(clone hEHK1.L) EHK1 receptor tyrosine kinase ligand (EFL-2) mRNA	0.5	2.2	-	0	7.7	0	-	~	0
U03105_at_	U03105	b4.2	B4-2 protein mRNA	29.4	107	8	11.4		أبر	1 0	2 0	5 6
J04111_at_	J04111	nní	C.jun proto oncogene (JUN), clone hCJ.1	2.2	4.2	2.4	19.1	5.6	13.4	1.6	0.5	4
M86400 at	M86400	vwha7	YWHAZ Tyrosine 3-monooxygenase/tryptophan 5 monooxygenase activation protein, zeta	Ų	C	((l.				
1118937 24	1118937		Anathra Anathr	0 !	7.0	7.7	o o	0.0	8	2.1	0.1	7
X05908 at	X05908	anxal	ANX1 Append ((incorpting)	7.7	1.6	1.3	3.6	5.6	5.4	8:0	0	1.4
2000	2222	100	Thursday recognition intercepts (TRIP)	2.2	2.9	6.4	ç:/	5.6	5.5	2.8	0.4	3.6
L40379_at_	L40379	trip10	end of cds	34.8	37.1	33	5.3	5.5	7.6	22.2	6	13
M23254_at_	M23254	capn2	CAPN2 Calpain, large polypeptide L2	2.2	2.3	4.4	2.4		2.3	0.7	3.1	4.6
X96506_s_at_ X96506	x96506	nc2a 🌲	NC2 alpha subunit	1.8	1.4	0.8	4.8	5.5	2.4	9.0	0	-
D00760_at	0900	hc3	PSMA3 Proteasome component C3	9.4	4.2	8.6	8	5.4	3.7	1.4	4.6	12.4
S54005_s_at_ S54005	S54005	thymosinb10		4.2	8.6	1.7	т	5.4	3.7	4.4	3.2	9.0
U22398_at	U22398	pws	Cdk-inhibitor p57KIP2 (KIP2) mRNA	0	1.7	0.1	5.1	5.4	11.7	0.7	-	2.2
U68063_at_	U68063	srfs10	Putative splice factor transformer2.beta mRNA	1.4	1.8	0	1.8	5.4	2 9	1 2	9	C
X56841_at_	X56841	hla·e	HLA-E MHC class I antigen HLA E	0.7		5.7	5.8	5.4	11		0 -	α
AF014958_at	AF014958	ccr6	Chemokine receptor X (CKRX) mRNA	3.6	9.2	36.3	3.7		9.9	1 12	, 4 E	
	НG2917. HT3061	n a	Major Histocompatibility Complex, Class I, E (Gb:M21533)	7.5	7 6	0	u c			, c	0 0	
at	M97935	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	4.1	7.9	10.5			200	άσ		36.7
	X94232	MAPRE2	Novel T-cell activation protein	0.4	1.2	1			3.2	0.0	6.0	80
U28124_at_	028124	d1s1733e	Unknown product	7.1	5	14.7	25.1	5.2	12	2.6	E	3.3

Figure 2K

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HG544.	10044						ŀ		ľ	-	-	
HT544_at_	HT544	ecgf	Endothelial Cell Growth Factor 1	5.9	15.3	4.8	10.4	5.2	2.1	26.7	16.5	
J00105_s_at_	J00105	b2m	BETA-2-MICROGLOBULIN PRECURSOR	5.7	3 6	ď		r,	u u	-	0	-
U56402_s_at	U56402	spt5h	Chromatin structural protein homolog (SUPT5H) mRNA	0) [) L			0 0	1
X85133 at	X85133	rbbb6	RBO-1 mRNA	7.7		0	0,0	2.7	7)	-	7	7.6
Z71389 at	271389	defensinh2	Skin antimicrobial pentide 1 (SAD1)	0.0	2.3	Δ, t	4.2	5.2	30.4	0.7		1.3
M21186 at	M21186	cyha	CVBA Cytochromo b 245 plane 1		0.5	/:/	12	5.2	6.4	1.2	5.3	0.3
		2,00	OTENITO CONTROLLE D'245, AIDNA POLYPEDTIDE	2.7	8 /	2	1.6	5.1	1.6	6.0	0.5	2.5
M93425_at	M93425	ptpg1	FIRM12 Protein tyrosine phosphatase, non- receptor type 12	0		C	L (ı	(-		
S78085 at	S78085	pdcd2	PDCD2 Programmed cell death 2	0 -	1.0	20.0	7.5	2.1	2.3	 	2.4	7
X74104 at	X74104	cero	SCD2 Cignal cognoper and the first	C: 1	7	0.6	9	5.1	3.3	ō	0	0.3
714978 at	71/078	33.55	ALLA OF MEDA OF MEDICAL PECEPTOR, DETA	0.8	2	0.1	5.1	5.1	1.7	1.3	9.0	2.1
75 0 015 T	0/6417		ALTHA-CENTRACTIN	0.5	9.0	0	1.1	5.1	5.6	0	0	0
D42040_s_at_	D42040	ring3	RING3 PROTEIN		1 7	α-	7 3	u		-	,	7
HG2639.					+	?	?		1		7:7	1.7
HT2735_s_at												
	HT2735		Single-Stranded Dna-Binding Protein Mssp-1	8	2.6	2.5	σ	ľ	0			O C
X63679_at_	X63679	tram	TRAMP protein	26	40	σ	7 7) u	200	1	1 0	0 0
X89750_at_	X89750	hpe4	TGIF protein	5 7	7	2 4	200	7 4	0 0	1 0	7:7	0.6
D30755_at	D30755	NAF1	VIM Vimentin	25.0	0.00	5 0	n 0			ρ.,		U.
HG987.	HG987.			20.0	7.07	13.6	19.9	9.4	5.9	14.1	5.3	7.9
HT987_at_		igfbp7	Mac25	2	7.7	α	α	0	,	,		ç
X57985_rna2 at	X57985		GL105 gene (histone H2B) extracted from			i			,	7.1	5	7.7
X78687 at	X78687	1 100	Co man propries for majorites men. I allo men	Σ.Ο.	0.8	10.9	2.1	4.9	49.9	0.1	1:1	15.8
V10032 24	V10032	100	do gene encounig standase	0.4	0.7	0.1	3.2	4.9	2.7	6.0	6.0	3.2
170035 91	110032	SEK	Putative serine/threonine protein kinase	0	0	1.6	2.5	4.9	5.4	8.0	0	0
U36341_rna1			SLC6A8 gene (creatine transporter) extracted from Human Xo28 cosmid pressing transporter		_							
at	U36341	slc6a8	(SLC6A8) gene, and CDM gene, partial cds	C	,-	1	0	α	7	0		,
U40369_rna1			Spermidine/spermine N1-acetyltransferase		+	-	1	7	;		5	7.7
at	U40369	sat	(SSAT) gene	9.1	5.3	12.1	10.6	4 8	σ	9	7 7	ά
									,	;	-	2

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	1000	0	Nuclear chloride ion channel protein (NCC27)		,							
U93205_at_	093205	nccz/	MKINA	2.7	3.2	c!	S.	8.	1.6	0.4	3.6	c1 C1
1			GGTB2 Glycoprotein-4-beta							<u> </u>		
D29805_at_	D29805	b4galt1	galactosyltransferase 2	13.4	6	12.9	6.1	4.7	m	0.7	3.5	4.5
M10901_at_	M10901	gcr	GRL Glucocorticoid receptor	1.9	2	3.9	4.2	4.7	11.5	1.2	1.5	1.4
U03851_at_	U03851	capza2	Capping protein alpha mRNA, partial cds	0.4	1.5	0	3.9	4.7	4.9	1.1	0.5	1.2
U37547_at_	U37547	ciap1	IAP homolog B (MIHB) mRNA	4 8	4 7	179	3.7	4 7	27.3	1.1	1.7	10.7
			NATURAL KILLER CELLS PROTEIN 4				-					Γ
M59807_at_	M59807	nk4	PRECURSOR	20.5	2.5	10.6	11.1	4.6	11.4	5.6	4.8	16.3
M63438_s_at	$\overline{}$		GLUL Glutamate-ammonia ligase (glutamine							-		
_	M63438		synthase)	1.6	0.2	0.2	2.6	4.6	137.4	0	0	1.2
X05855 s.at	X05855		EEF1G Translation elongation factor 1 gamma	4.0	2.2	0.3	4	4 6			C	C
			BTG1 B-cell translocation gene 1, anti-							2		T
X61123_at_	X61123	btg1	proliferative	30.4	26.8	14.4	% 4	4.6	4.4	3.6	7.4	9.7
AB006782_at												T .
	AB006782	gal9	Galectin-9 isoform	1.7	3.5	1.1	6.9	4.5	3.6	4.5	9.3	H
D14874_at_	D14874	adm	ADM Adrenomedullin	18	20.1	46.2	3.4	4.5	10.4	2.5	5.2	16.1
D29642_at_	D29642		HYPOTHETICAL MYELOID CELL LINE PROTEIN 3	9.6	15.1	10.3	2.2	4.5	3.4	0.4	3.8	9.5
	HG4297.									-		
HT4567_at_	HT4567	TCPC4	Transcriptional Coactivator Pc4	5.6	2.7	8.4	6.4	4.5	6.3	2.5	4.3	9.5
U57971_s_at							-				-	Γ
_	U57971	atp2b3	Calcium ATPase isoform 3x/a mRNA	വ	3.9	1.9	1.5	4.5	1.6	0	_	6.0
X92106_at_	X92106	blmh	Bleomycin hydrolase	1	1.4	0	1.6	4.5	5.5	0.3	1.4	0
			2',3' cyclic nucleotide 3' phosphodiesterase gene						-		-	
D13146_cds1		-	extracted from Human 2',3' cyclic nucleotide 3'									
at	D13146	cub	phosphodiesterase gene	15.9	13.4	25.3	6.2	4.4	10.1	5.6	33	11.2
D38551_at_	D38551	unknown	KIAA0078 gene	7.3	5.6	3.9	2.8	4.4	3.5	0	9.0	2.8
			INTERFERON GAMMA UP REGULATED 5111						-			
L07633_at_	L07633	pa28a	PROTEIN PRECURSOR	5.1	8.1	13.1	Ŋ	4.4	9.9	2.3	4.3	20.1
,	M82882	elt1	ELS-RELATED TRANSCRIPTION FACTOR ELF-1	1.4	0.7	0.8	3.2	4.4	4	1.1	1.3	9.0
- 1	S82297	b2m	BETA-2-MICROGLOBULIN PRECURSOR	9.5	1.6	3.1	6.3	4.4	3.4	1.3	0	1.4
U04209_at	U04209	mfap1	Associated microfibrillar protein mRNA	1	2	4.8	1.7	4.4	6.5	0	0	5.9

17 632000	2000		GAPD Glyceraldehyde-3 phosphate	-					-			
/63_at_	000/63	psma4	dehydrogenase	6.1	4.5	m	10.5	4.3	9	7	11.2	37
D78132_s_at_D78132	D78132	rheb2	Kas homologue enriched in brain (RHEB) gene, Ras-related GTP binding protein gene	1	2.2	o C	۲,	7	,	- 1		-
.76200_at_	L76200	guk1	Guanylate kinase (GUK1) mRNA	1	8.4	0.2	3.3		3.5	1-	0.3	3.1
нG2915. HT3059 <u>_f_</u> at_	НG2915. НТ3059	hla	Major Histocompatibility Complex, Class I, E (Gb:M20022)	ý	e G	α	ι, α		0	-	,	Ĺ
M19645_at_	M19645	grp78	78 KD GLUCOSE REGULATED PROTEIN PRECURSOR	4 2				2 6	0 0		0,0	0.0
M79463_s_at 	M79463	myl	PML Probable transcription factor PML (alternative products)		7.6	13.3		4 4		20 7	0 0	2 -
S68271_s_at_	S68271	crem	CREM CAMP responsive element modulator	=	0	0 0	1 2	,	0	: -		1 0
U28488_s_at	U28488	c3ar1	Putative G protein-coupled receptor (AZ3B) mRNA	9	6 6	2 - 6	0 7		10.7	1 0	0 0	20 0
X74039_at_	X74039	płaur	Variant urokinase plasminogen activator receptor (uPAR2) mRNA, partial cds	1.6	15	7.3		2, 4	φ. 4. α	5 -	j u	3.2
X75042_at	X75042	nfkb crei	REL V.rel avian reticuloendotheliosis viral oncogene homolog	8	200	2		1 0	0 1	2 0	1 .	0.7
D30655_at_	D30655	eif4a2	EIF4A2 Eukaryotic translation initiation factor 4A (eIF-4A) isoform 2	8	o -			4.4	0 0	0.0	0.	9.4
M94880 f at	M94880	6 6 6	HLA-A MHC class I protein HLA-A (HLA-A28,	7	, r	4.7	9:1	1.4	3.7	8.	0.3	2.1
U03644_at_	U03644	0.00	Recepin mRNA	10.9	4.3	5.3	6.1	4.1	2.4	1.3	1.7	2.9
U50327_s_at -	U50327		Protein kinase C substrate 80K·H gene (PRKCSH)	1.0	-1	4 0	0.1	4 1	6.9	6.0		8.3
U60519_at_	U60519	casp10	Aboptotic cysteine protesse Mchd (Mchd) DNIA	i		2 [1 7	1	t.	5	4	0.5
U83463_at	U83463	pbp1	Scaffold protein Pbp1 mRNA	10	0.0	0.7	3.1	4 4	7.1	0	6.4	15.4
X77366_at_	X77366	nfe2 1	TCF11 Transcription factor 11 (basic leucine zipper type)					;	1 0	?		6.5
M63838_s_at	M63838	ifi16	Interferon gamma indured protein /IEI 167	2, 0	2 ;	10.4	χ, υ,	1.4	4.5		6.4	15.7
M76766 at	M76766	ptf2h	GTEOR General transcription foots. Inc.	5	4.0	0	5.6	4	4	0.1	0.1	2.8
1	22.5	16116.0	Idil 20 delieral transcription factor IIB	2	1.1	5.1	m	3.9	2.2	0.7	2.3	5

						111	ven	lo	rs:		N	ır ŀ	łaco	he	Π, ε	et al												
(8,7	0 0	0.	0.8	ГŢ	1	14.5	0.0) -	1	α	70	7.1			55.9	,	7.	0	0 0	0.0	1.6	,	† C	7		
	0.5	7 -		0.5	0	2		0.7	-	1.1	5	r.		1.4	C		34	(0.0	7	2 0		0.8	0	7 0	7.7	5.1	1.2
	<u>ين -</u>	1 0	?	1.2	1		1.9	0.1	6	0.c	6:3	~~		7.7	0	1	22.7	,	1	~		5		1 7		0 1	2.5	1.4
	0 C	100		3.7	4		25.2	10.5	-	10	1	9		8.0	ō		31.5	,	7:7	ν	, ,		8.0	-	1 7		2.5	4.4
0				3.8	α m		χ,	3.8	,		;	3.7	1	7	3.7		3.7	7 6		7,	200	0 0	3,0	ر. بر	2 2			3.5
C		4.6		2	5.6		0.5	2.3	7	2 -		4.2	,	13.3	1.0		5.3	ς L		4			20	<u>.</u>	ی			2.5
- 2			,	7	7.3	,	0	175.8	0	0.0		41.8	0		-		62.2	7		4	C	2 0	7.0	0.7	α	0 0		α.υ
000	7.2	0.0		4./	<u>N</u>		, ,	0	C	4		21.8	7 %		0.5		48.6	'n	1	2.5	19	2 0		7.8	29	, u	2.5	3.1
, r	4 8	0.7		n	8.2	0	0.0	2.2	C	1.2		28.7	3.6	2	0		24.1	2.5		<u>C1</u>	1.3	90	0	5.6	1.3	7 2) u	0.0
RAF1 V-raf-1 murine leukemia viral oncogene homolog 1	JUNB Jun B proto-oncogene	SMT3B protein	H A.B. Line BNA	Sodium/potassium-transporting ATPase heta 3	subunit mRNA	Bci-2 binding component 3 (bbc3) mRNA, partial cds			Pre-mRNA splicing factor SRp20, 5'UTR (sequence from the 5'cap to the start codon)	Mr 110,000 antigen		PIM1 Pim-1 oncogene	C5R1 Complement component 5 receptor 1 (C5a ligand)	LIPA Lipase A, lysosomal acid. cholesterol	esterase	IAP homolog C (MIHC) as BNA		VIM Vimentin		Fas-binding protein (DAXX) mRNA, partial cds	KIAA0138 gene	CRM1 protein		Rer1 protein	Serine/threonine protein kinase	Major Histocompatibility Complex, Class I, C (Gb:X58536)	NP Nucleoside phosphorylase	20016 0014 001000000000000000000000000000
raf1	junb	smt3h2	hía-b		atp1b3							pim1	c5ar		lipa	cian		vim		daxx		crm1		pex10	dyrk1a	hla∙c	au	
X03484	X51345	X99585	D49824		U51478	U82987	0,100	A97748	D28423	D64154		M16750	M62505		U04285	U37546		219554		AF006041	050928	Y08614		AJ001421	D86550	HG658. HT658	K02574	
X03484_at_	X51345_at_	X99585_at	D49824 s at		U51478_at_	U82987_at_	072207	197740-5-dl	D28423_at_	D64154_at_	M16/50_s_at		M62505_at_	U04285_s_at	78 346	U3/546_s_at			AF006041_at	-	D50928_at_	Y08614_at_	AJ001421_at	\neg)_at	HG658. HT658_f_at_	K02574 at	1

							ln	ve	nto	S:		N	ir	Ha	aco	he	n,	et	al.											
32.5	-	1 6	23.5	0.0	0	200	11/2	α			2.0	1 4		2 4	1		200	17	3	2.0		0	116	0.0		4		3.4	161	3.2
11.8	6		1.61	P.	0	9	000	0			7.1	4 4			2	σ α		α	2 6	6.7		0	22		1	60		3.7	8.6	1.3
27.3	-	1 1	0.0	3.5	0.7	-		1			ρį	25		7 -	1	ľ		0	2	7		9.0	0	-		0		2.5		3.3
11.5	7 0		1.00	20.5	1.5		22	3.2		(77.7	3.6	23.4	0 0	5	8.9	4.3		2 -			8.3	22.2	4.6		2.9		6.9		2.5
3.5	C.			?	3.4		3.4	3.4		0	0.0	8	m m	3	1	3.2						3.2	3.2			3.2		3.1	3.1	3.1
5.6	σ		11.4		3.4	6.5	4.5	3.5		0		2.6	15.8	~	}	4.6	4.3	3.4	a		***	3.7	13.2	3.7		3.9		5.7	7.1	2.5
21	m	1 7	49.2	2	0	8.3	4.1	2				0.5	22.1	4 7		13.1	4.4	=	-	-		0	23.7	0		2.6		7.4	27.1	1.9
19.5	2.1	16.1	210.1		0	1.7	12.4	2			1	4.0	6.1	3.9		5.3	4.4	2.2	2 %			0.5	1.2	1.2		2.4	-	5.5	14.1	3
9	2.8		20.7		0.8	3.4	6.3	4.3		~		П	14.3	6.1		18.5	3.7	6.0	2.4	i		0	4.6	6.0		2.3		8.5	24.8	1.3
Mac-2 binding protein mRNA	Heat shock protein (hsp 70) gene	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2	ADENOSINE A2A RECEPTOR	mRNA fragment encoding beta tubulin. (from	clone D·beta·1)	Nuclear domain 10 protein (ndp52) mRNA	IRF4 Interferon regulatory factor 4	P97 mRNA		Splice 1	PAGA Proliferation associated gene A (natural	actor A)	PEBP2aC1 acute myeloid leukaemia mRNA	KIAA0005 gene		Tubulin, Beta	PGAM1 Phosphoglycerate mutase 1 (brain)	Integrin linked kinase (ILK) mRNA	Protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA		IFNA gene (interferon alpha h2) extracted from	Human gene for leukocyte (alpha) interferon H	BETA: DEFENSIN 1 PRECURSOR	HSPB1 Heat shock 27kD protein 1	PROBABLE PROTEIN DISULFIDE ISOMERASE ER	60 PRECURSOR	HLA.A MHC class I protein HLA.A (HLA.A28,	B40, .Cw3)	KIAA0084 gene, partial cds	EIF2A Eukaryotic translation initiation factor 2A
тас2ър	hspala	GBP2	adora2a			ndp52	irf4	dap5	,			paga	am12			tubulinB	pgaml	Ę	ptp4a1		;	itna14	defensinb1	hsp27	!	grp58	-	nla·a	KIAA0084	
L13210	M11717	M55543	X68486		J00314	U22897	U52682	U73824	HC1400	HT1400		X67951	Z35278	D13630	HG4322.	HT4592	J04173	U40282	U48296		000	V00533	792/44	223090		249835		032129	D42043	J02645
L13210_at_	M11/1/_rna1 _at_		!		J00314_at_	U22897_at_	U52682_at_	U73824_at_	HG1400. HT1400 s at				- 1	at	HG4322.	HT4592_at_	J041/3_at_	U40282_at_	U48296_at_		V00533_rna1	T at	T	223090_at_		249835_s_at_	00000	넱		J02645_at

M29064 at	M29064	hnrna2h1	HNRPA2B1 Heterogeneous nuclear	000	3 %	C.	л. С	۲,	7	α	1	000
M36341_at	M36341		ARF4 ADP-ribosylation factor 4		1.5			3.1	2.6	1.9	0.4	80
U48807_at_	U48807	dusp4	Dual specific protein phosphatase mRNA	5.6	29.6	7.4	2.4	3.1	8.6	9.7	2.6	21.7
			KAI1 Kangai 1 (suppression of tumorigenicity 6,									
-			prostate, CDoz alfrigeri (RZ leukocyte antigen, antigen detected by monoclonal and antibody									
U77948_at_	U77948	bap135	(441)	Ó	0.5	0	1.5	3.1	2.7	0	0.7	9.0
			GNB1 Guanine nucleotide binding protein (G				-	-			-	
X04526_at_	X04526	gnb1	protein), beta polypeptide 1	1.8	m	8.0	3.8	3.1	3.5	6.0	1.4	2.6
l i	X52425	il4r	1L4R Interleukin 4 receptor	8.6	10	10	5.9	3.1	4.4	1.8	2	9.7
D14695_at_	D14695		APOA2 Apolipoprotein A II	3.7	2.1	0.1	4.4	3	8.3	4.0	9.0	4.8
			PTGER2 Prostaglandin E receptor 2 (subtype							-	\vdash	Γ
L28175_at_	L28175	ptger4	EP2), 53kD	6.0	0	1.1	2.3	m	17.4	0	0.5	1.2
U23070_at_	U23070		Putative transmembrane protein (nma) mRNA	0.8	1.2	4.8	2.2	3	6.2	0.2	0.1	1.
U32944_at_	U32944	dic1	Cytoplasmic dynein light chain 1 (hdlc1) mRNA	2.9	4.3	2.6	3.4	m	2.4	П	0.2	1.4
X81198_at	X81198	arcn1	COATOMER DELTA SUBUNIT	1.9	m	2.6	2.4	m	2.5	0.7	6.0	1.4
Y08682_rna1	665600	114			,			-				[
s at	108682 563566	cpt1b	Carnitine paimitoyitransferase type	0.3	. I.	6.0	9.9	m	6.1	8.8	4.5	7.1
D63506_at_	D63506	unc18-c	Unc:18homologue	2.2	1.7	2.5	3.7	2.9	2.5	1.2	0.1	7
L19067_at	L19067	nfkb p65	TRANSCRIPTION FACTOR P65	7.9	5.4	3.9	8.2	5.9	9.9	6	1.6	5.9
U47634_at_	U47634	b-tub4	TUBB Beta-tubulin	3.8	2.3	2.2	2.8	2.9	4.3	1.1	6.0	9.0
D26599_at_	D26599	psmb2	Proteasome subunit HsC7.1	4.2	2.7	4.9	2.2	2.8	7	1.6	4	4.1
D87078_at_	D87078		KIAA0235 gene, partial cds	0	9.0	0	3.3	2.8	5.3	6.0	0	0.1
HG3076.						-						
HT3238_s_at HG3076- HT3238	HG3076 HT3238		Heterogeneous Nuclear Ribonucleoprotein K, Alt. Splice 1	1 4		Δ	α	α	17.3	0	2.1	r.
HG3954.												
HT4224_s_at HG3954	HG3954.		Landsteiner-Wiener Blood Group Glycoprotein									
	H14224	Icam4	(LW) (GD:L2/6/1)	2.4	4.8	1.2	3	2.8	m	1.5	0.5	6.0
S74017_at_	S74017	nrf2		3.8	6.3	3.7	3	2.8	1.8	3.1	2.8	1.9
U67319_at_	U67319	casp7	Mch3 isoform alpha (Mch3) mRNA	1.9	4.7	12.2	3.5	2.8	6.1	3.1	6.3	13.2
U76764_s_at	U76764	cd97	CD97 CD97 antigen (leucocyte antigen)	14.8	10.71	3.6	14.5	2.8	2.3	1 7	2.3	7.5
-						1		7	,	-	1,1	٠.

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190911 24	1190911		Close 03/170 08/4					,				
7,5-110,000	11000		CIONE 2303Z INKINA Sequence	2	2.7	5.5	3.7	2.8	5.8	1.3	0.7	4
X72727_at_	X72727	hnrpk	HINKEN HETEROGENEOUS NUCLEAR Inbonucleoprotein K	4 0	-	7 0	10.6	a c	1-	0		0
	_		P85 beta subunit of phosphatidyl inositol 3.			;	2.01	0.7	11.0	0	7.7	ا د.ع
X80907_at_	X80907	pik3r2	kinase	4.2	_	14	0	α	1		-	-
X98172_at	X98172	casp8	MACH-alpha-2 protein	1.3	14	000	1 6	2 0		1 12	- C	00
AB000896_at						i		j	7			0.7
I	AB000896		Cadherin FIB2, partial cds	1.5	0.3	4	2.7	2.7	5.2	C	α C	α
D49738_at_	D49738		Ovtoskeleton associated protein (CG22) mBNA	0	C	-		ľ				
HG2855.	HG2855.	-	WANTE (2200) Hotel de participation de la constant	0.5	ρ;	2.1	2.	2.7	3.3	1.1	6.0	3.3
HT2995_at_	HT2995	hsp70	Heat Shock Protein, 70 Kda (Gb:Y00371)	α	,	C	0	,		Č	-	
L26247_at_	L26247	sui1	RPL3 Ribosomal protein L3	37		2 4	100	j	2 .	5 .	1:4	7
M27749_at_	M27749	flambda1	Immunoglobulin-related 14.1 protein mRNA	0	i u	2 4	0.7	7.7	4.7	7.7		2.2
			IL12A Natural killer cell stimulatory factor		5	n	0.7	7	4.3	9.5	4.3	1.2
M65291_at_	M65291	ii12a	(IL12A)	2.8	0 7	0 700	(·	2 7	00	-	-	- (
	1	•	UBE2A Ubiquitin conjugating enzyme E2A (RAD6			1	1		50.5	-	1	50.3
	M/4524	rad6a	homolog)	1.3	1.1	2.7	1.6	2.7	18.7	2	0	0
M95/8/_at_	M95/8/	sm22	22kDa smooth muscle protein (SM22) mRNA	С	5	2 1	2,0	1 0	7.00		3.6	
			RNA polymerase II largest subunit gene	}	;	7.7	,,	, · ,	7.07	0.0	۷.۶	4
X74874_rna1	1		extracted from H.sapiens gene for RNA pol II									-
-s_at	X/4874	rpol2	largest subunit, exon 1	1.8	m	D	m	2.7			α	0
				-						-	2	1
103161 at	103161	ţ	SRF Serum response factor (c-fos serum									
101000	101000	- in	response element binding transcription factor)	1.3	0.5	0	5.1	2.6	4.4	0.3	1.5	C
J04456 at	104456	loals 1	LGALS 1 Ubiquinol-cytochrome c reductase core				-				-	
M33764 at	M33764	odc.		0.7	2.8	1.1	1.6	5.6	3.5	1.5	-	80.0
		Tabo	ODOL OTHER DECARDOXYIASE 1	1.4	1.4	0.3	2.5	5.6	1.9	0.7	0.7	0
			GLCLC Glutamate-cysteine ligase (gamma-								-	
M90656_at	M90656	glclc	glutamylcysteine synthetase), catalytic (72.8kD)	C	С	, L	o	2	Ç	C		Ļ
U90543_s_at	1			-	,	?		0.7	13	7	n.0	٥
	090543		Butyrophilin (BTF1) mRNA	1.1	1.5	2.4	r.	2	7	-	0	
714744 gr	714244		COX7B Cytochrome c oxidase subunit VIIb	9.0	12	0 2		0 0	10			7 0
D14812_at_	D14812		KIAA0026 gene	1.7	22	5.2	3.5	2 5	2 0	2 10		0 0
									?	5	ţ.	7:7

Figure 2R

			_			-	_ ,	
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HG4582.	HG4582			-	-					-		
HT4987_at	HT4987		Glucocorticoid Receptor, Beta	2	1.6	1.5	2.8	2.5	-	1.3	1.2	0.2
M91670_at_	M91670	psma2	Ubiquitin carrier protein (E2 EPF) mRNA	5.4	5.9	m	C1.	2.5	5.2	0.7	3.1	6.9
U14969_at_	U14969	rpl28	Ribosomal protein L28 mRNA	1.6	2.1	1.5	2.1	2.5	2.7	0.7	0.5	1.1
U41740_at_	U41740	golga4	Golgin-245 mRNA	3.3	7.1	17.2	5.9	2.5	6.7	0.3	1.7	6.3
U77846_rna1					-							
s at	U77846		Elastin gene, partial cds and partial 3'UTR	5.9	1.3	3.6	m	2.5	3.1	1.7	0.1	1.3
Y08409_at_	Y08409	thrsp	Spot14 gene	4.6	2.4	4.5	2.9	2.5	9.1	0	0.4	1.8
			INDUCED MYELOID LEUKEMIA CELL		-							
L08246_at_	L08246	mcl1	DIFFERENTIATION PROTEIN MCL1	3.3	5.6	4.6	4.1	2.4	7.6	1.4	1.5	3.8
U32519_at_	U32519		GAP SH3 binding protein mRNA	0.4	1.1	3.1	2.6	2.4	2.2	4.8	6.0	1.4
Z29678_at_	229678	mitf	MitF mRNA	9.0	1.5	5.9	7.1	2.4	9.4	0.5	6.0	
D28118_at_	D28118	db1	DB1	1.7	1.7	1.5	2.6	2.3	4.9	1.9	E	1.9
HG3597.			Major Histocompatibility Complex, Class I									
HT3800_f_at_	HT3800	hla	(Gb:X12432)	7	5.8	3.3	6.5	2.3	3.6	4	4.3	1.6
J00207_rna2 at	100207	ifna2	IFNA gene (interferon alpha-a) extracted from Human leukocyte interferon (leif) alpha-a gene	0	0	o		0	2		, c	-
				5	7.0		1.5	5.7	5.4.7	5	3	1
J04617_s_at_	J04617	ef1a	EEF1A1 Translation elongation factor 1 alpha 1	1.8	1.6	1.7	1.8	2.3	3.8	1.3	0.8	1.1
M63835_at_	M63835	fcgr1	HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR	0	2.6	C	en en	23	62	2.6	0	23.1
U07806_s_at	0			}								
	00/806	top1	IOPI DNA topoisomerase /	3.4	5.6	4.8	4.2	2.3	1.9	0	1.4	3.1
(C		,	CYTOCHROME C OXIDASE POLYPEPTIDE VIA.									
715341_at_	A15341	coxpai	LIVER PRECURSOR	0.5	1.4	0	1.6	2.3	4.2		9.0	1.1
AE001294 at	016600	Con	ros iliniva lor transmembrane protein	2.8	10.1	26.4	4.1	2.3	9.7	3.9	6.4	29.3
	AF001294	ldi	IPL (IPL) mRNA	2.6	2.3	· ·	4	2	00	0	-σ «	۲,
D31884_at_	D31884		KIAA0063 gene	3.5	1.3	3.4	5.9	2.2	6.9	2.4		19
D38128_at_	D38128	ptgir	PTGIR Prostaglandin 12 (prostacyclin) receptor (IP)	29.8	34.8	71.9	7.9	2.2	16.2		2.1	65.6

000101												
HT5143_s_at -	HG1322. HT5143		Small Nuclear Ribonucleoprotein, Polypeptide C, Alt. Splice 2	m	28	4	4	0	, ,	1 4	,	4
L17131_rna1 _at	L17131	hmgiv	High mobility group protein (HMG·I(Y)) gene exons 1-8		α		7 %	,			1 -	-
M17733_at_	M17733	ptmb4	Thymosin beta-4 mRNA	. T	1.4	12	17	2 2 2	4.3	0 0	100	ν C
M59371_at	M59371	eck	TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR		r	r.	0	0		-	2 -	0 0
M59815_at_	M59815	c4a	C4A Complement component 4A		3.9			12:2		0.5	1 8	2 <u>1</u>
M74447_at_	M74447	tap2	TAP2 Transporter 2, ABC (ATP binding cassette)	2	e 0	24 R	- 2	0	0.0	7	, C	25.2
M92843_s_at	M92843	tto	ZFP36 Zinc finger protein homologous to Zfp.36 in mouse			i u				,		1 0
X78925_at_	X78925		ZNF2 Zinc finger protein 2 (A1.5)		0 0	100		2.2	0.4	4.0	7.0	0 0
D87116_at_	D87116	mapkk3	DUAL SPECIFICITY MITOGEN.ACTIVATED PROTEIN KINASE KINASE 3	13.5	6 9	×	100		0	2 4	7	7
M54915_s_at _	M54915	pim1	PIM1 Pim-1 oncogene	17	13.7	37.2		2		0		, r,
U20734_s_at	U20734	quni	JUNB Jun B proto-oncogene	15.9	o C	7 4	σα	0		000	-	; -
U22431_s_at	U22431	hif1a	MODE FINAN		2 4	, ,		,		3 -		1 (
U24166_at_	U24166		EB1 mRNA	127	, <u>c</u>) -	0.4	2 - 2	2.5	1.6	0 0	5.0
U32680 at	U32680	bts	CLN3 Ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmever, voor disease)	, c	0		-		1 1			1 1
L36870_at_	136870	jnkk1	JNK ACTIVATING KINASE 1			7-1-	7 4	7.7	5.0	7 0	9 6	770
M13452_s_at	M13452	cmdla	LMNA Lamin A	0	α	- 2		1		1 0	2 -	1.7
U00115_at_	000115	bcl6	BCL6 B cell lymphoma protein 6 (zinc finger protein 51)	4.5		0		1 0	13.5	0	× ×	0 0
U04343_at_	U04343	98po	CD86 CD86 antigen (CD28 antigen ligand 2, B7. 2 antigen)	1.6	8.1	9		2			4 6	16.9
U80669_at_	080669	nkx3a	Androgen regulated homeobox protein (NKX3.1) mRNA	8.4	0	0.2	2.8	<u>c1</u>		0		4.0
Z29505_at_	229505		Aipha-CP1 mRNA	1.5	1.3	0.5	3.8	2	4.4	1.5	9.0	0.8

D00017_at_	D00017	anx2l4	ANX2 Annexin II (lipocortin II)	1 2	3.2	10	1 2	-	00	,	1	(
D10522 at	010522	300	MACS Myristoylated alanine-rich C-kinase	-	3.5		2	1.9	7.7	n Ti	2,	0
D25274 at	D25274	raci	Dandomly company DNA		3.2	10.3	4.7	1.9	2.9	2.3	3.2	5.1
141887 rna1		123	Selicina foota	2.9	4.7	6	3.6	1.9	8.3	0.7	1.2	7.8
at	L41887	sfrs7	Spilcing factor, arginine/serine-rich / (SFRS7)	o C	((
M73547_at_	M73547	d5s346	POLYPOSIS LOCI IS PROTEIN 1	0 0		5 0	7.7	6.	<u>ر</u> س	4.4	3.1	1.4
U62962_at	U62962	eif3s6	Int-6 mRNA	5 6	5 C	5 (2	1.9	10.6	1.5	0.5	0
	U89505	rbm4_lark	Hark BRNA	5.0	0.		1.2	1.9	0	0.4	1	1.3
V00536 rna1			LENG ACCO CATACONS	1.3	1.6	4.2	1.8	1.9	1.7	1.4	1.1	5.4
at_	00536	ifng	ir No gelle extracted from Human immune interferon (IFN:gamma) gana			,						
X75755_rna1		2	Series Series	3.4	7.7	124.2	46.7	6:1	25.7	6.0	1.4	27.8
_s_at_	X75755	sfrs2	PR264 gene	ı.	C	7		-			(,
X03000 at	CCCCCX	, , , , , , , , , , , , , , , , , , ,	Protein tyrosine phosphatase (tissue type:	2		3		1.9	2.3	4.0	7.0	o)
722250	02666	odsnn	Toreskin)	2.2	1.5	10.7	2.6	1.9	4.2	0.3	0	3,8
Y00285_s_at_	Y00285	igf2r	IGF2R Insulin-like growth factor 2 receptor	0.8	1 4	0	1	ō	-	2	,	,
038/01 34	039401								2		7	2
20401-at-	030431		ATPUTHETICAL MYELOID CELL LINE PROTEIN 7	0.7	0	1.2	1.7	1.8	7	0.4	0	00
D45370_at_	D45370		Apmiz mkina for GS2374 (unknown product specific to adipose tissue)	-	- 0	(
D49400_at_	D49400		Fetus brain mRNA for vacinalar ATPasa	1 0	2 0	3.6	7.7	χį	4	4.1	1.2	2
M26708_s_at				0.0	0.0	5	2.3	8.	1:9	-	6.0	5.2
ł	_	ptma	PTMA Prothymosin alpha		- 0	C	0	-	-	((- (
M94856_at_	M94856	fabp5	FATTY ACID BINDING PROTEIN, EPIDERMAI		1		0 0	0 0	י פ	4.0	8:0	1.3
X06614_at_	X06614	rara	Receptor of retinoic acid	0 0	10	5 5 6	n -	ρ.	Σį	77	1.4	2
X17093 at	X17093	hla-cda12	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F AI PHA CHAIN PBECLIBSOD	2				0	5	5	5.0	E.
			ATEA CAMP dependent transcription (2)	12.7	8.4	5.2	5.3	1.8	4.3	21.8	12.4	2.8
D90209_at	090209	atf4	4 (CREB2)	4.5	3.8	10.5	6.2	1.7	5.4	α	7	α
HG417.	HG417.											
H141/_s_at	H141/		Cathepsin B	0.3	1.5	1.1	1	1 7	2	, L		
M57710_at_	M57710	galbp	LGALS3 Lectin, galactoside binding, soluble, 3 (galectin 3) (NOTE: redefinition of symbol)	0.5	4.0		1	-	α -		1.2	5 6

	;	;	,)								
-	C	<u> </u>		o	0	7	1 7	7.	MANB Mannosidase alpha.B (Ivsosomal)	man2b1	1005572	10000/2_s_d
0.3	0.9	0.7	0	0.9	0.7	0	0	0	protein 1 (51C protein)	Inppl1	L36818	L36818_at_
	-	i	-						INPPL1 Inositol polyphosphate phosphatase like	:	0	(
0	0.1	1.3	0	6.0	9.0	0	0.7	0.1	mRNA	iqgap1	L33075	L33075_at_
									Ras GTPase activating like protein (IQGAP1)			
0.8		1.2	0	6.0	0.3	0	11	0.5	ANT3 Adenine nucleotide translocator 3 (liver)	ant3	J03592	J03592_at_
C	ō	0	0		0	0	6.0	0.1	mitochondrial (aspartate aminotransferase 2)	got2	M22632	M22632_at_
					-				GOT2 Glutamic oxaloacetic transaminase 2,			
0	0	0	0	1.1	9.0	0	0.1	0	KIAA0131 gene, partial cds	RhoGAP4	X78817	X78817_at_
0.5	0.8	0.1	0	1 1	. 5	0	60	0 8	PABPL1 Poly(A)-binding protein-like 1		U68105	
9		3	,									U68105_s_at
α	7	0 7	α	-	4 7	en en	2	21.8	DAF Decay accelerating factor for complement (CD55, Cromer blood group system)	daf	M31516	M31516_s_at
	>		1	?	7		,	}				
	- (,	,	,	(((Clone CIITA-8 MHC class II transactivator CIITA	÷	118259	1118259 at
0.1	4.3	0.5	0	1.3	1.7	0	0.2	1	PRECURSOR	hspa9	L11066	L11066_at_
									MITOCHONDRIAL STRESS-70 PROTEIN			
0.8		13	0	1.3	2.2	0.3		0.7	KIAA0168 gene		029990	D79990_at_
0.5	9.0	0	0	1.3	0	0	0	0	PUTATIVE PROTEIN PHOSPHATASE 2C	pp2c-like	D13640	D13640_at_
0	0	0.2	0	1.4	1.1	0	0.7	6.0	Nucleolar protein p40 mRNA		U86602	U86602_at
2.1	0.8	Ó	3.2	1.4	1.4	2	-	0.7	Muscarinic acetylcholine receptor gene	chrm1	M35128	M35128_at
0.1	2.8	Ö	11.2	1.5	2.3	9.0	1.3	1.6	homologue (C-terminus)		X04347	X04347_s_atX04347
				_					Liver mRNA fragment DNA binding protein UPI			
0	0.2	0.1	0	1.5	0.5	0	0.7	0	Uncoupling protein homolog (UCPH) mRNA	ucp2	094592	U94592_at
0.4	0.5	1.6	O	1.5	0	0	1.4	0	Clone 23665 mRNA sequence	unknown	U90913	U90913_at_
2.5	O	2.4	2.4	1.5	6.3	0	2.6	0	TESK1	tesk1	D50863	D50863_at_
1.3	0.3	1.2	1.8	1.5	2.2	0	1.2	1.3	(Icap·1a) mRNA	icap-1b	AF012024	at
									Integrin cytoplasmic domain associated protein		_	AF012024_s_
3.5	0.7	0.4	2.7	1.6	4	1.4	9.0	1.4	Orphan nuclear hormone receptor		230425	Z30425_at_
1.5	3.3	2.9	4.4	1.6	4.2	3.4	m	6.1	PRG1 Proteoglycan 1, secretory granule	prg	X17042	X17042_at_
4.2	m	0.4	133	1.6	2.2	2.2	2.1	0.5	TFIID subunit TAFII55 (TAFII55) mRNA		U18062	U18062_at_
0	0.8	6.0	0	1.6	0.5	0	ī	0	CD33 CD33 antigen (differentiation antigen)	cd33	M23197	M23197_at_

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									_															
	2.4	-	C	0.8				10	0 4		4.0	0	0.5	,	7.7	0			2.3	0		0	0	0
-	4	6.0	to		İ		1 4	0	9.0		9.0	o		ά	0.	4.			0	0	T	0	0.1	0.5
	0.3			1.5			0	1.2	8.0		3.2	0.7	2.5	7	2	0			0	1.4	\vdash	9.0	1.2	9.0
	0	0	0	0	-			0	0		0	0	0	-	7		_		0	0	\vdash	0	0	0
0	6.0	6.0	80	0.8	İ		α C	0.8	0.8		0.8	0.8	0.7	7.0	 	0.7			0.7	0.7	-	0.7	0.7	9.0
)1	2.1	0	0.4			00	8.0	3.5	-	0.1	0	8.0	, m		0,2	<u> </u>		0	0.3		1.4	1.4	0
	4.7	2.5	0	0	-		ر ا	0.3	0		0	1.8	0	0		0			0	0		0	0	0
7 0	3.7	0		0	-		1 2	6.0	9.0		6.0	0	0.4	0	4.	- 0			1.1	6.0	_	0.2	0.7	1
	210	0	0	0	_		-9	0	9.	_	2	7		0					0	1		0	0	0
		O					ō		-1		0.2	0.7	0.1							0.1				
Tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds	Biliverdin-IXalpha reductase mRNA	ALPHA CENTRACTIN	NADPH-flavin reductase	KIAA0179 gene, partial cds	ITGAM Integrin, alpha M (complement	COMPonent receptor 3, alpha; also known as CO11b (0170) macrophage antigen alpha	polypeptide)	M6PR Mannose receptor	SSBP Single-stranded DNA-binding protein	Silencing mediator of retinoid and thyroid	normone action (SMRT) mRNA	Translation initiation factor elF-4gamma (partial)	ORF, Xq terminal portion	DNA-DIRECTED RNA PÖLYMERASE II 23 KD POLYPEPTIDE		Tyrosine Kinase Syk	ERCC1 Excision repair cross-complementing	rodent repair deficiency, complementation group	I (includes overlapping antisense sequence)	Clone 23693 mRNA sequence	ATP5D ATP synthase, H+ transporting,	mitochondrial F1 complex, delta subunit	RETINOBLASTOMA BINDING PROTEIN P48	KIAA0037 gene
	blvra		blvrb	kiaa0179			cd11b	mmr	ssbp	Ç	ncorz			polr2e		syk			ercc1		7 12 14	атрэд	rbp48	adcy/
U12595	U34877	X82206	D26308	D80001			J03925	M93221	M94556	27146	03/146	234918	D16469	D38251		HG3730. HT4000		2010184	WI13194	U79254	00400	A03422	X/4262	1025538
U12595_at_	U34877_at_	X82206_s_at_ X82206	D26308_at_	D80001_at_			J03925_at_	M93221_at_	M94556_at_	1071701	U3/146_at_	Z34918_at_	D16469_at_	D38251_s_at_	HG3730.	HT4000_s_at HG3730		1010104	M13134 dt	U79254_at	2000	Ab3422 at	X/4262_at_	U25538_at

Figure 2W

							111	ve	ntors		-	Nir Ha	ac	ohen,	et	' a	l.										
	0	0.7		3	ा	0			0.0		0		0		0	0	0	0.4	0	3.8	0	6.0			0	ा	-
	0	3.2	C	7.0	2	0.1	Ċ	0.0	0.0	0.3	0		1.8		0.7	0	0	0	9.0	3.8	0	0.7		(3 r	0.0	Ċ
	0	0.7	0	0 0	ر د د	0	Ó	? > -			0.2	,	9.0			0	1.7	1.7	0	0	0	2.3		0	χ. Σ.	5	
	Ó	0	C	5 0	5 0	5				5	0	,	5		5	0	0	0	0	1.9	0	0		Č	5 0	5	
	9.0	9.0	0	5 0	0 0	9.0	C				0.5		0.5			0.4	0.4	4.0	0.3	0.3	0.2	0.2		0	7.0	7.0	0
	0.7	2.1	C		5 6	5.0	-	100			0		0.5		1.4	1.1	3.5	1.2	0	0	0	0		-	10	+	~
	0	0				7	C	5 0			0		5		5	0	0	7.7	0	3.8	0	1.7					C
L	0.4	1.3		0			0	0			0.8	C	>		0.0	0.7	0.5	2)	0.9	0	0	1.4	<u>.</u>	0	1 0		0.3
	0	1.2	0.3	C		2	1.2	-	· C		٥	-	2	- 6			0.5		5	0.6	5	8.		40	- C		_
	4	-				-									1									_	1		
PTGS1 Prostaglandin endoperoxide synthase 1 (prostaglandin G/H synthase and	(cyclooxygenase)	ryndoxal kinase mKNA	SNRP70 U1 snRNP 70K protein	SCA1 Ataxin 1	Sds22-like mRNA		A2M Alpha-2-macroglobulin	ESD Esterase D/formylglutathione hydrolase	Membrane-associated protein (HEM.1) mBNA	PCCA Proniony.coa carboxylasa schoic	י בייין יייין	LIMIKI gene (LIMIKInasel) extracted from Human LIMIKinasel and alternatively spliced [LIMIKinasel (LIMKI) gene		PACE Paired basic amino acid cleaving enzyme (furin, membrane associated recentor protein)	MAPKAP kinasa (3nK) mPNA	Transcriptional potitional College	Dynamitin mBNA	KIAAO246 good partial ada	Brk mDNA for tyroning Line	Stac	KIAAA332 martial ada	innouzza gene, parnai cus		Transcription Factor liia	ADORA3 Adenosine receptor A3	Chromosome 16p11.2 BAC Clone CIT987SK.	234F9 complete sequence
	COXI		rnpulz		ppp1r7		a2m	esd	hem1	Dcca		limk1		fur	3pk			kiaa0246		stac				TFliia	adora3		
000	909811	000000	X04654	X79204	67/057		M11313	M13450	M58285	879219		U62293		X17094	U09578	1129175	U50733	D87433	X78549	D86640	D86976	2	HG4312.	HT4582	L77730		U46025
ME0070	189606 at	00000	ţ		Z50749_at_	M11313_s_at		M13450_at	M58285_at_	S79219_s_at	1	U62293_rna1 _s_at_		X17094_at_	U09578_at	Ι		Γ	T	T	Τ		s_at		L77730_at_		U46025_at_

Figure 2X

			Naip gene (neuronal apoptosis inhibitory		-		-		-		-	ſ
			protein) extracted from Human basic									
0			partial cds, neuronal apoptosis inhibitory protein									
U80017_rnaz _at_	U80017	gtf2h2	(naip) and survival motor neuron protein (smn) genes	C	C	C	, ,	C		(7	(
			H-IDH gamma gene (NAD(H) specific isocitrate		5		3	7.7	5	1		9.
			dehydrogenase gamma-subunit precursor)									
18b2_621897			extracted from H.sapiens IDH gamma gene and									
_at	268129	idh3g	TRAP delta gene	0	0.2	0	C	0.0		1 7	~	
M64009 24	0000	1 1 1	High density lipoprotein binding protein (HBP)				-		,			
111701	111110	daini	TIKINA	0.5	0.1	0	0.3	0.1	0	9.0	0.6	0
ı,	011/91	cak	CCNH Cyclin H	0.7	2	0	c	0	c	000	α	0
D38521_at_	038521		KIAA0077 gene, partial cds	0.2	0	C	C	c		100	0 0	
D80000_at_	080000		KIAA0178 gene, partial cds	1.1	0	c	0		o	0 0	0.0	7 0
HG2274.	HG2274.							,	5		2	5
HT2370_at_	HT2370		Rna Polymerase Ii, 14.5 Kda Subunit	0	C		C			-	0	0
			INTERFERON-ALPHA/BETA RECEPTOR ALPHA		,	1	,	-		+	0.0	וֹה
J03171_at	J03171	ifnar1	CHAIN PRECURSOR	Ö	0.1	ď	C	С	σ	0		
			HMGCL 3-hydroxymethyl-3-methylglutaryl-		-		,	,		3	-	7.0
			Coenzyme A lyase									
L07033_at_	L07033	hmgcl	(hydroxymethylglutaricaciduria)	0	-	2.3	C	C	C	α		0
			GNA11 Guanine nucleotide binding protein (G					,	,	2	1	7
M69013_at	M69013	gnal1	protein), alpha 11 (Gq class)	0	0	0	C	C	C	Č	Ċ	
M80397_s_at			POLD1 Polymerase (DNA directed), delta 1,			-			,	+	}	
	M80397	pold1	catalytic subunit (125kD)	0	0.2	0	Ċ	C	C	-	-	
M956/8_at_	M95678	plcb2	PLCB2 Phospholipase C, beta 2	0	0	0	c	0	0 0	1 0	5 0	
			Fatty acid synthase {3' region} [human, breast			-	+	,		-	7	7
580437_s_at	580437		and HepG2 cells, mRNA Partial, 2237 nt]	0.4	Ó	0	0	C	C	7	۲	0
1			Putative holocytochrome c-type synthetase	-				+	,	 	-	31
U36/87_at_	U36787	hccs	mRNA	0	0	C	C	_		-		
U51269_at_	U51269	arvcf	Armadillo repeat protein mRNA	0	C	c	0			-	7 0	7
U51333_s_at					,		1		5	7	0.5	-
) () () () () () () () () () () () () ()	U51333	hk3	HK3 Hexokinase 3 (white cell)	1.5	9.0	ō	0	Ö	-	0 7	Ġ	ď
U51336_at_	U51336	itrpk1	Inositol 1,3,4-trisphosphate 5/6-kinase mRNA	0	C	c	0.5	0	, -		; -)) (
				,	>	5	5	>	5	5	7:7	7.0

	_										
	dab2	micegan esponsive prosprioprotein (DOC-Z)	C	C	č		-		-	-	<u> </u>
		Mitochondrial NADH dehydrogenase-ubiquinone	<u>, </u>	,		5	5	5	5	0.4	5
		Fe-S protein 8, 23 kDa subunit precursor									
		(NDUFS8) nuclear mRNA encoding	-			-					_
U65579	ndufs8	mitochondrial protein	C	-0	-	_	(-		
172514		C2f mRNA		0 0	5	5	5	5	1.5	0	0
17766E			j	0	0	0.3	0	0	0.5	2.8	C
3		RIVASEP protein p30 (RPP30) mRNA	6.0	60	C	7 0	c	c	9 0)
		RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASF		-	,			7	0.0	0.0	9
X59543	rrm1	M1 CHAIN			C	L.	-	-	1		
		Cellular adhesion regulatory molecule Thuman		1	5	0.0	5	5	5	0	0
(65784_s_at_ X65784	car	mRNA, 429 nt]	0	-	,	(
(91257_at_ X91257		SERYL TRNA SYNTHETASE	0.0	10	7.7	5	5	0	3.3	9.0	1.5
X92762		Tafazzine protein	0.0	7.7	12.2	0.4	0	0	1.4		6.2
V07750	41.0		2.8	0	0.5	0.7	ō	ō	С	1	0
	11131112	Myosin heavy chain 12	0.7	0.8	0.7	С	c	C	- 2	0	0
6	,					+	}	7	7:5	2	7.7
411559_at(411559	acol	IREB1 Iron-responsive element binding protein 1	0.1	0.2	0	C			<u> </u>		-

Figure 2Z

affylD	GBA	gene symbol	gene Name	4000	1000			- [į
X67325_at_	X67325	ifi27	INTERFERON-ALPHA INDUCED 11.5 KD		0.00	ופרח	ıpra	npr8	tpr8	ican	mcan	tcan
X02530 at	YOOKSO		INP10 Interferon (gamma) induced cell line;	135.8	143.4	618.8	265.8	192.2	498.1	20	212.1	604.2
3	005000	010	protein 10 from	12.5	13.1	442.2	137.9	290.4	501.4	5.4	205.9	451.4
M65290_at_	M65290	i12b/p40	(IL128)	71.0	261 5	r 300	(0				
U59286_at_	U59286	itac	Beta-R1 mRNA, partial cds	27.5	27.02	0.00	5	2.3	- 1	32.8	76	412.7
M13690_s_at			C1NH Complement component 1 inhibitor	04.0	9./2	237.9	201.6	207.8	340.8	3.8	74.4	389.7
	M13690	clnh	(angioedema, hereditary)	16.9	34 1	200	ď	100		((
U37518 at	U37518	trail	TNF-related apoptosis inducing ligand TRAIL		,	200	0.01	7.5.0	7.00	0.0	30.1	358.9
U29680_at	U29680	bcl2a1	Bci-2 related (Bfl.1) mRNA	14.7	34.2	134.3	171	7	590.2	5.7	109.1	318.2
X72755_at_	X72755	mig	Himip mRNA	105.3	97.9	678.7	40.7	35.7	117.5	4	8.3	1791
X07834_at_	X07834	sod2	SOD2 Superoxide dismitase 2	3.2	5.2	68.3	59.4	52.3	58.6	1.6	77.5	1286
U88964_at_	U88964	hem45	HEMAS mena	2/./	104.1	240.9	34.7	92.1	91.6	9.6	17	1165
				34.6	43.7	191	27.2	15.5	73.3	80.80	43.4	1161
X04602_s_at_ X04602	X04602	il6	IL6 Interleukin 6 (B cell stimulatory factor 2)	408 5	370 2	2 7 2 6 1	L C	I.				
X65965 s at X65965	X65965	CPCG	SOD-2 gene for manganese superoxide	000	3,2,5	C./021	0.0/	0.0	269.4	14.6	43	目
M62403 s at	20222		Usmutase ICEDB4 Issuer III.	233.7	149.2	204	143.7	86.3	86.3	10.6	35.0	100 3
	M62403	igfbp4	der brite insulin ilke growth factor binding protein 4	L	i						3	100.5
				5.01	2.5	32.7	61.8	17.5	37.9	6.8	9.1	104.6
M33882_at_	M33882	mx1	MX1 Myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein 578)		(i						
U52513_at_	U52513	ifit4	RIG-G mRNA	25.1	100.8	84.7	80.3	152.2	89.8	34	397.3	102
M24594_at_	M24594	g10p1	IFI56 Interferon induced protein 56	100	27.5	20.07	32.1	84.6	86		39.1	94.7
1133017 at	1133017		Signaling lymphocytic activation molecule	2	01)	0://	90.0g	99,7	141.1	18.6	248.6	89.6
	022017	Sidili	(SLAM) MKNA	320.7	343.9	685.7	4.8	25.8	m	2.7	24.4	84.5
X02875_s_at_	X02875	oas1	OIAS (2'.5') oligoadenylate synthetase	16.7	30	48.7	41.5	58	1177	C A	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	0
at	98866X	mcp2	MCP.2 gene	ĭ							2	†
V00594_at_	V00594	mt2a	Metallothionein isoform 2	1,5021	51	26.3	42.9	82.6	47.9	4.8	23.8	79.5
				1003.1	1098.4	143.4	3/1.1	414.5	107.8	3.3	261	74.2

Figure 3A

			PTGIR Prostaglandin 12 (prostagyclin) receptor									
D38128_at	D38128	ptgir	(P)	α ος	0 7 0	,	٢	(,	,		
U77643_at_	U77643	k12	K12 protein precursor mRNA	0.7	04.0		, u	7.7	16.2		2.1	65.6
			TUMOR NECROSIS FACTOR: INDUCIBLE	,	2.5	0,00	4.0	7.7	11.4	7 / 7	9.4	63.3
M31165_at_	M31165	tnfaip6	PROTEIN TSG-6 PRECURSOR	172.2	163.5	624 1	80.8	100	0	ı	L	
L31584_at	L31584	ccr7	CMKBR7 Chemokine (C.C) receptor 7	58.1	87.3	980	22.00	7.00		7 / 0	0.0	28.6
U3/546_s_at	1137546				5	1200	5:53	03.0	0.50	6.07	=	56.3
U04636 rna1	+-	Clapz	IAP nomolog C (MIHC) mRNA	54.1	48.6	62.2	5.3	3.7	31.5	22.7	34	55.9
at	004636	cox2	Cyclooxygenase-2 (hCox-2) gene	-	0	(
M57731_s_at			Supering Chack El Barre		120.8	908.6	15.3	13.8	87.4	5	4.7	54.9
-	M57731	gro2	GRO2 GRO2 oncogene	30.1	7	5 507						
U72882_s_at	_		Interferon induced leucine zipper protein (IFP35)		† †	0.00	7	δ.4	32.2	13.8	11.7	53.6
U50527 s at	U72882	ifi35	mRNA, partial cds	23.2	58.9	39.5	22	26.7	21.2	20.3	29.3	50 B
	U50527		BRCA2 region, mRNA sequence CG018		,		-					
				ה ה	10.4	/0.1		3.3	18.4	3.3	13.9	50.7
L05072_s_at_ L05072	L05072	irf1	IRF1 Interferon regulatory factor 1	48.2	24.5	9	63.7	ä	7 00	C		
AU45UU_at_	X04500	1115	IL1B Interleukin 1, beta	100 3	508 2	0 7 7	3	200	47.67	10.0	34.0	20.5
			Hepatitis Cassociated microfubillar aggregate	5:27	220.3	104.4	7	17.0	20.2	24		48.7
D28915_at	D28915	mtap44	protein p44	α	200	73.6		1, 7,		(i t	1
U53830_at_	053830	irf7	Interferon regulatory factor 7 (humirf7) mRNA	426	130	30.0	. 0	1 2	244.0	13.3	15.5	48
M21121_at_	M21121	rantes	SCYA5 Small inducible cytokine A5 (RANTES)	7287	5617	01 40	38.8	72.5	49.2	51.4	43.1	47.5
			MX2 Myxovirus (influenza) resistance 2 homologia):100	4.00	1	396.6	115.3	113.6	87.4	43.7
M30818_at_	M30818	mx2	of murine	21	74.4	100	0	0	Ç	(
X02910_at	X02910	tnfa	TNF Tumor necrosis factor	144.1	225.5	115.7	72.7	506.3	400	27.00	39.4	43.2
0450/3 al	D42073	rcn1	Reticulocalbin	5.7	18.4	61.3	10	7.5	13.7	2.6	110	43.7
X57522_at_	X57522	tap1	TAP1 Transporter 1, ABC (ATP hinding cassette.)	0	,				-			
U03891_at	103891	unknown	Phorbolin I mRNA nartial cds	04.0	442.3	48.3	/6.1	53.3	47.7	11.6	31.7	41.3
AB000115_at			coo ma no f	43.8	28.9	21.9	189.3	58.3	23.3	4.4	9.6	39.3
ı	AB000115	unknown	mRNA .	σ	- 6	2	C			-		
M9/935_s_at			SIGNAL TRANSDUCER AND ACTIVATOR OF			24.3		20.3	7.87	3.4	6.1	37.6
104164 21	M97935	stat1	TRANSCRIPTION 1. ALPHA/BETA	4.1	7.9	10.5	2.5	r,	12.2	σ	17.0	26 7
304104 at	304104	11117	RPS3 Ribosomal protein S3 /wrong name	25.8	57.2	37.7	34.5	45.6	79.3		50.5	25.7
									2	,	2.5	٠ ٢

- nesp	onse of Denantie Cens to u	
Inventors:	Nir Hacohen, et al.	

-	_		G1P2 Interferon, alpha-inducible protein (clone						-		-	
M13755_at_	M13755	isg15	[F] 15K)	214.1	545.6	57.4	253	662	100.2	302.7	208.8	34.3
S59049_at_	S59049	ier1	RGS1 Regulator of G-protein signalling 1	4.5	25.9	15.9	2.2	5.8	9.1	9.9	10.8	34
L15702_at_	L15702	bf .	BF B-factor, properdin	46.3	64.4	85.6	3.3	7.9	7.8	5.4	6.5	33.8
L19779_at_	L19779	h2a	Histone H2A.2 mRNA	53.2	154	83.4	40.2	122.8	65.8	7.9	10.8	33.4
M14660 at	M14660	910n2	ISG-54K gene (interferon stimulated gene)	C u	ď	0,00	-		2	(1	3
L13210 at	L13210	mac2bp	Mac-2 binding profein mRNA		19 5	27.3	109	312.4 2 E	200	2 2 2	o	33.4
X66401 cds1			LMP2 gene extracted from H sapiens genes	1	2	17	5	?	71.0	6.12	0.1	32.3
_at	X66401	tap2	TAP1, TAP2, LMP2, LMP7 and DOB	30.6	20.6	32.4	12.9	9.6	6.3	6.1	23.6	31.0
D50663_at_	D20663	tctel1	CW-1 mRNA	23.1	17.9	33.6	16.9	13.3	15.1	5.1	13.5	300
			PROBABLE G PROTEIN COUPLED RECEPTOR									
L06797_s_at_		cxcr4	LCR1 HOMOLOG	12.7	19.2	30.6	89.	7.9	19	14.9	4.1	30.7
U72661_at_	U72661	ninj1	Ninjurin1 mRNA	43.8	31.1	48.8	22	17	7.4	2.6	9.6	30.3
X69910_at_	X69910	p63	P63 mRNA for transmembrane protein	5.8	10.1	26.4	4.1	2.3	9.7	3.9	6.4	29.3
M92357_at_	M92357	tnfaip2	B94 PROTEIN	29.6	39.7	104.2	20.5	31.8	34	m	13.9	287
M97936_at_	M97936	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	7.4	11.4	16.9	13.4	7.7	11.4	48.3	40	28.5
D28137_at_	D28137	bst2	BONE MARROW STROMAL ANTIGEN 2 (BST.2)	LC.	0	12.0	=	ō	0 4	0	, c	970
				-						?	7	5
X57579_s_at_		activinba	Activin beta A subunit (exon 2)	166.9	233.7	47.2	22.8	16.8	9.4	14.1	19.3	24.6
D10040_at_	D10040	fac12	FACL1 Long chain fatty acid acyl coA ligase	24.7	15.2	26.2	13.5	5.9	12.4	2.2	4.4	24.1
U32849_at_	U32849	imi	Hou mRNA	5.5	9	16.1	10.4	10.5	24.4	2.7	12.3	23.9
M55543_at_	M55543	GBP2	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2	30.7	161	47 1	11	7	, c	7	10	23 E
M29696_at_	M29696	il7r	IL7R Interleukin 7 receptor	61.7	36.8	55.8	27.5		15	50	11.5	23.2
X54489_rna1						-						
at	X54489	grol	Melanoma growth stimulatory activity (MGSA)	49.6	130.6	644.5	6.0	3.2	7.5	4.6	14.6	22.8
U83461_at_	U83461	copt2	Putative copper uptake protein (hCTR2) mRNA	3.6	13.4	19.1	2.9	10.1	12	ı.	4 7	22 6
L22342_at_	L22342	unknown	Nuclear phosphoprotein mRNA	3.8	9.7	11.4	4	6.1	1	11.5	12.2	21/2
U48807_at_	U48807	dusp4	Dual specific protein phosphatase mRNA	5.6	29.6	7.4	2.4	3.1	9.8	9.7	2.6	21.7
M31166_at_	M31166	ptx3	PTX3 Pentaxin-related gene, rapidly induced by IL-1 beta	82.7	- 0 88	807.3	2	27.2	1222	r,	с п	6
					2.55	2: :22	,	11	1777	3.6	6.3	60.0

	20.5		20.2	20.2	20.1		19.8	19.6	19.3		19.1	19		18.9	-	18.7	0	1 0	175	175	17.3	?	17.2		16.9	16.2	16.3	15.7
	4		6.8	18	4.3		3.2	4.2	2.6		24.8	8.6	,	6.4		21.3	7 6	2 (%)	77	4 5	31		9.8		4.6	Δ	0 0	
	2.9		4.6	12.8	2.3		2.5	7.6	2.1	-	40.1	χ χ	î	2,	(10.4	~	2.1	2.5	2 2	9		4.4	1	5	2	2 2	24.6
	5,3		2.5	7:07	9.9		0.9	23.4	4.2			ψ. U.		31.4	L	0.3	η. 4		16.5	5.1	2.6		22.1	(6.7	11.4	10.4	13.7
	1.8		3.5	0.60	4.4		2.2	3.3	1		y c	3.1	0	0.0	ď	7.0	5.9	15.4	33.1	0.5	2.8		28.5	- (7	4.6	4.5	
	2.3		2.0.2		5	• •	2.5	15.8	0.3	7	1/.0	7.	u	0	0	0.01	0.7	7.8	15.4	1.7	0		19.1	,		11.1	3.4	37.8
	16.9	10.0		32.3	13.1		15.2	22.1	3.5	22.2	27.3	7:/7	616	2.10	0 //		37.9	13.1	21.2	5.2	16.6		24.2	u		10.6	46.2	17.1
	5	7 01	10.7	S	8.1		5.5		6.5	ας	141		126		38	3	18.5	7	8.6	4.4	3.7		12.6	ά	5	2.5	20.1	39.4
	3.6	0	40.0	7:01	5.1	- 1	7.7	14.3	5.5	σ, α	24.8		4.2		126.1		7.8	10	11.8	0.5	2		2.2	<u>.</u>		20.5	18	49.2
	MUC1 Mucin 1, transmembrane	INF receptor 1 associated protein (TRADD) mRNA, 3' end of cds	TRYPTOPHANYL-TRNA SYNTHETASE	INTERFERON GAMMA UP-REGULATED 1-5111	PROTEIN PRECURSOR	MTHFD NAD-dependent methylene	PERPOACT acute myaloid laukagenia	Transmembrane protein	Interferon inducible PNA depondent access	kinase (Pkr) gene	KIAA0084 gene, partial cds	C1S Complement component 1. s	subcomponent	GOS2 gene extracted from Human GOS2 gene,	flank and cds	Caspase-like apoptosis regulatory protein 2	(clarp) mRNA, alternatively spliced	Starbu mkna	OBSET OF THE	GRAFT GIRCH KNA sequence binding factor 1	Lysophiospholipase nomolog (HU-K5) mRNA	INCLEASE PROTEIN	CD86 CD86 antigen (CD28 antigen ligand 2 B7	2 antigen)	NATURAL KILLER CELLS PROTEIN 4	L MECURSOR	AUM Adrenomedullin	Mitogen induced nuclear orphan receptor (MINOR) mRNA
	muc1	tradd	wars	00	pazoa	MTHFD2	am12	adam8		pkr	KIAA0084		c1s		G0S2		flip ctoff	Station Dae 2	3000	h, iv	Cupi	ncf1		cd86	240	1 TO C	anıı	minor
	105582	L41690	X59892	663701	LU/033	X16396	235278	D26579		U50648	D42043		J04080	0	M/2885	7000	AF005//5	M87434	1107231	1167963	200	M55067		U04343	M59807	D14874	10110	U12767
	J05582_s_at_ J05582		X59892_at_	107633 24	T	X16396_at	Г		ä		D42043_at_		-+		S at		X82200 at	T	T	1 10	Τ	M55067_at_		U04343_at	M59807 at	Ţ	T	U12767_at_

Figure 3D

HT1612_at	HG1612. HT1612	macmarcks	Macmarcks	19.2	30	44.7	11.5	30.2	16.9	3.4	11.8	15.6
X64177_f_at_ X64177	X64177	mt1h	Metallothionein	761.9	728.2	93.6	73.7	6.99	27.4	10.4	27.4	14 9
Z14982_rna1 _at_	214982	7aml	MHC-encoded proteasome subunit gene LAMP7. E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility complex encoded proteasome subunit MP7.	(
L06633_at_	L06633	pscdbp	Transcription factor mRNA	3.0	9.5	9.6	4.2	8.7	8.6	5.1	2.9	13.9
L40379_at_	L40379	trip10	Thyroid receptor interactor (TRIP10) mRNA, 3'			10.4	j i	2.	١	4.0	2.2	13.6
U15932_at_	U15932	5dsnp	Protein tyrosine phosphatase mBNA	34.8	3/.1	33	5.3	5.5	7.6	22.2	8.9	13.5
U67319_at_	U67319	casp7	Mch3 isoform alpha (Mch3) mRNA	/6 -	(6,5	44.5		11.1	8.8	2.4	4.4	13.4
U45878_s_at				C:1	į	16.6	3.5	8.7	6.1	3.1	6.3	13.2
M13792 at	U45878 M13792	ciap2	Inhibitor of apoptosis protein 1 mRNA	2.6	2.7	19.1	ō	0.4	10.9	1	7 1	13.1
15-16 (01)	70,000	aga	AUA Adenosine deaminase	13.5	14.9	108.1	0.7	1.6	9.9	3.6	2.1	123
M86707_at	M86707		TETRADECANOYLTRANSFERASE	2.4	9	2.7		0	-	,	,	
MO92U3_s_at	M69203	mip1b	SCYA4 Small inducible cytokine A4 (homologous to mouse Min.1h)		;	į	1	7	1	0.7	0.0	12.2
D63881_at_	D63881		KIAA0160 gene, partial cds	104.9	44.6	19.3	372.7	82	10.5	4.6	30.1	11.6
U07158_at_	U07158		Syntaxin mRNA	000	7 (10.	2.0	7	10.1	5.3	2.9	11.4
D13146_cds1			2,3'cyclic.nucleotide 3'phosphodiesterase gene extracted from Human 2,3'cyclic.nucleotide 3'.	6.3	4:7	1.0	2.3	2.4	0	3.2	<u></u>	11.4
_at	D13146	cub	phosphodiesterase gene	15.9	13.4	25.3	6.2	4.4	10.1	5.	ď	11
	M22403		PRECURSOR	4	-	7 00	, c	-				
M/9463_s_at 	M79463	lým	PML Probable transcription factor PML falternative products		1 1	35.7		<u> </u>	<u>v.</u>	<u> </u>	3.7	11.1
	HG4322.			0.0	0.	13.3	2	4.2	4.1	7.1	5.9	=
HT4592_at_ J04056_at	HT4592 J04056	tubulinB	Tubulin, Beta	18.5	5.3	13.1	9.4	3.2	8.9	2	6	
U15460 at	1115460		RZip protein B ATE mbNA	0.1	3.9	9.0	3.7	20.5	7.4	4.2		
	22.22		אוצוון ווינון מוסוסות לוקס	19.8	17.1	56	1.5	0.4	6.0	m	33	=

Inv...aors: Nir Hacohen, et al.

HT1102_at_	HT1102	ras·related	Ras-Related C3 Botulinum Toxin Substrate	0	,	-		,				
U22662_at	U22662	lxra	Nuclear orphan receptor LXR-alpha mRNA	1.5	7.3	13.4	8.1 ×	1 2	1.4	4 ×	2.1	10.9
Y00787_s_at_	Y00787	8!!	INTERLEUKIN.8 PRECIESOR	0							77	10.0
AF000234_at				09.1	234.5	40.9	8.6	13.1	8.4	8.2	10.8	10.5
_	AF000234	p2x4	P2x purinoceptor mRNA	2.5	32.4	00	σ	0	-	r.	<u>u</u>	
M81750_at_	M81750	mnda	MNDA Myeloid cell nuclear differentiation antigen		0			1	+		0.	4.
HG2239.	HG2239-			5	7.7	4.0	3	4.4	8.	1.7	4.3	10.4
HT2324_at_	HT2324	-	Potassium Channel Protein (Gb:711585)	c	C		1	(
AF014958_at				ט פ	7	7.1	5	0.3	0	1.7	5.6	10.1
I		ccr6	Chemokine receptor X (CKRX) mRNA	3.6	0	36.3	n	r,	9 9	u	- (
U57721_at_	U57721	kynu	L-kynurenine hydrolase mRNA	25.2	32 5	2000	0	5.0) -	1 0	4 ·	
X70340_at	X70340	tgfa	TGFA Transforming growth factor, alpha	0	7.3	7 -	200	ò	1	0.0	11.	2) (2)
					?	1		7	5	5.3	4.4	χ. Σ
X61123_at_	X61123	btg1	proliferative	30.4	26.8	14.4	α	7		C	١	1
X66899_at_	66899X	ews	EWSR1 Ewing sarcoma breakpoint region 1	4.9	6.2	7.5	7	1 -	1 0	0.0	t <) C
			Proteasome-like subunit MECL-1 gene extracted			?	?	?	7.1		1 1	y.
_			from H.sapiens genes for proteasome-like						-			
			subunit (MECL-1), chymotrypsin-like protease									
X71874_cds1			(CTRL-1) and protein serine kinase (PSK-H1) last	-					_			
at	X71874	lmp10	exon	3.4	5	7 7	٠,	-			,	1
M59465_at_	M59465	a20	TNFAIP1 Tumor necrosis factor alpha inducible protein A20	į į		;	7	1	5	12	0	أم
HG4297-	HG4297.			ò	128./	41.1	65.3	/3.5	22.9	7.6	5.9	9.6
HT4567_at_	HT4567	TCPC4	Transcriptional Coactivator Pc4	2 6	27	ά	7	<u>u</u>	- 0	C	•	ı
V00594 s at	700594	m+23							5	2	φ. 10.	0.5
	10000	111750	Metallotilionelli isotorm Z	167.1	337.3	15	64.9	122.8	34.8	69.4	52.2	46
M24283_at_	M24283	icam1	ICAM I Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	202	, , ,	5	6	:	,			-
HG4069.				2,	32.4	Z0.7	87	7.1.7	3.4	9.5	9	9.3
HT4339_s_at HG4069.	HG4069.											
	HT4339	mcp1	Monocyte Chemotactic Protein 1	2.9	2.5	2.8	38.4	16.9	10.3	~	10.7	σ
Uby546_at_	U69546		RNA binding protein Etr-3 mRNA	2.5	7.1	6.4	7	2 1	2	1 0	, , ,	10

1									ŀ	-	
2 3	ak3	AK3 mRNA for adenylate kinase 3	15	38	35.3	4.5	7.4	0	3	10	C
1/649/1	map4	MAP4 Microtubule associated protein 4	4.3	4.8			0	0 0	5 0	7 2	
U28386		RCH1 RAG (recombination activating gene)	0	-;			2		1		o.
690801	hspf4	DNAJ PROTFIN HOMOLOG 2	8.2	2.4	15.4	2.6	-	8.9	2.7	2.7	8.9
D42087		KIAA0118 gene partial cds	12.8	11.1	12.7	10.9	20.7	9.7	1.7	3.9	8.8
		ATF4 CAMP-dependent transcription factor ATE	1:	2.3	10.9	2.8	1.6	0	2	3.5	8.5
D90209	atf4	4 (CREB2)	4 5	ď	0	ď	,	·			
M32886	scn	SRI Sorcin) j	2 -	2.0	7 7	4.0	Σįς	5.1	8.4
X90858	dn	Uridine phosphorylase	13.1	11.4	10.9	100	ο α	5 0	ا ا ا	9,0	ω c
M16750	nin 1	MI O		<u> </u>				1	2	<u>- 1</u>	0.0
U19261	traf1	Fostein Barr views induced access	28.7	21.8	41.8	4.2	3.7	9.4	m	5.9	8.2
		Spermidine/sperming N1 0000 11	25.7	15.4	25.2	8	12.7	9	5.8	9.5	8.1
U40369	sat	(SSAT) gene	σ	r,	2	001	-		-	-	
D30755	NAF1	VIM Vimentin	5.03	5 6	1	0.0	O	2.8	6.3	4.1	8.1
X14448	gla	ALPHA GALACTOSIDASE A PRECIIBSOR	200	7.07	13.0	2.5.	2.5	5.9	14.1		7.9
		STAT4 Signal transducer and activator of	7.7	7.7	4	1	9.0	1.3	4.8	2.9	7.9
L/8440	stat4	transcription 4	6.4	16.4	40.6	0	1.4	6.5	 	0 0	α
M31642	T Dort	HPRT1 Hypoxanthine phosphoribosyltransferase									D
		Putative outer mitage and	5.2	5.4	6.2	2.5	6.0	0.3	2.9	2.4	77
U58970	tom34	translocase hTOM34 mRNA	0	2 1	,		-	,			
X79882	mvp	Lrp mRNA		7 4	1.0	5	5 (9.	9.6	2.7	7.7
U76764	7907	7000 7000		?	0,	1	6.3	4	77	9	7.6
		cos, cos, annigen (reucocyte antigen)	14.8	10.7	3.4	14.5	2.8	2.3	1.7	2.3	7.5
X57351	ifitm2	RPS3 Ribosomal protein S3 / wrong name	13	84.2	13.1	15.3	81.7	30.3	55.9	20.8	7.5
D14826	crem	CREM CAMP responsive element modulator	3.4	~~	7	127	7 0	0	ī	ļ-,	$\prod_{i=1}^{n}$
268	map3k4	KIAA0213 gene, partial cds		117	7 0	/ 0	0 1	0.00	2.0	9	4.
M87284	oas2	69/71 KD	000	, , ,	7.0	0 -	C: 2	7	3.6	1.8	7.4
M31724	ptp1b	PTPN1 Tyrosine phosphatase 1	7 7 7		0 0	2	5.3	9.5	5.9	2.2	7.4
		1 0000000	17.47	ĭ	7	2	0	,		-	,

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Invena	rs.	Nii	- 14	Iacobe	n e	t /	. 1

Z11697_at_	211697	cd83	CD83 ANTIGEN PRECURSOR	18.7	12.6	9.8	19.6	9.5	9	4.1	10.4	7.2
	0		LYN V-yes-1 Yamaguchi sarcoma viral related					-				
M16038_at_	M16038	lyn	oncogene homolog	7.9	5.6	9.1	11.6	6.7	ú	1.6	4.7	7.1
1170451 at	170451	887/488	Myleoid differentiation primary response protein		7	(,		j	,		
Y08682 rna1	1010	2006	AND DOOR	7.7	1	2.2	6.3	7/.2	7	1.6	2.4	7.1
s_at_	Y08682	cpt1b	Carnitine palmitovitransferase type	0	00	c	9	~	4	α		7 1
HG544.	HG544-							,	;			1
HT544_at_	HT544	ecgf	Endothelial Cell Growth Factor 1	5.9	15.3	4.8	10.4	5.2	2.1	26.7	16.5	
			ANPEP Alanyl (membrane) aminopeptidase								2	
			(aminopeptidase N, aminopeptidase M,	_								
M22324_at_	M22324	anpep	microsomal aminopeptidase, CD13)	5.4	10.4	7.5	1.9	1 9	0	2.2	33	7
U43185_s_at		!	STAT5A Signal transducer and activator of									
	U43185	stat5a	transcription 5A	7.6	8.5	14.5	1.2	0.8	1.1	15.9	10.5	7
			Protein tyrosine phosphatase PTPCAAX1									
U48296_at_	U48296	ptp4a1	(hPTPCAAX1) mRNA	2.4	3.7	14	2.8	3.2	14.7	2	2.3	6.9
D43949_at_	D43949		KIAA0082 gene, partial cds	2.7	6.7	5.6	0.3	0.7	2.6	6.5	m	89
			PML Probable transcription factor PML									
M79462_at_	M79462	myl	{alternative products}	3.1	8.9	6.2	2.7	6.7	6.2	33	3.8	89
U28014_at_	U28014	casp4	ICH.2 PROTEASE PRECURSOR	13.5	4.4	9	9.2	1.5	3.2	7.2	7.2	8 9
			PML Probable transcription factor PML									3
X63131_s_at_ X63131	X63131	lyn	{alternative products}	9.9	4.7	4	4	0.5	50	4.3	10.3	8
M23178_s_at			MACROPHAGE INFLAMMATORY PROTEIN 1.									
	M23178	mip1a	ALPHA PRECURSOR	73.8	125	11.4	52.8	73.8	8.5	7.4	96	9
M37435_at_	M37435	mcsf	CSF1 Colony-stimulating factor 1 (M-CSF)	7	12.8	9	37.5	12.1	0.4	4.1	9.6	6.3
HG2917.	HG2917.		Major Histocompatibility Complex Class F									
HT3061_f_at_	HT3061	hla	(Gb:M21533)	5.7	7.6	0	Γ.	ب ب	٣	ر بر	ď	ď
			Modulator recognition factor I (MRF.1) mRNA, 3'				3		,			3.0
M62324_at_	M62324	mrf.1	end	4.8	8.6	10.2	7.9	6.1	14.3	18	3.4	62
U70660_at	U70660	atox1	Copper transport protein HAH1 (HAH1) mRNA	3.8	8.1	6.0	1.8	2.2	0.4	13.5		6 2
U76189_at_	U76189	ext12	EXTL2 (EXTL2) mRNA, partial cds	0.7	7.3	13.5	1.7		0.1	4.4	5.3	9
+c 2 30005U	300070	7										
U/3600_3_al_[U/3600	002670	3004	JOUCH Syndecan 4 (amphigiycan, ryudocan)	6.3	9.9	21.1	15.2	11.	10.2	2.7	2.7	9

Figure 3H

, resp	onse of Deligitic Cells to a
Inventors:	Nir Hacohen, et al.

			SSB Sjogren syndrome antigen B (autoantigen		-		-	-	-	-	-	
X14684_s_at_	_	qss	(La)	2.7	4.2	1.5	8.	6.7	12.1	7.4	4.6	9
U59863_at_	U59863	itraf	TRAF-interacting protein I-TRAF mRNA	1.3	5.5	4.5	4.7	7.1	7.7	2.1	6.4	5.9
			EIF5 Eukaryotic translation initiation factor 5			-					-	
U49436_at_	U49436	eif5	(eIF5)	5.6	7.7	16.1	1.2	5.5	0	1.4	2:2	5.7
HG2915.	HG2915.		Major Histocompatibility Complex, Class I. E									<u> </u>
HT3059_f_at_	HT3059	hla	(Gb:M20022)	6.1	6.3	8.8	5.8	4.2	2.8	-8	3.6	92
			Receptor protein tyrosine kinase (HEK5) mRNA,		-		-	-		-	-	
L41939_at_	L41939	drt	3'end	0	0	1.9	0.4	0	1.7	3.6	4 4	5,6
X07743_at_	X07743	plek	PLECKSTRIN	9.7	2.1	5.7	13.9	10.7	2.7	3.6	1.6	5.6
D45248_at_	D45248	pa28b	Proteasome activator hPA28 subunit beta	13.1	17.2	6.2	17.1	8.2	5.7	34.3	17.3	5.5
D87076_at_	D87076		KIAA0239 gene, partial cds	0	2.7	2	1.2	3.2	5.8	3.2	2.7	5.5
			6-16 gene (interferon-inducible peptide					-	-			
U22970_rna1	_		precursor) extracted from Human interferon-									
_s_at_	U22970	g1p3	inducible peptide (6·16) gene	115.3	68.2	5.8	70.6	97.1	13.7	13.1	15.6	5.5
U41654_at_	U41654		RagA protein	2.8	3.9	6.5	1.8	1.5	0	1.5	1.8	
			DNA-binding protein CPBP (CPBP) mRNA,		_		\vdash	-	-		F	
U44975_at_	U44975	bcd1	partial cds	2.4	11.3	8.9	3.7	7.1	7.8	1.5	4.2	5.3
X56468_at	X56468	tan	14-3-3 PROTEIN TAU	1.1	1.9	4.9	5.5	9.3	8.3	1	1.8	5.2
			MACS Myristoylated alanine-rich C-kinase		_		-			-	-	
D10522_at_	D10522	macs	substrate	4	3.2	10.3	4.7	1.9	5.9	2.3	3.2	5.1
U00672_at_	U00672	il10ra	IL10R Interleukin 10 receptor	9.5	14.1	9.1	10.6	15	9.5	4.2	5.9	5.1
			Variant urokinase plasminogen activator			-		-		-		I
X74039_at_	X74039	plaur	receptor (uPAR2) mRNA, partial cds	1.6	15	7.3	1.6	4.2	2.8	1.5	5.4	5.1
D11428_at_	D11428		PMP22 Peripheral myelin protein 22	2	7.7	1.2	5.9	1.4	٦	1.9	2.1	2
			MAJOR HISTOCOMPATIBILITY COMPLEX				-	-		 	-	Τ
	M69043	ikba	ENHANCER-BINDING PROTEIN MAD3	23.9	19.6	11	14.8	9.5	4.7	4.3	3.7	8.4
M31627_at_	M31627	xbp1	X BOX BINDING PROTEIN:1	4.4	δ	15.4	16.7	20.6	27.1	3.2	3.1	4.6
U90313_at_	U90313		Glutathione-S transferase homolog mRNA	4.1	m	3.7	2.9	6.0	0	1.8	3.9	4.6
249107_s_at_	249107	lgals9	Galectin	6.1	3.1	5	17.1	12.1	3.7	2 2	5.7	4 6
D38048_at_	D38048		Proteasome subunit z	9.0	1.2	1.7	3.6	6.0	1 4	5.2	14	4
HG3415.	HG3415.	i i				-					-	?
H13598_at_	H13598	cd155	Poliovirus Receptor	43.5	39.6	38.5	1.7	0	0	4.2	9.9	4.5
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Incontore	Nir Ugoobon at al	

								Inver	itors:		Ni	r Hac	cohe	en, e	et al.								
4.5		4	43	4.2	4	5.	4	3.9	0 %	0 00	a c	3.7		3.7	2 %	9 6	7	3	3.6	u c	o.	3.4	, ,
3.1	1	2.2	2.2	17	2.1	3.3	7 7	2.6		- F	α κ	11.2		3.5		3.1	,		3.9	0.0		2	, L
2.9			2.5	2.9		6.2	4 3	1 9		2 4	4 7	_		m	-	9.5	0		2.3	1		25	
4.5	0.7	1.5	0	5.2	5.1	3.1	4 6		C	1 6	Ĉ	9		2.4			r v		8 0		5	6.9	
0.3	3.2	0	1.9	9.5	1.5	0	14.4	18		0.5	1 4	4.3		10.7	6	m	o C	3	7.7	1 0	5	3.1	-
2.4	19	8.0	1.1	8.2	0.3	0	28.7	1.3		3.9		10.5		12.5	0	2.1	۲.		4 -	t C	>	5.7	c
5.2		18	10	4.2	1.9	4 3	6.9	9.0	6.0	1.6	6.2	m		14.5	33	0.2	7 2		<u> </u>	5	1	7.4	C
2.1	m	0.3	8.1	2.4	2.8	1.5	26.4	1.2	3.1	2.4	11.8	4.5		26.9	2 6	3.7			0.7		,	5.5	10.8
0.8		0.4	7.9	2.8	0.1	0.3	65.5	0	4.8	14.6	2.9	6.1		17	5.0	0.7	1.6		φ. α	2 0)	8.5	60
LOT1 mRNA	Globin gene	CD19 CD19 antigen	IEX∙1	PROTEASOME COMPONENT C8	KIAA0151 gene	Fork head domain protein (FKHR) mRNA. 3' end	IL1RN Interleukin 1 receptor antagonist	METALLOPROTEINASE INHIBITOR 3 PRECURSOR	Novel glucocorticoid receptor associated protein	ID2 Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ZNF151 Zinc finger protein 151 (pHZ-67)	GAPD Glyceraldehyde-3 phosphate dehydrogenase	Urokinase-type plasminogen activator receptor	plasminogen receptor	IL3RA Interleukin 3 receptor, alpha (low affinity)	KIAA0226 gene	Phosphatase 2A mRNA, partial cds	Phosphotyrosine independent ligand p62 for the	SERUM PROTEIN MSF55	Clones 23549 and 23762 mRNA	ass I	B40, Cw3)	MMP2 Matrix metalloproteinase 2 (gelatinase A; collagenase type IV)
		cd19	iex-1	psma3	IKKE	fkhr	illrn	timp3	bag1	id2b	znf151	psma4		plaur	il3ra			262	200			hla·a	6dmm
U72621	M69023	M28170	S81914	D00762	D63485	U36922	X53296	U14394	235491	M96843	U20647	D00763		U09937	D49410	626980	103805	1146751	M88338	806060		D32129	02020
U72621_at_	M69023_at_	M28170_at_	S81914_at_	D00762_at_	D63485_at_	U36922_at_	X53296_s_at_	U14394_at_	Z35491_at_	M96843_at_	U20647_at_	D00763_at_	1109937 rna1	_s_at_	D49410_at_	D86979_at_	J03805_s_at_	1146751 24	M88338 at	U90908 at		D32129_f_at_	J05070_at_

						- ;	vesh	onse oi	Den	arı	ne C	CII	, (t	, a						_
					Inv	ento	rs:	Nir I	lacol	lei.	i, et a	ıl.								
3.3	3.1	3.1	m	2.9	2.9	2.9	2.8	2.8	2.8	2.7	2.7	2.6	2.6	2.5	2.5	2.4		2.3		
2.3		2.6	4.1	1.6	4.6	1.4	1.6	3.5	12.4	1.3		3.4		1	8	.33		3		
æ		9		2.6	6.6	7.9	4.2	3.7	21.8	C1	4.9	2.3	2.	1.8	3.8			2.6		
3.4	2.8		0	0	6.5	2.4	7.8	0.1	4.3	1.4	0.7		0.2	1	7.9	2.5		0.1	1.6	
12.6	2.2	5.7	0.4	1	51.6	14.7	3.6	0	1.8	0.8	2.8	3	1.1		18.4	κi ·	0.3	o.	0.8	
∞	4.5	11.4	1.3	8	70.3	16.2	4.1	3.4	5.3	0.2	1.2	7.5	4.2	6.0	16.8	1.8	2.4		4.4	
8.6	9		2.7	3.1	5.7	6.1	4.7	6.3	5.2	6.0	3.1	0.1	0	3.3	5.2	0	0.1	1.4	3.7	

8.4

9.3

9.9 12.7

sapiens cDNA clone memd, mRNA sequence HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F ALPHA CHAIN PRECURSOR

J30999 Homo sapiens MV3 melanoma Homo

Fas-binding protein (DAXX) mRNA, partial cds

84.9

14.6

177.6 2.5

52.1

42.2

SCYA4 Small inducible cytokine A4 (homologous to mouse Mip-1b)

Nuclear Factor Nf-116

nfi16

HT3688 J04130 L11329

HT3688 at

U09587 HG3494.

U09587 HG3494

DUAL SPECIFICITY PROTEIN PHOSPHATASE

PAC.1

dusp2

daxx

AF006041

AF006041_at

L11329 at

mip1b

104130_s_at_

11.4 81.9

<u>8</u> 2.8

2.3 10.7

2.6

B4.2 protein mRNA GARS Glycyl tRNA synthetase

IPL (IPL) mRNA

ipl b4:2

AF001294

4F001294_at

003105

J03105_at

3.7

76 kDa tyrosine phosphoprotein SLP-76 mRNA

Receptor 4 1BB ligand mRNA

41bbl

U03398_at_

lcp2

U20158

U20158_at_

9.2

Figure 3K

2.3

2.1

0.8

8.4

1.9

0.7

38.2

ID2 Inhibitor of DNA binding 2, dominant

Homologue of yeast sec7 mRNA negative helix-loop-helix protein

KIAA0070 gene, partial cds

kars d17s811e

M85169

D31890_at_ M85169_at_

M97796_s_at

92

M97796

6.0

3.3 0.0

3.6

22.4

PTPRC Protein tyrosine phosphatase, receptor

type, c polypeptide TXN Thioredoxin

cd45

Y00062 Y07566 D31890

Y00062_at_ Y07566_at_

Rit mRNA

Uridine diphosphoglucose pyrophosphorylase

FRG1 mRNA

mRNA

ugp2

U27460 X77584

U27460_at_ X77584_at_

(macrophage elastase) 26S PROTEASE REGULATORY SUBUNIT 4

mmp12

psmcl

L23808 L02426 L76159

L02426_at_ L76159_at_

.23808_at

irg]

MMP12 Matrix metalloproteinase 12

KIAA0122 gene, partial cds

hla.cda12

X17093

X17093_at_

)50912_at_

cd166

030999

U30999_at_

39.5

U03057 at	103057	snl	Actin bundling protein mRNA	20.2	27 5	Vα	1 1	10.4	11 11	30	13.4	6 6
XROKG2 at	XROGGS		FDK3 protein binace mDNA	0.0	5, 5		j (1 -		35,	1.0.4	0.7
126247 at	126247	Sui 1	RPI 3 Ribosomal protein I 3	3.7	2.7	J Z	0.7	1,0	5 -	0 -	Σ. σ	2.3
1			CDKN1A Cyclin dependent kinase inhibitor 1A	,	1.7		3.1	7.7	7.7		0.4	7.7
U09579_at_	009579	cpne5	(p21. Cip1)	12	9 5	5.1	5.6	2.4	1.2	2.3	3.4	c.
D86550_at_	D86550	dyrkla	Serine/threonine protein kinase	1.3	2.9	8.9	9		7.3			
HG1879.	HG1879.		F								1	1
574017 at	574017	Chris	NAS-LIKE FIOLEIT 1010				0		0	7.3	2.9	1.9
3/401/ 41	2/401/	71111	ואווע	3.8	6.3	3.7	3	2.8	1.8	3.1	5.8	1.9
U20758_rna1 _at_	U20758	osteopontin	Osteopontin gene	2.1	5	0.5	-	5.3	1.2	4	6.3	6
V00599_s_at	000599	tubulinB like	mRNA fragment encoding beta-tubulin. (from clone D-beta-1)	9	3	, c	7.	r.	C	C		-
HG2981.								?	1	1		
HT3125_s_at HG2981	HG2981.		:									
1	HT3125	cd44	Epican, Alt. Splice 1	13.1	9.7	8.1	2	1.4	0	2.7	2.3	1.7
U16811_s_at _	U16811	bak1	Bak protein mRNA	6.0	3.7	1.9	3.9	99	3.7	0	٠-	1 7
Z17227_at_	Z17227	il10rb	CRFB4 Cytokine receptor family II, member 4	1.9	3.4	3.7		1.2	17		2.1	1.7
							i				İ	
at		hla	Major Histocompatibility Complex, Class I (Gb:X12432)		5.8		6.5	2.3	3.6	4	4	-
U91616_at_	091616	ikbe	I kappa B epsiton (IkBe) mRNA	16.3	12.4	3.3	12.6	4.5	0	4	9	2
					-							
			TWHAZ Lyrosine 3-monooxygenase/tryptophan 5		-							
D78134 at	078134	Cirbo	nioriooxygenase activation protein, zeta	C	÷			ŗ	(,		•
		22	PAGA Proliferation associated gene A (matural	0.0	1	0.	7.7	0.0	5	3.1	7.7	4:1
X67951_at_	X67951	рада	Killer-enhancing factor A)		0	0	0	7	0	0		
			Partial cDNA sequence, farnesyl pyrophosphate					?	;			
Z47055_s_at_			synthetase like-4	4.4	1.4	1.3		m	-c	2	7	7
L40377_at_	L40377	cap2	Cytoplasmic antiproteinase 2 (CAP2) mRNA	7.4	8.1	7	2.7	0.5	0	2.2		-
Z28407_at_	228407	rpl8	RPL8 Ribosomal protein L8	1.2	0.4	0.8	2.1		2.7	1.5		
HG33.									+			
HT33_at_	HG33-HT33		Ribosomal Protein S4, X-Linked	0.4	1.9	0	0	1.1	0.6		-	

Figure 3L

							mve	entors	S:		NI	r Ha	co	ne	n,	et.	al.											
0.8	0 7	5	0 0	0	1 4	0.3		0 0	0.5	0.2	0.2	0.1	0	0	TC	Ö	0	C	ì	C			C	Ì	Ĉ	ि		0
6.0	1	0	0.7	c	- 0	0	-	6 -	1	О	0	0.5			C	0.3	90	C	,	0			C	1	C	0		0.2
1.7	80		m	0	0			5 -	<u>, (</u>	0.8	0	0.5	0	0.4		0	0	. 5		0.4	-	1	6 0		0 4			Э
0	0.5		0	c	0	0				0.4	o	0	0	0	0	0	0	Ĉ	-	0	-		0		Ö	ō	+ (5
1.1			90	0	0.5		9			O.4	0.5	1.7	0.3	2.8	0.8	0	0.3	С	-	0.5	0		0.7	-	6.0		 	1.5
0	0.5		0.5		0.20				0	5	0	1.3	0	0	0	0	0	0	-	0	2 0	2	0		0	0		5
2.2	9.0	0	0	C	0	0	-			4.1	0	0	0	0	0	0	0	0		0	č		0		0	0		5
4.7		0	0.2	0	80	0.8	α				9.0	1.5	0	9.0	-	0.4	6.0	0		1.1	ā	2	· 0		9.0	0	-	7.7
0.4	0.5	0	0	0	0.7	0	C			٥	0	0	0	9.0	0	0	0	0		0			0		0	0		5
Adenosine triphosphatase mRNA	RpS8 gene for ribosomal protein S8	PUTATIVE PROTEIN PHOSPHATASE 2C	KIAA0232 gene	Skeletal beta-tropomyosin	Plectin (PLEC1) mRNA	KIAA0159 gene	GNAS1 Guanine nucleotide binding protein (G protein), alpha stimulating activity polypeotide 1	RET ligand 2 (RETL2) mRNA	Oncontatein 18 (On 18)	Circopiotelli 10 (Op10) gelle	Acetolactate synthase homolog mRNA	Hematopoietic progenitor kinase (HPK1) mRNA	HRH1 Histamine receptor H1	KIAA0112 gene, partial cds	NADPH-flavin reductase	Rhodanese	KIAA0246 gene, partial cds	KIAA0264 gene, partial cds		Male Enhanced Antigen	SPTAN1 Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	IMPDH1 IMP (inosine monophosphate)	dehydrogenase 1	TKT Transketolase (Wernicke-Korsakoff	syndrome)	ADORA3 Adenosine receptor A3	Endogenous retrovirus envelope region mRNA	\(\subset = 1 \)
atp2b1	rps8	pp2c-like		tmsb			ard1	gdnfrb	lan18	0145			hrh1		blvrb	rds	kiaa0246				sptan1		impdh1		tkt	adora3	1 10	
J04027	X67247	D13640	D86985	M12125	U53204	D63880	X77588	AF002700	M31303	2007	U61263	U66464	Z34897	D25218	D26308	D87292	D87433	D87453	HG1869.	HT1904	J05243		J05272		L12711	L77730	M11119	21111
٦.		40_at_	_	ļ	,	D63880_at_	X77588_s_at	AF002700_at	M31303_rna1	1- 000	U61263_at_		\neg	D25218_at_			ig	D87453_at		HT1904_at_	J05243 at		J05272_at_		L12711_s_at_ L12711	L77730_at_	M11110	

M19/20_rna2			L-mvc gene (1-mvc protein) extracted from	-		-		-	$\frac{1}{2}$	-	-	ſ
at	M19720	Imyc	Human L-myc protein gene				0	C				-
M23197_at_	M23197	cd33	CD33 CD33 antigen (differentiation antigen)	0		0	2 0	2 4	5 0	5 0	5 0	7
			PTGS1 Prostaglandin-endoperoxide synthase 1		•	,		2	5	n:	0.5	7
			(prostaglandin G/H synthase and								_	
M59979_at_	M59979	cox1	(cyclooxygenase)	c			7	C		-	_	
M95678_at_	M95678	plcb2	PLCB2 Phospholipase C. beta 2	o	1 0	0	5	0 0	5 0	5 0	5 0	D
U06631_at_	U06631	H326	ILEF SSP 9502 mRNA		5 0		5 0	5 7	5 0	5 0	5 0	7
				5	5	0.7	O.3	1.3	n	χ.	0	0
153446 at	1153446	りんちん	Mitogen-responsive phosphoprotein (DOC.2)									Γ
		3000	CANTIL	S	ò	0	0	0	0	0	0.5	0
										-		
			FACE Faired basic amino acid cleaving enzyme				_	_	-			
X17094_at_	X17094	fur	(furin, membrane associated receptor protein)	6.0	0.6	C	1 4	C	C	Ĉ	7	C
			FES Feline sarcoma (Snyder-Theilen) viral (v.		-	+	+	2	5			7
			fes)/Fujinami avian sarcoma (PRCII) viral (v.fps)	_								
X52192_at_	X52192	fes	oncogene homolog	~ <u>~</u>	~ <u>~</u>	C		Ċ		· ·		
			Ung gene (uracil DNA glycosylase, UNG2)			1			5	7.7	3	5
X89398_cds2	-		extracted from H.sapiens ung gene for uracil									
_at	X89398	dgu	DNA glycosylase	0	C		C.		,	C	_	
X95735_at_	X95735	zyx	Zyxin	17		5 0	5,0	2 0	-	770	5	्र
X97335 at	X97335	akan1	Kinase A anchor protein		5 0	5 0	7.7	0.0	2	0.7	7)
			יייייייייייייייייייייייייייייייייייייי	5	D	o l	0	ō	0	0.5	ō	0
	1		I Fivit Tropomyosin alpha chain (skeletal		_					_	-	Γ
T	224/2/	,	muscle)	0	-	0	0	1.7	0	0	0	c
250/49_at_	250/49	ppplr/	Sds22-like mRNA	C	c	c	<u>د</u>	90	C	-	5	10

Figure 3N

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affyID	GBA	gene symbol	gene Name	feco	heco	teco	fpr8	hpr8	tpr8	ican	mcan 1	tcan
V00594_at_	V00594	mt2a	Metallothionein isoform 2	1683.1	1698.4	143.4	371.1	5	107.8	3.3	261	74.2
X64177 f at	X64177	mt1h	Metallothionein	761.9	7282	93.6	73.7	699	27.4	10.4	27.4	14.9
_		1116	IL1B Interleukin 1, beta	199.3	598.3	184.4	9.1	12.6	1	24	11.1	48.7
J03910_rna1 _at_	J03910	mt1g	(clone 14VS) metallothionein IG (MT1G) gene	602.9	500.2	138.9	1.1	1.9	ō	0	2.7	0.3
X04602_s_at_ X04602	X04602	91!	IL6 Interleukin 6 (B cell stimulatory factor 2)	408.5	379.2	1267.5	70.5	76.5	269.4	14.6	43	111
U33017_at_	U33017	slam	Signaling lymphocytic activation molecule (SLAM) mRNA	320.7	343.9	1	8.4	25.8	<u></u>	2.7	24.4	84.5
M65290_at_	M65290	i125/p40	IL12B Natural killer cell stimulatory factor (IL12B)	71.2	261.5	825 7	0	2 3	4.7	32.8	9/	412 7
Y00787_s_at_	Y00787	118	INTERLEUKIN-8 PRECURSOR	89.1	234.5	40.9	9.8	13.1	8.4	8.2	10.8	10.5
X57579_s_at	X57579	activinba	Activin beta-A subunit (exon 2)	166.9	233.7	47.2	22.8	16.8	9.6	14.1	19.3	24.6
L11329_at_	L11329	dusp2	DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC:1	52.1	177.6	16.1	16.2	14.7	2.4	7.9	1.4	2.9
X54489_rna1 _at_	X54489	gro1	Melanoma growth stimulatory activity (MGSA)	49.6	130.6	644.5	6.0	3.2	7.5	4.6	14.6	22.8
X54925_at_	X54925	mmp1	MMP1 Matrix metalloproteinase 1 (interstitial collagenase)	74.3	127.2	147.8	0.5	0	0.4	4.0	0.4	0.7
U04636_rna1 _at_	004636	cox2	Cyclooxygenase-2 (hCox-2) gene	110	120.8	9.809	15.3	13.8	87.4	2	4.7	54.9
M57731_s_at	M57731	gro2	GRO2 GRO2 oncogene	39.1	114.4	703.3	~	4.8	32.2	13.8	11.7	53.6
M28130_rna1 _s_at_	M28130	811	Interleukin 8 (IL8) gene	109.8	107.8	333.5	9	8.3	1		1 9	9.5
M26311_s_at	M26311	cagb	Cystic fibrosis antigen mRNA	45.8	106.5		6.0	4	0.0	23	C	0 6
U29680_at_	U29680	bcl2a1	Bcl-2 related (Bfl-1) mRNA	105.3	97.9	678.7	40.7	35.7	117.5	4	8.3	179.1
M10942 at	M10942	mt1e	Metallothionein-le gene (hMT-le)	50.5	90.3	63.6	1.4	9	1.8	0.8	9.0	0.2

Figure 4A

		674	PTX3 Pentaxin-related gene, rapidly induced	82.7	88.9	807.3	21	27.2	122.2	5.2	2.5	20.9
M31166_at	M31166	ptx3	MMP12 Matrix metalloproteinase 12		-	,	-	0	7	0	u u	2 7
L23808 at	L23808	mmp12	(macrophage elastase)	14.6	84.9	3 0 1	γ α ο		ά	2 4	4 4	13.4
Γ	U15932	gdsnp	Protein tyrosine phosphatase mKNA	2)	0.0	1	2	-			-	
		Ų.	II 6 Interleukin 6 (B cell stimillatory factor 2)	144.3	71.8	1281.1	39.5	22.4	95.7	0.5	158	39.3
j,	Y00081	OII	COS COS Satisfact (PAS)	32.4	70.8	168.3	6.1	9.9	20.8	0.2	34.9	132
	D84276	2502	CUSO CUSO allugali (P45)	46.3	64.4	85.6	3.3	7.9	7.8	5.4	6.5	33.8
	L15702	Di.	Br Bilactor, properties	13	55.5	212.3	3.2	8.2	44.4	1.1	8.4	83.6
U31628_at_	U31628	il15ra	ILISKA Interleukiii 13 leceptol alpiia citaiii	-			İ					
100100	KO1396	- ta	Pl Protease innibitor 1 (anti-elastase), alpila-11 antitrosin	47.3	55.4	72.2	4.7	5.7	2.9	6.0	4.7	m
	200100			0	Ω.	49.2		5.2	5.4	1.7	0.6	æ
X53800_s_at_	X53800	gro3	GRU3 GRU3 oncogene	201								
M60974_s_at	M60974	gadd45	DDIT1 DNA damage inducible transcript 1	30.7	43.6	78.3	4.0	4.4	5.1	1.4	=	6.7
HG3415	HG3415			43.5	39.6	38.5	1.7	0	0	4.2	9.9	4.5
HT3598_at_	HT3598	cd155	Pollovirus Receptor									
M72885_rna1	M72885	G0S2	GOS2 gene extracted from Human GUSZ gene, 5' flank and cds	126.1	38	44.9	10.8	6.2	5.3	10.4	11.3	18.7
X60673_rna1		٠	s asserted at the second at th	7.	38	35.3	4.5	7.4	0.3	3.6	10.5	6
at	X60673	ak3	MT11 Metallothionein 11	5.7	37.4	8.9	0	3	2.1	1.1	0.2	0
X/6/1/_at_	۸/۵/۱/	111111	Thyroid receptor interactor (TRIP10) mRNA,			C		L	7 6	22.2	α	125
1 40379 at	1 40379	trip10	3' end of cds	34.8	3/.1	255	5.0		2.	77	3	
			PTGIR Prostaglandin I2 (prostacyclin)	29.8	34.8	71.9	7.9	2.2	16.2		2.1	65.6
D38128_at_	038128	prgir	Lyminepine hydrolase mRNA	25.2	32.5	20.4	5.9	6.7	1	3.5	11.7	6.6
U57721_at_	17//50	WALIO	ICAM1 Intercellular adhesion molecule 1									
000	200707	- medi		70.6	32.4	20.7	28	11.1		σ.	9	6.9
M24283 at	M24203	Chail	(57.0 // 1.1 1	3.9	31.6	25.9	0.8	3.6	7.		1:1	10.9
045906_at_	D45906	NAFI	ViM Vimentin	56.3	28.2	19.6	19.9	4.9	5.9	14.1	5.3	9.
U30/33_81_			BTG1 B-cell translocation gene 1, anti-			,	o	7	-	36	7 4	0 7
X61123_at_	X61123	btg1	proliferative	30.4	26.8	37.4			14	5 0	-	8.5
U02020_at	U02020	ppef	Pre-B cell enhancing factor (PBEF) mKNA	70.3			j		1			

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110011												
M10943_at_	M10943	mtIt	Metallothionein-If gene (hMT-If)	5.5	26.1	26.6	C	C	27	-	0	C
			PTGS2 Prostaglandin-endoperoxide synthase									
L15326_s_at_	_	cox2	cyclooxygenase)	30	7 50	0.00	Ċ	Ċ	(
M86849_at	M86849	cx26	Connexin 26 (GJB2) mRNA	000	22.7	27.4	V (7.7	0.0	17.7	5	2.4
M21005_at_	M21005	caga	CALGRANULIN A	20	22.7	31.0	4.0	1	7,1	4 0		4.5
M90657_at_	M90657	m3s1	TUMOR ASSOCIATED ANTIGEN I &	t u	47.77	0.001	5 6	4.1	0.0	8.0	ਾ	0.9
M16750_s_at				10.0	7:77	30.1	5.0	0.3	0	0	0	ा
i	_	pim1	PIM1 Pim-1 oncogene	28.7	α	α.	7	0			ı	(
D86967_at_	D86967		KIAA0212 gene	29.0	21.0	2 7	7 0	5.7	y C	7 0	υ. υ.	3.2
M32315_at_	M32315	tnfr2	TNFR2 Tumor necrosis factor receptor 2 (75kD)	9 9	1 6) (d	5 0	ò	0.0	0	77	<u>4</u>
U64197_at	U64197	mip3a/larc	ICC chemokine I ABC precingor	0.01	70.7	28.5	0.3	ري د ک	9.0	5.4	1	2.5
D14874_at	D14874	adm	ADM Adrenomedullin	10.8	20.7	164.2	1.7	12.2	16.1	0	3.9	6.4
M36284_s_at	+			21	20.1	46.2	3.4	4.5	10.4	2.5	5.2	16.1
	M36284	ge	GYPC Glycophorin C (Gerbich blood group)	4.6	9	7 1		U	1	-	0	(
×20710 24	V 70710	1741	MTF-1 mRNA for metal-regulatory						1	9	2	2.3
7/0/10 at	01/0/	THUT	transcription factor	8.7	19.7	8.9	2.9	2	1.1	0	ıc.	0
U08021_at_	U08021	nnmt	Nicotinamide N-methyltransferase (NNMT) mRNA	3.7	0.0	1	0					
1			Activin beta-A gene, regulatory sequence of	5		`.	2	2	5	8:0	5	0.4
D17357_at_	017357	actbA	5'upstream region	29.4	18.8	0.0	0	o	7	0	_	
AF005//5_at	11		Caspase-like apoptosis regulatory protein 2				;		?		7	4
AE00044E 2+	AF005//5	dill	(clarp) mRNA, alternatively spliced	7.8	18.5	37.9	0.7	5.9	5.4	m	7 6	18.4
7 0004+57_a1	AF008445	plscr1	Phospholipid scramblase	000						-	-	
U15460_at_	U15460	batf	BZip protein B.ATF mRNA	19.0	17.1	17/71	7 4	9.7	38.3	27.0	6.3	88.5
				2		07	2	2	ر در	7	3.3	
X65724_at	X65724	dpu	NDP Norrie disease (pseudoglioma) protein	33.4	17.1	39.4	-0	1.2	C	رن بر	C.	C T
L78440_at_	L78440	stat4	STAT4 Signal transducer and activator of transcription 4		1					3		
Z48481_at	248481	mmp14	MT.MMP protein	4.0	10.4	40.6	0		6.5	3.1	2.4	7.8
				12.2	15.6	10.1	1.3	<u>∞</u>	2.7	~	0	2.4
X03656_rna1			gene for gene extracted from Human gene for granulocyte colony-stimulating factor							-	 	
at	X03656	gcsf	(G·CSF)	19.4	15.2	37.6	C C		Ľ.			
					;	5	5	7.7	7	-	5	-

	_		WNT5A Wingless type MMTV integration site	-	ŀ			ŀ			-	
L20861_at_	L20861	wnt5a	5A, human homolog		ū		C	-		•	•	,
M13792_at_	M13792	ada	ADA Adenosine deaminase	13.5	170		2 0	1 -	5 0	7	 	4.6
X05232_at_		mmp3	MMP3 Stromelysin	20.00		100.1	3 0	0.1	0.0	3.6	7.7	12.3
D87953_at_	D87953	rtp	RTP	27.1	1 0	0.00	200	7.0	7 0	5	0	
M54915_s_at				2	7.1	40.0	7	20	0.5	7.7	0.8	5
1	M54915	pim1	PIM1 Pim-1 oncogene	11	13.7	37.2	2	2 1	0	o	7	ď
D12775_s_at	D12775	ampd3	AMPD3 Adenosine monophosphate	1				1	4.5		<u> </u>	
M68840 at	M68840	maga	MAOA Monoamine oxidasa A	14.7	13.1	18.9	7	2.7	0.9	0.8	1.2	4.5
			TGB3 Integrin beta 3 (platelot glucoscotti	11.2	13	11.7	8.0	3.4	0	0.7	2.1	0.7
M35999_at_	M35999	itgb3	illa, antigen CD61)	8	12.8	2.0	C			1 7		
0000	0		MITOCHONDRIAL ELONGATION FACTOR TS					+	-	-	1	
L3/936_at_	L3/936		PRECURSOR	6.1	12.5	19.6	9.0	5.5	0.4	9.0	5.6	5.1
S66896_at_	968998	scca1	SCCA1 Squamous cell carcinoma antigen 1	ά	10.0	27	-	C	(,	,	
			SERINE/THREONINE PROTEIN KINASF	2	25.3	0.	>	0.7	λ. λ.	1	0.2	1.5
X66363_at_	X66363	pctk1	PCTAIRE-1	11.2	11.9	32.3	C	7 0				C L
USDSDS_at_	USGSGS	тар3к4	KIAA0213 gene, partial cds	10.8	117	7.0	000		;		2 0	0 1
U15174_at	U15174	nip3	Nip3 (NIP3) mRNA	0	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	7.70	0.7	0.0	-	3.0	2	4.
X90858_at_	X90858	an	Uridine phosphonylase	200	1	5/2		7.7	0.8	0.3	1.7	11.1
			acet foundation of the	13.1	11.4	10.9	2.4	1.8	0	4.5	1.9	8.3
			ANPEP Alanyl (membrane) aminopeptidase									
M22324_at_	M22324	anpep	(aminopeptidase N, aminopeptidase M, microsomal aminopeptidase CD13)	U		1						
L08187_at_	L08187	ebi3	Ovtokine receptor (FBI3) mRNA	10.1	4.0	ر د ز	5.1	6.1	0	2.2	3.1	7
HG2981.				‡.	10.2	54.9	5	9.0	m	0	2.1	12.5
H13125_s_at												-
_	HT3125	cd44	Epican, Alt. Splice 1	13	7 0	α	c				(- 1
104100			ETS2 Vets avian erythroblastosis virus E26			5	7		1	7.7	2.3	
J04102_at_	304102	ets2	oncogene homolog 2	23.3	9.6	53.3	0.7	4.7	C	С	r.	'n
014407 24	7077	4	COT Proto oncogene c cot (protein.		-		_		,	1		?
71443/ al	014497	103	serine/threonine kinase)	4.1	9.5	27	0	9.0	4.4	0.5		10
U09579_at	009579	cone5	CUKN1A Cyclin-dependent kinase inhibitor 1A			- ;	;			2	1	1
7		22:042	(PC+, OP+)	12	9.5		2	C.	C.	c c	7	0

X01060_at_	X01060	cd71	TFRC Transferrin receptor (p90, CD71)	26.3	8.9	13.7	0.3	2.6	0.5	1.2	4.9	8.6
L22524_s_at_	L22524	mmp7	MATRILYSIN PRECURSOR	9.6	8.6	63.7	0	0	5.1	0.4	0.1	1.9
X07820_at_	X07820	mmp10	MMP10 Matrix metalloproteinase 10 (stromelysin 2)	13.3	9.8	8.86	0	0	1.5		000	3.4
U19557_s_at	£33011	C	Squamous cell carcinoma antigen 2 (SCCA2)								-	
Т	/66510	sccaz	MKIVA	17.5	8.5	24.2	0	0.6	1.5	0	0.1	0
1	581914	lex-1	EX:1	7.9	8.1	10	1.1	1.9	0	2.5	2.2	4.3
	M30894	tcrg	TCRG T cell receptor gamma chain	8.9	80	40.3	0	0.7	m	1.8	0	1.4
M93056_at_	M93056	ei	LEUKOCYTE ELASTASE INHIBITOR	23.4	∞	30.8	3.7	1.8	0.7	1.6	4 8	0
U43522_at_	U43522	fak2	Protein tyrosine kinase PYK2 mRNA	5.2	7.9	16.3	Ī	1.6	5.8	0	129	25.9
	M24069	csda	DNA BINDING PROTEIN A	14	7.8	12.1	ō	0.8	C	0.3	C	- -
X01057_at	X01057	il2r	IL2RA Interleukin 2 receptor, alpha	9.3	7.4	39.3	0	9.0	0.3	2.8	0.4	-
			Phosphoribosypyrophosphate synthetase									
D61391_at_	D61391	prpsap1	associated protein 39	2.1	7.3	6.4	0	0.7	0	0	0	2.8
D88422_at_	D88422	csta	CYSTATIN A	12.8	7.1	6.5	3.8	-	-	2.2	0.5	0.5
J04501_at_	J04501	gys	GYS1 Glycogen synthase 1 (muscle)	9.8	6.9	4.1	0	8.0	0	1	0.3	2.2
2000	000107		Metallothionein-I-A gene, complete coding									Γ
KU1383_at_	KU1383	mtia	sednence	3.7	6.5	23.6	0.4	6.0	1.6	1.2	6.0	0
D28235_s_at_	D28235	cox2	Cyclooxygenase-2 (hCox-2) gene	28.6	6.4	147.9	1.3	1.5	21.9	0	7 0	7 7
U76421_at_	U76421	adarb1	DSRNA adenosine deaminase DRADA2b (DRADA2b) mRNA	2.6	93	8	C	C			-	-
U16720_rna1 _s_at_	U16720	110	Interleukin 10 (IL10) gene	17.1		83.6	0	0	0 0	1	0	, ,
			815A9.1 gene (myosin heavy chain) extracted									i
AF001548_rn al at	AF001548	mvh11	from Homo sapiens chromosome 16 BAC clone CIT987SK-815A9 complete sequence	27	ر ب	300	7	0	u	C	· ·	u
D78156_at_	D78156	gaplm	RasGTPase activating protein, partial cds	7.2	5 0	30.0	C	9 0		40	200	2.0
U42408_at_	U42408	lad1	Ladinin (LAD) mRNA	6.3	5.9	67.8	03	4	2 0	000	0	ο σ
			GRANULOCYTE.MACROPHAGE COLONY. STIMULATING FACTOR RECEPTOR ALPHA									
X17648_at	X17648	gmcsfR	CHAIN PRECURSOR	9	5.9	12.9	0	1.9	0	0.5	6.0	8.4

Figure 4E

	_		INON-IENS Deta gamma-crystallin like protein	_				-	-	-		ſ
U83115_at_	U83115	aim1	(AIM1) mRNA, partial cds	0	7	19.3	1		7	1	<u> </u>	0
Z24725_at_	224725		Mitogen inducible gene mig.2	4.8	5.2	17.8	; C	70	200	1	200	0 0
M31551_s_at			PAI2 Plasminogen activator inhibitor, type II				7	-	7.7	5	2	9
ı	M31551	pai2	(arginine serpin)	1 3	ır	7 70		c	-	_	-	(
X55740_at	X55740	nt5	NT5 5' nucleotidase (CD73)	0.9	47.7	101		5 0	5	5 0	5	
M28983_at_	M28983	illa	IL1A Interleukin 1. alpha) L	, ,	17.7	2 0		1.1	7.7	9 0	200
				1.7	7.7	17:4	ر ن	4.0	5.3	2.0	5	3.6
D79984_s_at_ D79984	D79984	supt6h	KIAA0162 gene	4.4	4.1	2	1 7	0		0		0
			Heparan N-deacetylase/N-sulfotransferase-2				+	2		111	>	6.3
U36601_at_	U36601	ncst2	mRNA	3,3	4.1	11.2	С	C		C		0
U34877_at_	U34877	blvra	Biliverdin-IXalpha reductase mRNA	2	3.7	4 7	 -	000		0	5 -	3 6
U77180_at_	U77180	mip3b/elc	EBI1-ligand chemokine	12.5	37	2332	90		000	2 4	1 00	1 00
			SCYA1 gene (secreted protein 1.309)		+	1	2	7	2	?	7.07	35./
M57506_rna1			extracted from Human secreted protein (1.				-					_
at	M57506	i309	(309) gene	2.3	ď	916	0	0	7		c	-
			CAB3b mRNA for calcium channel beta3					2	2	7	5	1
U07139_at_	U07139		subunit	^	0	ιι		-			- (C
HG3494.	HG3494.			1		5.5		1	0.4	7	2	0.7
HT3688_at_	HT3688	nfil6	Nuclear Factor Nf.II6	11.4	α	ς,	α		C	c	,	
			VDR Vitamin D (1,25- dihydroxyvitamin D3))	;		+	7	0.7	0	2.3
J03258_at_	103258	vdr	receptor	9 1	0	2 6	- ~	,	C		-	,
X15306_rna1					2	51	?	2.1		5	1	7.7
at	X15306	nefh	NF.H gene, exon 1 (and joined CDS)	œ	α	36.6	-		C	0		-
				+		2	2	+	7	62	7	
X95325_s_at_ X95325	X95325	csda	DNA BINDING PROTEIN A	37.7	2.7	7.2	1 7		C.	7	1 7	C
M13452_s_at						+		1	?	1	1)
	M13452	cmd1a	LMNA Lamin A	0	α C	2 1	o c		ŗ	1		- 0
				1	5	7.11	Ö	<	ē	17 (1	-	<u> </u>

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affyID	GBA	gene symbol	gene Name	feco	hero	100	fors	0,4	9,00		ĺ	
M14660_at_	M14660	g10p2	ISG-54K gene (interferon stimulated gene) encoding a 54 kDA protein, exon 2	_			-	0.00		icail	IIICALI	ıcan
X02530_at_	X02530	inp10	INP10 Interferon (gamma) induced cell line; protein 10 from		2	6.73		- 1	706	.7	2	33.4
			TNF-related aboutosis inducing ligand TDA!	12.5	13.1	442.2	137.9	290.4	501.4	5.4	205.9	451.4
U37518_at	U37518	trail	MRNA	14.7	34.2	134 3	171 9	230 1	700	T.	,	0
U59286_at_	059286	itac	Beta-R1 mRNA, partial cds	34.9	27.6	237.9			370.2	7.0	109.1	318.2
L40387_at_	L40387	oasi	Thyroid receptor interactor (TRIP14) gene, 3' end of cds	4	7 2	5	1		1	9 .	†	309.7
Y00451 s at	Y00451	100	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	7	?	3	103.3	7.001	124.5	-	0.4	13.6
X72755 at	X72755	mig	Himia mena	17.8	8.2	14.6	62	53	23.9	1.2	12.2	7.7
		0	GEBP6 Inclination grounds for the contract of	3.2	5.2	68.3	59.4	52.3	58.6	1.6	77.5	128.6
M62402_at	M62402	igfbp6	6		-	7.	7 0	0		-		
			IFNA gene (interferon alpha.d) extracted from	7	5	1	4.00	4.σ α	9/9	0	0	0.4
J00210_rna1			Human leukocyte interferon (IFN:alpha) alpha.d						_			
_at	J00210	ifna13	gene general de la companya de la co	c	C		L.	L	0	-		_
V00535_rna2			Interferon beta 1 gene extracted from Gene for	;	7		0.0	4α.υ	192.3	5	0	0
s_at_	V00535	ifnb1	human fibroblast interferon beta 1	0	×	187.4	7 89	22.0	166.4	,	-	- (
JUDU3/_at_		sps	L-SERINE DEHYDRATASE	C	-	1	5 5	33.50	4.001	7.7	5)
M22976_at_	M22976	cyb5	CYB5 Cytochrome b-5	5 0	- C	4:4		31.6	15.8	0.1	0	4.8
			Eyon 1b. used only in this 2 this	2.7	4.2	7	5.5	30.2	4.6	1.7	2.1	5.6
X94563_xpt2	2040		H. sapiens dbi/acbp gene exon 1 & 2./ntype=DNA		<u>.</u>							
-1-91-	V34303		/annot=exon	14.2	က	m	4.6	29	89	8	0	-
at		pmaip1	LRP1 ATL-derived PMA-responsive (APR) nentide	-			,					
U80073_at_	U80073	tap	Tip associating protein (TAP) mbNA	2 6	7,	172.0	16.9	24.1	249.1	0	0.4	11.1
			PRG2 Proteoplycan 2 hone marrow (patrice) billion	6.3	1.5	6.1	19.7	21.8	31.1	0.1	5.6	7.6
			cell activator, eosinophil granule major basic									
s_at_	226248	prg2	protein)	C	7	-	0	,	r	(•	
HG2/24.	HG2724.				J . 1	-	6:3	51.3	5	5	0	0
11 2020 at			Oncogene Tis/Chop, Fusion Activated	0	0	20	8	19.3	000		0	
003576_at	8/7600	tap	Fibroblast activation protein mRNA	Ō	С	c	148	17.0	27.0		5 0	101.1

HG4069.				ŀ	-		_		-	-	-	Γ
s_at									_			
1		mcp1	Monocyte Chemotactic Protein 1	5.9	2.5	2.8	38.4	16.9	10.3	<u>C1</u>	10.7	9.5
M62831_at_	M62831	etr101	Transcription factor ETR101 mRNA	4.6	20.4	4.3	9.3	16.6	11.2	9.0	0.5	1.2
10 0000	79000		Annexin II, 5'UTR (sequence from the 5'cap to the	í	,							
U20304 at	720304		Start codon)	8.2	0.1	4.1	14.2	15.2	6.1	1.4	0	3.1
	D25696	prsc1	Cysteine protease	0	6.0	1.2	2.5	14.3	3.8	0.1	0.1	6.4
			ZNF183 gene	0	0	9.0	6.6	13.7	34.5	0.5	0	0
D86962_at_		grb10	KIAA0207 gene	2.2	1.7	37.1	19.5	12	108.7	1.3	1.3	9.5
X78992_at_		erf2	ERF.2 mRNA	0	6.0	1.5	20.6	11.9	24.9	0.2	0	0
U22662_at_		lxra	Nuclear orphan receptor LXR-alpha mRNA	1.5	7.3	9.6	34.8	11.4	9.4	8.4	3.1	10.9
U07802_at_		erf2	ERF.2 mRNA	0	2.6	2.1 21.2	6.4	11.3	21.6	0.7	0.1	0
HG3884.	HG3884.									-		
HT4154_at	HT4154	hpx42	Homeotic Protein Hpx.42	-	0	m	4.3	11	2.8	0	0	0
X97324_at_	X97324		Adipophilin	0	9.0	2.8	2	10.8	5.7	0	0	9.9
X07743_at_	X07743	plek	PLECKSTRIN	9.7	2.1	5.7	13.9	10.7	2.7	3.6	1.6	5.6
L01664_at_	L01664	clc	CLC Charot-Leyden crystal protein	0.5	2.7	8.0	2.6	10.2	15.8	0.3	0.8	1.6
X57351_at_	X57351		RPS3 Ribosomal protein S3	8.0	3	26.5	8.2	10	43	1.4	5	72.9
Z11518 s at Z11518	211518		HISTIDY! TRNA SYNTHETASE	C	7		7	,	0	-	u C	,
						† ;	2	2	0	1		7./
U70663_at_	U70663	ezf	Zinc finger transcription factor hEZF (EZF) mRNA	0	0	0	10.2	9.9	55.7		0	-0
U65093_at_	065093	mrgl	Msg1-related gene 1 (mrg1) mRNA	0	0.7	0.4	7.2	9.6	10.4	0.2	0	0.4
U27699_at_	U27699	slc6a12	SODIUM- AND CHLORIDE-ÖEPENDENT BETÄINE TRANSPORTER	6.0	0	51.9	14.9	000	99	0.5	C	42 B
X05345_at_	X05345	hars	HARS Histidyl tRNA synthetase	9.0	2.2		28.5		7.7	0	2.6	3.2
M95809_at_	M95809	gtf2h1	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT	-	£.	0.2	3.1	8 1	16.7	0.1	0.5	3.3
D14826_s_at_D14826	D14826	crem	CREM CAMP responsive element modulator	3.4	2	6.3	13.7	7.8	50.6	5.1	1.6	7.4
U59748_at_	U59748	dhh	Desert hedgehog (hDHH) mRNA, partial cds	9.0	0	2.4	5.4	7.3	24.5	0	0.1	000
M16707_rna1 _s_at_	M16707		Histone H4 gene, clone F0108	0.3	8.0	1.4	8.4	7	2.8	4.0	0	1 7
		•						-		-		
[S77154_s_at_[S77154	S77154	nurrl	TINUR	0.2	5.1	0.3	8.6	6.8	9.8	0.7	0	0.7

X96719_at_	X96719	aicl	AICL (activation induced C type lectin)	Ь	1.7	O	4.9	5.9	5.9	0.5	6.0	8 6
			ACTIN, AORTIC SMOOTH MUSCLE (ALPHA-ACTIN		\vdash							T
X13839_at	X13839	acta2	(2)	0.1	0.7	1.2	7.5	5.8	5,6	0	5.4	3.4
J04111_at_	J04111	nni	C-jun proto oncogene (JUN), clone hCJ-1	2.2	4.2	2.4	19.1	5.6	13.4	1.6	0.5	4
Z14978_at_	214978		ALPHA.CENTRACTIN	0.5	9.0	0	1.1	5.1	5.6	0	0	0
D42040_s_at_D42040	D42040	ring3	RING3 PROTEIN	1.3	1	- 00	7.3	ιc	7	1		7 0
Y10032_at_	Y10032	sgk	Putative serine/threonine protein kinase	0	0	1.6	2.5	0 4	5.4	80		0
M63438_s_at			GLUL Glutamate ammonia ligase (glutamine		t							
	M63438		synthase)	1.6	0.2	0.2	2.6	4.6	137.4	0	0	1.2
X92106_at	X92106	blmh	Bleomycin hydrolase	-	1.4	0	1.6	4.5	5,5	0.3	1.4	0
					-					T		
S68271_s_at_ S68271	S68271	crem	CREM CAMP responsive element modulator	1.1	6.0	4.2	12.6	4.2	18.2	1.1	6.0	3.8
M63838_s_at					-		<u> </u>					
_	M63838	ifi16	Interferon gamma induced protein (IFI 16) gene	0	0.4	0	2.6	4	4	0.1	0.1	2.8
			Pre-mRNA splicing factor SRp20, 5'UTR		-							
D28423_at	D28423		(sequence from the 5'cap to the start codon)	0	0	6.0	7.5	3.7	4	0.2	1.1	0.7
U04285_s_at			LIPA Lipase A, lysosomal acid, cholesterol	-		ľ						I
1	U04285	lipa	esterase	0	0.5		1.9	3.7	1.9	~	0	1 1
			CLN3 Ceroid lipofuscinosis, neuronal 3, juvenile		\mid		1					
U32680_at_	U32680	bts	(Batten, Spielmeyer-vogt disease)	2.5	8.0	2.1	10.1	2.1	7.3	0.1	9.0	2.7
U94592_at	U94592	ucp2	Uncoupling protein homolog (UCPH) mRNA	0	0.7	0	0.5	1.5	0	0.1	0.2	0
U50733_at_	U50733		Dynamitin mRNA	1.1	1.9	1.7	1.2	0.4	0	1.7	0	0.4
			Fatty acid synthase {3' region} [human, breast							\mid		
S80437_s_at_ S80437	S80437		and HepG2 cells, mRNA Partial, 2237 nt]	4.0	0	0	0	C	-c	0.7	1 3	0.0

Figure 5C

affyiD	GBA	gene symbol gene Name		feco	heco	teco	fpr8	hpr8	tpr8	ican	mcan	tcan
V00594_at_	V00594	mt2a	Metallothionein isoform 2	1683.1	1698.4	143.4	371.1	414.5	107.8	3.3	261	74.2
X64177_f_at_ X64177	X64177	mt1h	Metallothionein	761.9	728.2	93.6	73.7	6.99	27.4	10.4	27.4	14.9
M21121_at_	M21121	rantes	SCYA5 Small inducible cytokine A5 (RANTES)	728.7	661.7	83.4	717	396.6	115.3	113.6	87.4	43.7
1	X04500	ii1b	IL1B Interleukin 1, beta	199.3	598.3	Γ	9.1	12.6	1	1		
M13755_at_	M13755	isg15	G1P2 Interferon, alpha-inducible protein (clone IFI-15K)	214 1	545 6	57.4	253	662	100.2	302.7	208.8	34.3
X04602_s_at_ X04602	X04602	911	IL6 Interleukin 6 (B cell stimulatory factor 2)	408.5	379.2	1267.5	70.5	76.5	269.4	14.6	43	
U33017_at_	U33017	slam	Signaling lymphocytic activation molecule (SLAM) mRNA	320.7	343.9	685.7	4.8	25.8	e e	2.7	24.4	84.5
V00594_s_at_	V00594	mt2a	Metallothionein isoform 2	167.1	337.3	15	64.9	122.8	34.8	69.4	52.2	9.4
Y00787_s_at_ Y00787	Y00787	81	INTERLEUKIN.8 PRECURSOR	89.1	234.5	40.9	9.8	13.1	8.4	8.2	10.8	10.5
X57579_s_at_ X57579	X57579	activinba	Activin beta-A subunit (exon 2)	1669	233 7	47.2	22.8	16.8	9.6	14.1	19.3	24.6
X02910_at_	X02910	tnfa	TNF Tumor necrosis factor	144.1	225.5	115.7	73.8	58.6	48.5	27.2	81.1	1
L11329_at_	L11329	dusp2	DUAL SPECIFICITY PROTEIN PHOSPHATASE	52.1	177.6	16.1	16.2	14.7	2.4	7.9	1.4	2.9
M33882 at	M33882	m×1	MX1 Myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p.78)	14	x 991	Δ να	6 00	1500	a a	78	6	<u> </u>
M31165_at_	M31165	tnfaip6	TUMOR NECROSIS FACTOR INDUCIBLE PROTEIN TSG-6 PRECURSOR	172.2		624.		100	-		1	
M59465_at_	M59465	a20	TNFAIP1 Tumor necrosis factor alpha inducible protein A20	87	158.7	41.1	65.3	ł	22.9	7.6		1
L19779_at_	L19779	h2a	Histone H2A.2 mRNA	53.2	154	83.4	40.2	'			Γ	m
X65965_s_at_ X65965	X65965	sod2	SOD-2 gene for manganese superoxide dismutase	233.7	149.2	204	143.7	86.3	86.3	10.6	35.9	109.3
X67325_at_	x67325	1627	INTERFERON ALPHA INDUCED 11.5 KD PROTEIN	136.8	143.4	618.8	265.8	-	498.1	50	212	1

Figure 6A

In ... htors: Nir Hacohen, et al.

U53830_at	U53830	irf7	Interferon regulatory factor 7 (hymirf?) mRNA	42.6	130	70	8 88	7.0 5.	0 0	, ,	,	Ĺ
M23178_s_at	M23178	mip1a	MACROPHAGE INFLAMMATORY PROTÉIN 1. ALPHA PRECURSOR		125	-	ς ς α	0.27	0 0	7 7	1,00	0./4
U04636_rna1 _at_	U04636	cox2	Cyclooxygenase-2 (hCox-2) gene	110	120.8	9.809	15.3	13.8	87.4	j r.	0. 4	5.0 A7.
X07834_at	X07834	sod2	SOD2 Superoxide dismutase 2, mitochondrial	57.7	104.1	240.9	34.7	92.1	91.6	6.6	17	116.5
023000_al	023000	DCIZAI	BCI-Z related (BfI-1) mRNA	105.3	97.9	678.7	40.7	35.7	117.5	4	8.3	179.1
M31166_at_	M31166	ptx3	P.1X.3 Pentaxin-related gene, rapidly induced by IL.1 beta	82 7	88.9	807.3	21	27.2	122.2	5.2	2.5	20.0
L31304_d1	L31384	ccr/	CMKBK/ Chemokine (C.C) receptor 7	58.1	87.3	98.2	23.3	9.69	83.5	26.5	11	56.3
X57351_s_at_ X57351	X57351	ifitm2	RPS3 Ribosomal protein S3 / wrong name	13	84.2	13.1	15.3	81.7	30.3	55.9	20.8	7.5
01335_al	28610	cdsnp	Protein tyrosine phosphatase mRNA	57	76.5	44.5	9.8	11.1	8.8	2.4	4 4	13.4
M30818_at	M30818	mx2	MXZ Myxovirus (influenza) resistance 2, homolog of murine	21	74.4	42.6	40.9	82		ά	30,7	000
M24594_at	M24594	g10p1	IFI56 Interferon-induced protein 56	19.8	71.6	77.5	8.06	266	141	180	248 6	20.6
000			6·16 gene (interferon-inducible peptide								0.01	5
U229/U_rna1	020201	, ,	precursor) extracted from Human interferon.									
Y50902 24	VEC970	81p3	inducible peptide (6·16) gene	115.3	68.2	5.8	9.07	97.1	13.7	13.1	15.6	5.5
15702 at	115702	wars	DE P. CHANYL I KNA SYNTHETASE	40.2	6.99	32.5	56.1	59.5	25.2	12.8	18	20.2
1172002 6 24	27/05	2	Br B-tactor, properdin	46.3	64.4	85.6	3.3	7.9	7.8	5.4	6.5	33.8
0/2002_s_at	U72882	ifi35	Interreron-induced leucine zipper protein (IFP35) mRNA, partial cds	23.2	220	30 7	, ,	7 30	5	000	6	L
J04164_at_	J04164	ifi17	RPS3 Ribosomal protein S3 /wrong name	25.8	57.2	37.7	34.5	45.6	793	11.5	60.3	35.1
X99886_s_at_	98866X	mcp2	MCP.2 gene	0		0,00			1			
U37546_s_at					15	20.3	44.3	97.0	¥ \	χ.	23.8	/9.5
	U37546	ciap2	IAP homolog C (MIHC) mRNA	54.1	48.6	62.2	5.3	3.7	315	7 2 7	34	ה
M692U3_s_at	MEGOODS		SCYA4 Small inducible cytokine A4					-			5	
1188967 34	188967	mip10	(nomologous to mouse Mip-1b)	164.9	44.6	19.3	372.7	82	10.5	4.6	30.1	11.6
,	000000	11611143	HEM45 mKINA	34.6	43.7	191	27.2	15.5	73.3	8.8	43.4	1161
X57522 at	YE7E22	1	TAP1 Transporter 1, ABC (ATP binding									
7	A37.366	lapı	casserre)	34.3	42.3	48.3	76.1	53.3	47.7	11.6	31.7	413

J04130_s_atJ04130 M92357_atM92357	J04130	•									_	
57_at_		mipib	(homologous to mouse Mip.1b)	81.9	42.2	7 7	703	71	r.	0	7	Ċ
	M92357	tnfaip2	B94 PROTEIN		39.7	1042	20.5	31.0 X	3.7	<u>, u</u>	1 0	20.7
X77584_at_	X77584	txn	TXN Thioredoxin	22.4	39.5	5.2	16.8	18.0	0 /	α	ς α	20.7 D.D.D.
J12767_at_	U12767	minor	Mitogen induced nuclear orphan receptor (MINOR) mRNA	700	000		7		1			3
U52513_at_	U52513	ifit4	RIG-G mRNA	25.1	39.3	7.77	0.70	84.6	13.7	13.0	20.3	15.7
85_rna1	110000	0	G0S2 gene extracted from Human G0S2					2	3	7:51	7	ì
_s_at_	W/2885	G0S2	gene, 5' flank and cds	126.1	38	44.9	10.8	6.2	5.3	10.4	11.3	18.7
,			Thyroid receptor interactor (TRIP10) mRNA,							5	?	ò
403/9 at	L403/9	trip10	3' end of cds	34.8	37.1	33	5.3	5.5	7.6	22.2	8	13.5
MZ9696_at	M29696	11/1	IL/R Interleukin 7 receptor	61.7	36.8	55.8	27.5	13.7	1.5	σ	11	22.0
			PTGIR Prostaglandin 12 (prostacyclin)							,		7.67
D38128_at_	D38128	ptgir	receptor (IP)	29 8	34.8	71.9	7.9	0	16.2	-		55.6
	1		TNF-related apoptosis inducing ligand TRAIL		-		-			:		
J37518_at_	U37518	trail	mRNA	14.7	34.2	134.3	171.9	230 1	590.2	5 7	1001	210
M13690_s_at			C1NH Complement component 1 inhibitor					-	1.222		2	210.6
	M13690	clnh	(angioedema, hereditary)	16.9	34.1	209.8	13.8	12.6	26.2	9	30.1	2580
			ICAM1 Intercellular adhesion molecule 1							;		0.00
	M24283	icam1	(CD54), human rhinovirus receptor	70.6	32.4	20.7	200	11.1	3.4	9	Œ	σ
U/2661_at_	0/2661	ninj1	Ninjurin1 mRNA	43.8	31.1	48.8	CC	7			0	5 0
HG1612.	HG1612.					2	1	†				5.00
HT1612_at_	HT1612	macmarcks	Macmarcks	19.2	30	44.7	11.5	30.2	16.9	3.4	00	15.6
5_s_at_	X02875_s_at_ X02875	oas1	OIAS (2'-5') oligoadenylate synthetase	16.7	5	787	<u>r</u>	0	117		9 6	
			Hepatitis Cassociated microtubular			50		0		1.1	c.U.3	80.4
D28915_at_	D28915	mtap44	aggregate protein p44	8.5	29.6	53.6	10.7	47 1	44 3	13.3	n n	Q
	U48807	dusp4	Dual specific protein phosphatase mRNA	5.6	29.6	7.4	2.4	3.1			20.5	217
J03891_at_	U03891	unknown	Phorbolin I mRNA, partial cds	43.8	28.9	210	1803	200) U	20.7
U50648_s_at			Interferon inducible RNA dependent protein					0.00	63.3	i	0.0	09.9
	U50648	pkr	kinase (Pkr) gene	19.8	28.4	22.3	17.8	6,3	22.1	40 1	24.8	101
U3U/55_at	D30/55	NAF1	VIM Vimentin	56.3	28.2	19.6	19.9	4 9	40	141	7 0	10
	U59286		Beta-R1 mRNA, partial cds	34.9	27.6	237.9	201.6		340.8	3 8	74.4	389.7
UU3U5/ at	/505001	Snl	Actin bundling protein mRNA	59.8	27.5	8.4	4 1	1_	14 1	32	12/	2000

Figure 6C

			Urokinase type plasminogen activator							-		
U0993/_rna1	100001		receptor gene extracted from Human									
-s_ar_	00993/	plaur	urokinase type plasminogen receptor	17	26.9	14.5	12.5	10.7	2.4	m	3.5	3.7
X61123_at_	X61123	btg1	BIG1 Brell translocation gene 1, anti- proliferative	30.4	26.8	1.4.4	α	2		0 0	,	0
					2	r r		t o		0	7	7.
X53296_s_at_		illrn	IL1RN Interleukin 1 receptor antagonist	65.5	26.4	9	787	14 4	4	4	7 7	-
S59049_at_	S59049	ier1	RGS1 Regulator of G-protein signalling 1	4.5	25.9		22	000	0	2 1	α 0 ι	7 7
M14660_at_	M14660	g10p2	ISG-54K gene (interferon stimulated gene) encoding a 54 kDA protein, exon 2	5.9	7,7	27.0	0	310 4	300	0 0	2	
L05072_s_at	L05072	irf1	IRF1 Interferon regulatory factor 1		27 2	C	2 2 2	000	3 8	y .	0 7	4.00
M16750 s at				1	64.3	3	3	30.5	42.4	t.	34.0	50.5
l I	M16750	pim1	PIM1 Pim-1 oncogene	28.7	21.8	418	0	۲ د	0	0	C L	C
X66401_cds1			LMP2 gene extracted from H.sapiens genes							7		0.6
_at	_	tap2	TAP1, TAP2, LMP2, LMP7 and DOB	30.6	20.6	32.4	12.9	9	7	6 1	23.6	21.0
D14874_at_	D14874	adm	ADM Adrenomedullin	18	20 1	46.2	3.4	4.5	10.5	7 2	1 Э г.	15.1
			MAJOR HISTOCOMPATIBILITY COMPLEX					?	F	21	7:5	1
M69043_at_	M69043	ikba	ENHANCER BINDING PROTEIN MAD3	23.9	19.6	11	14.8	9.5	4 7	4	3.7	α
L13210_at_	L13210	mac2bp	Mac-2 binding protein mRNA	9	19.5	12	5.6	25	 			20.00
			PROBABLE G PROTEIN COUPLED RECEPTOR						2	5,7	0.11	32.3
L06797_s_at_		cxcr4	LCR1 HOMOLOG	12.7	19.2	30.6	80	7 9	0	14 9	7	20.7
D42073_at_	D42073	rcn1	Reticulocalbin	5.7	18.4	613	2	7.7	137	000	110	20.7
D50663_at	D50663	tctel1	CW.1 mRNA	23.1	17.9	33.6	16.9	13.3	15.1	7 -	12 5	000
D45248_at_	D45248	pa28b	Proteasome activator hPA28 subunit beta	13.1	17.2	0 9	171	200	1 2	1 6	17.0	0 1
1			INTERFERON-INDUCED GUANYLATE-BINDING					1	;	51	?	0
M55543_at	M55543	GBP2	PROTEIN 2	30.7	16.1	47.1	11.4	3.5	9	7	-101	23.5
M31724_at_	M31724	ptp1b	PTPN1 Tyrosine phosphatase 1	14.7	15.8	162	67	ά		2 2	17.7	2.5
U19261_at	U19261	traf1	Epstein-Barr virus-induced protein mRNA	25.7	15.4	25.2	ά	10.1	1 0	j u) u	ن د
HG544.	HG544.					11.51		3,1		0		-
HT544_at_	HT544	ecgf	Endothelial Cell Growth Factor 1	5.9	15.3	Δ	10.0	n C	,	7 30	7	٦
D10040_at_	D10040	faci2	FACL1 Long chain fatty acid acyl-coA ligase	24.7	15.2	26.2	13 0	7 0	1201	20.7	10.0	7
X74039 at	X74039	nlaur	Variant urokinase plasminogen activator	,	:		2	;	17.7	7.7	† 	7.4.7
1	20000	2000	I COCPTO (UI MICE) IIIMIN, PALIIAI COS	1.0	12	7.3	1.6	4.2	2.8	1.5	5.4	5.1
U42043_at_	D42043	MIAAUU84	KIAA0084 gene, partial cds	24.8	14.1	27.1	7.1	3.1	4 5	α α	8	ō

0000/2_41_ 0000/2	7/0000	IIIUra	IL10R Interleukin 10 receptor	9.5	14.1	9.1	10.6	15	9.5	42	5 9	5
D13146_cds1 _at_	D13146	cub	2,3'-cyclic-nucleotide 3'-phosphodiesterase gene extracted from Human 2',3'-cyclic-nucleotide 3'-phosphodiesterase gene	0 4	0	c u				1		
U83461_at_	U83461	copt2	Putative copper uptake protein (hCTR2) mRNA	0.00	2	50.3	7.0	4 4	101	0.0	8.	11.2
AB000115_at	+			0.5	13.4	19.1	6.2	10:1	12	വ	4.7	22.6
	AB000115	unknown	mRNA	9.8	13.1	24.9	8.4	26.9	28.7	3.4	6.1	37.6
X02530_at_	X02530	inp10	INP10 Interferon (gamma)-induced cell line; protein 10 from	12.5	13.1	2 6 6 7 9	1370	7000	7 104	, u	200	
J04080_at_	104080	cls	C1S Complement component 1, s			1		1.00.4	1	4	6.602	4.104
			NCF1 47 kD autosomal obropio	7.7	17.0	01.0	5.6	χ. υ.	31.4	3.7	6.4	18.9
	M55067	ncf1	granulomatous disease protein	2.5	12.6	24.5	19.1	28.5	22.1	4 4	σ	17.0
41109/_at_	7,1109/	cd83	CD83 ANTIGEN PRECURSOR	18.7	12.6	8.6	19.6	9.5	9	4	10.0	7 / 2
M97936_at_	M97936	stat1	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.ALPHA/BETA	7.4	11 4	16.9	12	77	-	0,0		4, 00
	1		DNA-binding protein CPBP (CPBP) mRNA,						1	0.0	1	78.3
044975_at	044975	bcd1	partial cds	2.4	11.3	6.8	3.7	7.1	7.8	1.5	4 2	n n
1	LUGUOS	nspr4	DNAJ PROJEIN HOMOLOG 2	12.8	11.1	12.7	10.9	20.7	9.7	17	30	200
176767 6 0t	003100	7-40	B4-2 protein mRNA	29.4	10.7	8.2	11.4	5.7	2	6.4	26	7
0/0/04_s_dl	U76764	cd97	CD97 CD97 antigen (leucocyte antigen)	0 7 1	1	,	:		1			;
X69910_at_	X69910	p63	P63 mRNA for transmembrane protein	2 5	10.	26.4	0.4	2.0	2.3	7.7	2.3	7.5
D79206_s_at_D79206	D79206	sdc4	SDC4 Synderan 4 (amphighydrus 2008)					2,4	, ,	υ υ	4.0	29.3
L22342_at_	L22342	unknown	Nuclear phosphoprotein mRNA	0.0	ט נט	7	15.2	11.2	10.2	2.7	2.7	9
AF014958_at				0.0	7.7	11.4	4.1	0 1	+	11.5	12.2	21.7
_	AF014958	ccr6	Chemokine receptor X (CKRX) mRNA	3.6	0	36.3	7 2	n n	v	ч	,	,
			MHC-encoded proteasome subunit gene LAMP7-E1 gene (proteasome subunit LMP7)									
Z14982 rna1			extracted from H.sapiens gene for major histocompatibility complex encoded									
	214982	lmp7	proteasome subunit LMP7	3.6	9.5	9 4	4	α	σ	r.	0	0
								;	5	7	,	i

			BONE MADDOW STROMAL ANTICENS SEET	-	-							
D28137_at_	D28137	bst2	2)	i.C	σ	120			- 5	7 0	4	0 7 0
M31627_at_	M31627	xbp1	X BOX BINDING PROTEIN 1	4.4	6	15.4	167	206	27.1	, r	7 - ~	0.10
M79462_at	M79462	- A	PML Probable transcription factor PML (alternative products)	2	0	-	,	5 7		j (1 0	r (
M62324 at	M62324	mrf.1	Modulator recognition factor I (MRF-1) mRNA, 3' end	0		200	/ V	ò			χ, (0
M87434_at_	M87434	oas2	69/71 KD		0 0	210.6	7 7.0	33.1	14.3	2 2	3.4	6.2
X17093_at_	X17093	hla-cda12	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F ALPHA CHAIN PRECURSOR		0 0	7 0 4	r c	-	2 -	2 5	2	0. /1
L07633 at	L07633	pa28a	INTERFERON GAMMA UP: REGULATED 1-5111 PROTEIN PRECURSOR	i u	t e					61.0		8.7
M97935_s_at	MAO 703E	1 1 1 1	SIGNAL TRANSDUCER AND ACTIVATOR OF		0	10.1	C	4.4	9 9	5.3	φ. Ψ.	20.1
	M9/935	stati	IRANSCRIPTION 1 ALPHA/BETA	4.1	7.9	10.5	2.5	5.3	12.2	9.8	17.2	36.7
U20158_at_	U20158	lcp2	76 KD3 tyrosine phosphoprotein SLP:76 mRNA	3.7	7.8	9.8	8	12.6	3.4	ю	2.3	3.3
HG2917. HT3061_f_at_	HG2917. HT3061	hla	Major Histocompatibility Complex, Class I, E (Gb:M21533)	5.7	7 6	0	r. u	n,	~	, ,	C	(
M79463_s_at			PML Probable transcription factor PML			;	?	3			0.0	0.0
	M79463	myl	{alternative products}	5.8	7.6	13.3	5	4.2	4.1	7 1	ις O	111
U22662_at_	U22662	lxra	Nuclear orphan receptor LXR alpha mRNA	1.5	7.3	9.6	34.8		9.4	8.4	m	100
U70451_at_	U70451	myd88	Myleoid differentiation primary response protein MyD88 mRNA	0		α	0	1 2		-		1
X82200_at_	X82200	staf50	Staf50 mRNA	10	, /			15.4	16.7		3 1.4	181
HG2915. HT3059_f_at_ HT3059	HG2915. HT3059	hla	Major Histocompatibility Complex, Class I, E (Gb:M20022)	6.1	m vc	α	0	0	α	α -	0	u u
S74017_at_	S74017	nrf2	Nrf2	3.8	6.3				2 00) (C	0 0
Z35278_at_	235278	am12	PEBP2aC1 acute myeloid leukaemia mRNA	14.3	6.1	C1	0.21	m	23	7 6	1,1	19.61
U32849_at_	U32849	nmi	Hou mRNA	5.2	9	16.1	10.4	10.5	24.4			23.9
HG3597- HG3597 HT3800_f_at_HT3800	HG3597. HT3800	hla	Major Histocompatibility Complex, Class I (Gb:X12432)	۲.	τ. αύ	(n)	נט פו	c.	<u>w</u>	<1	4	7

Figure 6F

M16038_at_ M D32129_f_at_ D U59863_at_ U HG45322. H HT4592_at_ H U40369_rna1 at_ at_	M16038 D32129 U59863 HG4322- HT4592 U40369 M62403 X72755 U67319	lyn hla-a itraf tubulinB sat	Oncogene homolog HLA-A MHC class I protein HLA-A (HLA-A28, B40, Cw3)	7.9	5.6	9.1	11.6	6.7	5	1.6	4.7	7.1
** .!· !! ! ! !!- !	132129 159863 164322- 174592 140369 162403 172755 167319		HLA-A MHC class i protein HLA-A (HLA-A28, B40, Cw3)									
 	159863 164322 174592 140369 162403 167319 167319		TPAE interacting protein TDAE		L	1		-				
11 111	IG4322. I40369 I40369 I62403 I67319 I67319	[5]		0.0	0.0	4.4	5.7	3.7	6.9	2.5	3.7	3.4
	14592 140369 162403 72755 167319	ili	CANULI INTELLIGIONE SUIDONOMI SUIDONOMI INTELLIGIONE SUIDONOMI SUI	2.7	0.0	4.0	4	7.	/:/	2.1	4.9	5.9
 	140369 162403 72755 167319 000763	sat	Tubulin, Beta	20.77	r.	12	0	'n	Q	L	0	;
 	140369 162403 72755 167319	sat	Spermidine/spermine N1-acetyltransferase		?	1:51	1			7		7
	462403 72755 67319 000763		(SSAT) gene	σ	ro C	5.	10 6	00 *1	σ	ď	-	0
- 	162403 72755 167319 000763		IGFBP4 Insulin-like growth factor binding					2		2	1	ö
	72755 167319 000763	igfbp4	protein 4	15.9	r.	32.7	ά	17.5	27.0	CC C	0	0,01
	000763	mig	Humig mRNA	3.2	5.2	683	59.4	50.00	200	0 4	17.0	1000
	000763	casp7	Mch3 isoform alpha (Mch3) mRNA	0	4.7	1.0	2	0.00	2 -	1 0	5 6	120.0
	000763		GAPD Glyceraldehyde-3-phosphate			1			5	7	2.5	13.2
D00763_atD		psma4	dehydrogenase	6.1	4.5	m	10.5	4	Ψ		11.0	Ç
	0000		ATF4 CAMP dependent transcription factor			1					7.1.7	?
D90209_atD	D90209	atf4	ATF-4 (CREB2)	4.5	3.8	10.5	6	1.	7.	α	u u	α
			Protein tyrosine phosphatase PTPCAAX1							1	1.5	į.
U48296_atU	U48296	ptp4a1	(hPTPCAAX1) mRNA	2.4	3.7	14	C.	۲,	1.1.7	C	0	Ų
			MACS Myristoylated alanine-rich C-kinase	-				1		1	5.7	0
D10522_atD	D10522	macs	substrate	4	3.2	10.3	4.7	1.9	5.9	2.3	3.2	7
749107 s at 749107	49107	02/66/								-		
HG4297.	HG4297.	-Ea137	משומרווו	6.1	3.1	2.6	17.1	12.1	3.7	2.7	5.7	4.6
at	HT4567	TCPC4	Transcriptional Coactivator Pc4	0	,	Ç	·	ī		(- 1	,
#				0.7	7.7	0.7	4.0	4.0	6.3	5.5	4.3	9.5
	AF006041	daxx	Fas-binding protein (DAXX) mRNA, partial cds	C	C Tr	ζ,	•	7 0	-0			(
HG4069.				1			,	0.0		1.1	0.1	Σ! V
HT4339_s_at HG4069-	IG4069.											
Ξ_	HT4339	mcp1	Monocyte Chemotactic Protein 1	00	2	o o	28	70	10	C	-	c
	1		NATURAL KILLER CELLS PROTEIN 4					1	2	1		y.
1	M5980/	nk4	PRECURSOR	20.5	2.5	10.6	11.1	4.6	11.4	2.6	4	16.3
	D00762	рѕтаЗ	PROTEASOME COMPONENT C8	2.8	2.4	4	o Ci	9.2	r. c.i	6.2	1 2	4.2
	12624/	Sui 1	RPL3 Ribosomal protein L3	3.7	2 4	4 5	C.1	2.7	2.1	1.7	5.6	1,01

Figure 6G

AF001294_at -	AF001294	ā	IPL (IPL) mRNA	3 6	C							
X07743 at	X07743	nlek	PI FOKSTBIN	0.7	2.3	ام		7.7	2.8	2.9	3.9	3.1
				7.6	2.1	5.7	13.9	10.7	2.7	3.6	1.6	5.6
D14826_s_at_D14826	D14826	crem	CREM CAMP responsive element modulator	3.4	~	u u	0	7	(L	,	,
U90913_at_	U90913	unknown	Clone 23665 mRNA sequence	5	7 7	200	7.51	0	0.00	7.0	1.0	4.4
D26308 at	D26308	blvrb	NADPH-flavin reductase	0	1	5	5	1.5	5	1.6	0.5	0.4
				5	7	٥	5	0.8	0	=	0	0
L13939_s_at_	L13939	ap1b1	Beta adaptin protein mRNA		-	С	C	0 7	- C	C	<u>u</u>	Č
M22107 at	70100M	7					1			5		
D87/33 at	D87433	cuss kise0346	CU33 CU33 antigen (differentiation antigen)	0	1	0	0.5	1.6	0	6.0	0.8	0
00/433_al	00/433	KIGGUZ40	NIAAUZ46 gene, partial cds	0	0.9	0	0	0.3	0	0	9.0	0
M22632_at_	M22632	got2	GOT2 Glutamic oxaloacetic transaminase 2, mitochondria (aspartate aminotransferase 2)	C	C	-	C	,	,			
M93221_at_	M93221	mmr	M6PR Mannose receptor	1.0		2 6	ο α	7 0	5 0) c	5	ा
			DTGC1 Drostonica dia anti-	7	2	?	0.0	0.0	0	7.7	- T.O	0
0	() () () () () () () () () ()	,	r i co. 1 Prostagiandin-endoperoxide synthase 1 (prostagiandin G/H synthase and									
MD99/9 at	W599/9	cox1	cyclooxygenase)	0	0.4	0	0.7	0	C	C	C	
HG4312. HT4582 s at	HG4312.								,	1		
1	HT4582	TFIiia	Transcription Factor lija	0	0			C		0	((
			ATP5D ATP synthase, H+ transporting		7:5		7	7.0	5	ρ	5	ो
	X63422	atp5d	mitochondrial F1 complex, delta subunit	C	0	C	-		C	0		(
- 1	X78817	RhoGAP4	KIAA0131 gene, partial cds	C	110	0	יו) -	5 0		5 6) (
D13640_at_	D13640	pp2c-like	PUTATIVE PROTEIN PHOSPHATASE 2C		100	5 0	5	10	5	5 0	- I	5](
1	D80001	kiaa0179	KIAA0179 gene, partial cds		0 0	5 0		2 0	5 0	ا _د	و اد	0.5
D83597_at_	D83597	RP105	RP105			5	‡ (0.0		C. T	7	8.0
l					٦	5	5	2.0	0.3		6.0	1.4
HT4000_s_at HG3730	HG3730.											
	HT4000	syk	Tyrosine Kinase Syk	0	C	C	0	7	C	-	-	
1 26010	01000		INPPL1 Inositol polyphosphate phosphatase.			5	7			5	4	ी
177730 at	17730	Inppi1	like protein 1 (51C protein)	0	0	0	0.7	6.0	0	0.7	6	0.3
L/ / 30 al	L///30	auoras	ADURAS Adenosine receptor A3	0	0	0	0	0.2	0	0	0 7	
M22638_at_	M22638	y 1	LYL-1 protein gene	c	C	c	C		-	1	,	7

M95678_at_	M95678	plcb2	PLCB2 Phospholipase C, beta 2	0	0	0	0	0	0	0	0	0
U06631_at_	U06631	H326	IEF SSP 9502 mRNA	0	0	0.2	0.3	1.3	0	8.0	0	0
			Mitogen-responsive phosphoprotein (DOC-2)	-	-		_				-	
U53446_at_	U53446	dab2	mRNA	0	0	0	0	0	0	0	0.2	0
U70439_s_at							_					
	U70439	ssp29	PHAPI2b protein	0	0	0	0.7	0.7	0	Ó	6.0	0.4
Z34897_at_	234897	hrh1	HRH1 Histamine receptor H1	0	0	0	0	0.3	O	0	9.0	0.1
Z50749 at	250749	ppp1r7	Sds22-like mRNA	0	0	0	0.3	9.0	0	0.1	0.1	С

Figure 61

ecsponse of Dendittic Cells to a...

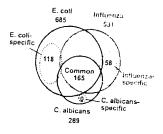


Figure 7A

Title. sesponse of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

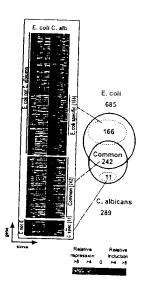


Figure 7B

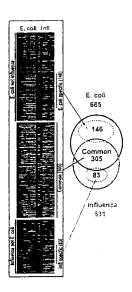


Figure 7C



Figure 7D



Figure 7E

Invo. .ors: Nir Hacohen, et al.

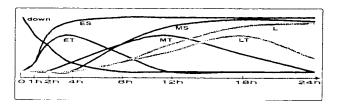


Figure 8A

E.A	RLY	MIDD	LE	1.4	TE
Transient	Sustained	Transient	Sustained	/Transiero	
	clathrin coat, MMH			11000000	SOUREITHE
	ribosomal genes, sur!	wars		+	
tnia, il6, mip1a, mip1b, a20, cox-2, oas2	#1b, #8, histamineR cox1, rp105	it1m, ptger			
macs, o-subulin,	sni	ictal 1		-	
ipi	CIBO2, CBSQ7	trad bot2-a1		+	
core	#10ra_cd33			0007	nk4
ptp4a1,lcp2, minor, pkr.	ptp1b.pim1.traf1.lkba dusp2, tes syk lxra adenosineH.plcb2 lipk.ppp1/7.RhoGapa	mx1, mx2, dusp4, igfbp4, ecgf, igais9, myd88, lyn	adm. plaur. bst2 tnfaip6	-	
uf1, tcpc4 nd2	ati4	stail, id7, id1,	myl	 -	
		psma4. psma3			
	icam1	rentes, slem, mcp1, inp10, mid			ncp2
	niny1, ncf1	mt2a,hspi4,ron1	copt2, sod2,	milh	
	pa28a	pa28b	hia. imp2, top1, tap2		mp7, hla
	Transient Inta, #6, mp1a, mp1b, #20, cos-2, cas2 macs, b-tubulin, oil cor8 ptp4a1,kp2, minor, px;	Para-sideptin appmin Para-sideptin appmin Para-sideptin appmin Para-sideptin appmin Para-sideptin appmin Para-sideptin appmin Para-sideptin P	Transient	Sustained Transient Sustained Sust	Transient Sustained Transient Sustained Transient

Figure 8B

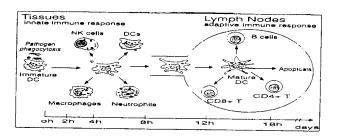


Figure 8C

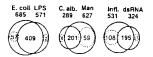


Figure 9A

In. Interes: Nir Hacohen, et al.

E. coli Man 685 627 E. coli daRNA 685 324 (201) 366 (1) (177 245 2

Figure 9B

Gene	GenBank accession no.	E. coli	C. albicans	Influenza
		Innate		
Neutrophil				
il8	Y00787	+++	+	+
gro1	XS4489	+++	+	+/~
gro2	M57731	. +++	+	+/-
gro3	×53800	++	+/-	+/~
Inflammation				
tnfa	K02910	++	+	+
il1b	K04500	+++	+	+
il6	X04602	++	+	+
illa	M28983	+		
gcsf	X03656	++	_	_
mip1b	M69203	++	+	++
mip3a/larc	U64197	++	+/-	+/-
mip3b/elc	U77180		+/-	+/-
bf	L15702	++	+	
			т	+/-
Prostaglandin/leukoti				
ptgir	D38*28	++	+	+
ptger4a	L28175	-	-	+
cox2	U04€36	++	+	+
		Adaptive		
T cell: T _H 1				
il12b/p40	M65290	++	+	
itac	U59286	+	+ .	++
mig	X72755	+	+	++
inp 10	X02530	+	+	+ +
ifnb1	V0053S	+	-	+ +
ifna2	J00207	-	-	+
ifna 13	J00210	_	_	+++
ifna 14	V00533	-	_	+
ifna 16	M28585	-	_	+
Tcell: T _H Z				
tarc	D43767	++	+	+/-
mdc	U83171	+	+	+/-
T cell stimulation	00317.1		т	+/-
41bbL	1103230			
	U03398	++	-	+/-
slam	U33017	+++	+	+
cd86	U04343	+	+	+
icam1	M24283	++	+	++
ebi3	L08187	++	+	_
Antigen presentation				
b2m	J00 10 5	++	_	++
lmp 10	X71874	+	+	+/-
cell				.,
pbef	U02020	+++	+	
Fy			Ψ.	τ
		nune receptor		
il15ra	U31628	++	+/-	+
il7r	M29696	++	+	+
il2r	X01057	+	+/-	-
il4r	X52425	+	+	+/-
g mcsfr	X17648	+	+/-	_
il3r	D49410	+	+	_
41bb	U03397	+++	+/-	++
tnfr2	M32315	++		_
il13ra1	Y10659	4.4	++	
cd155	M24406	+++	**	-
cd83	Z11697	+++	++	-
2203		++ ne transcription	TT	++
nfkb p52	\$76638	•		
		++	+/-	+
nfkbp50	M58603	++	+/-	++
nfkb p65	L19067	+	+	+
nfkb rei8 statSa	M83221 U43185	++	+/- +	-

Figure 10A

Gene	GenBank	C 11	<i>c</i>	, -
Gene	accession no.	E. coli	C. albicans	Influenz
stat4	L78440	**	+	
stat3	L29277	+	+ +	+/-
irf2	X15949	+		+
irf4	U52682	+	+/-	+/-
isgf3	M87503	+	+/-	+
csda	M24069	++		-
		lysis and energy		
eno1	M14328	+		ď
pk3	X56494	+ +	-	+/~
tpi	104603	+	_	
gys	J04501	+	-	ď
pgm1	M83088	+	+/-	ď
gk	×69886	+	+/-	_
pfkp	D25328	+		_
pgk1	V00572	+	_	+/-
g3pdh	X01677	+	_	+/-
ldh1	X02152	+	_	+/-
pgd	U30255	+	_	+/-
pgam1	J04173	+	+	+
hif1a	U22431	+	-	+/-
		Apoptosis		
Inhibitor				
pai2	M31551	++	_	_
iex-1	\$81914	++	+	_
tax1bp1	U33821	+	_	+/-
flip	AF005775	++	+	+/-
bag1	Z35491	+	+	+/-
ciap2	U37546	++	++	+
bcl2-a1	U29680	++	+	+
mcl1	L08246	+	_	+
tau	X56468	+/-	+/-	++
Activator				
casp4	U28:014	++	+	+/-
nip3	U15174	++	+/-	
trail	U37518	+	+	++
fas	X63717	+	+	+
casp5	U28015	+	-	+
bak1	U16811	+/-	+/-	+
pmaip1	D90070	+	-	++
casp10	U60519	+/-	+	+
_		tors and receptors		
tgfa	አ70340	+	_	_
ndp	λ65724	+++	Ann	-
wnt5a	L20861	+++	+/-	-
activinba	X57579	+++	++	+
p2x4	AF000234	+	+	_
vdr	J03258	+	+/-	_
	Tissue	remodeling		
mmp9	J 05 070	+/-	+	
mmp7	L22524	++	<u>.</u>	_
ттр3	X05232	+	_	_
mmp19	X92521	+	+/~	+/~
mmp 1 4	Z48481	++		+/-
mmp12	L23808	++	+	_
ттр 10	X07820	+	_	_
mmp1	X54925	+	-	_
lad i	U42408	+	- + - - - +	+/
extl2	U76189	+/-	+	+/-
collagen-a 1	M55998	+	_	_
tnr	X98085	+	-	+/-
		l stress		
nt1g	J03910	+++	+/-	+/-
ntle	M10942	+++	+/-	+/-
tg2	U72649	++	+/-	-
th1	L20941	++	+	_
quiescin	L42379	++	+/-	-
agb	MZ6311	++	_	+/-

Figure 10B

Gene	GenBank accession no.	E. coli	C. albicans	influenza
ddit1	M60974	++	-	+/-
map3k4	D86968	++	+/	+/-
mt1l	X76717	+ +	-	+/-
mt1h	×64177	+ +	+	+
mt2a	V00594	++	+	+
hspa1a	M11717	+ +	+/-	+ +
ninj1	U72661	++	+	++
sodZ	X07834	++	+	+ +
atox1	u70660	+	+	-
hspa6	X51757	+	+/-	-
krs1	U26424	+	+/-	-
mt1a	k01383	++	-	-
mt1f	M10943	+	-	-
rtp	D87953	++	+/-	-
cyp450db1	x07619	+	+/-	+/-
ast12	U46499	+	-	+/~
hsf4	D87673	+	-	+/-
hspa4	£12723	+	-	+/-
dusp1	×68277	+	-	+
mtf	¥78710	+	-	+
hsp70	U10284	+/-	-	+
hsp27	223090	-	+/-	+ + +
cbr1	104056	+/-	+	+
	In	nmune inhibitors		
тср1	\$69738	+	++	++
1110	U16720	++	-	-
hla-e	×56841	-	-	+
gfrp	U7B190	d	-	+
ido	M34455	++	+/-	++

Figure 10C

s, at the interfeuchtien is stated to the cell stimulatory factor 2, cytotoxic EDN1 J05008 44444 761-6 at the interfeuchtien is the cell stimulatory factor 2, cytotoxic IL12B M65290 2449.1 761-6 at interfeuchtin B B-factor, propered in actual by Cos-Cys), member 20 IL15702 2300.5 32-6 at small inducible cytokine subfamily A (Cys-Cys), member 10 SCYA20 U64197 931-7 28-3 at pertain reasted gene, rapidly induced by IL-1 beta GRO2 M3105-6 37-7 28-3 at pertain reasted gene, rapidly induced by IL-1 beta GRO2 M3105-6 37-7 38-3 at pertain reasted gene, rapidly induced by IL-1 beta GRO2 M320-7 38-3 37-7 at pertain reasted gene, rapidly induced by IL-1 beta GRO2 M320-7 38-3 37-3 at pertain reasted gene, rapidly induced by IL-1 beta GRO2 M320-7 38-3 37-3 at the consideration of the pertain of the profile of prof	1	della Italiie	Gene Symbol	GBA	Score Froli	Score Candida	Const lating
Interleukin 128 (natural killer cell stimulatory factor 2, cytotoxic 11,128 M65990 2444.1 7615 11,158 11,15702 12,157 11,158 11,15702 12,157 11,158 11,15702 12,157 11,158 11,15702 12,157 11,158 11,15702 12,157 11,158 11,15702 12,155 12,157 11,158 11,15702 12,156,4 11,157 11,158 11,15702 12,156,4 11,157 11,158 11,15702 12,156,4 11,158 11,15702 12,157 12,	1520_s_at	endothelin 1	FDN1	OEOOO	200	Score Call	score_tnriuenza
Unpulpocyce maturation factor 2, p40) Unbulpocyce maturation factor 2, p40 Unbulpocyce maturation factor 2, p40 Unbulpocyce maturation factor 2, p40 Unbulpocyce maturation factor 2, p40 Unbulpocyce maturation factor 2, p40 Unbulpocyce maturation factor 3, p40 Unbulpocyce maturation 6, p40 Unbulpocyce maturation 6, p40 Unbulpocyce maturation 6, p40 Unbulpocyce maturation 6, p40 Unbulpocyce maturation 6, p40 Unbulpocyce maturation 6, p40 Unbulpocyce maturation 6, p40 Unbulpocyce maturation 6, p40 Unbulpocyce maturation 6, p4	563_at	interleukin 12B (natural killer cell stimulatory factor 2 cytotoxic	1,00	1	444		113.7
## Bifaction, properdin at interleukin 8		lymphocyte maturation factor 2, p40)	1778		2449.		1.2
Bractor, properding	w.						
Interfeukin 6 (Interfeuch, beta 2) Interfeukin 6 (Interfeuch, beta 2) Interfeukin 6 (Interfeuch, beta 2) Interfeukin 6 (Interfeuch, beta 2) Interfeukin 6 (Interfeuch, beta 2) Interfeukin 6 (Interfeuch, beta 2) Interfeuch 6 (Interfeuch, beta 2) Interfeuch 6 (Interfeuch, beta 2) Interfeuch 6 (Interfeuch, beta 2) Interfeuch 6 (Interfeuch, beta 2) Interfeuch 6 (Interfeuch 6	۱"	B-factor, properdin	IL8	M28130	2300.5	2	
Example inducible cyclotine subfamily A (Cys Cys), member 20 SCYA20 U5664 1013 23	38299 at	Interleukin 6 (interferon heta 2)	BF	L15702	1635.7	,	17.3
the pentaxin-related gene, rapidly induced by IL-1 beta and factorial processes and conceaused by IL-1 beta and factorial processes and factorial proc	40385 at	small inducible exterior cuttaming A (Co. Co.)	116	X04430	1566.4		
The formation related gene, rapidly induced by IL-1 beta PTX3 M31166 827.3 8.9 All Concogene A	91636 at	and the manager of towning subjecting A (cys.cys), member 20	SCYA20	U64197	943.4		
SCYALOR SECTION STOCK ST	1491 at	Dentaxip:related gene rapidly induced by 11 1 5 25		AI652725	886.7		
t tumor necrosis factor, alpha-induced protein 6 tumor necrosis factor, alpha-induced protein 6 tumor necrosis factor, alpha-induced protein 6 tumor necrosis factor, alpha-induced protein 77 tumor necrosis factor, alpha-induced 77 tumor necrosis factor, alpha-induced 77 tumor necrosis factor, alpha-induced 77 tumor necrosis factor, alpha-induced 77 tumor necrosis factor 17 tumor necrosis f		á	PTX3	M31166	827.3		97
Interferon, beta Librobiast		17	GR02	M36820	785		
Interferon, alpha-inducible protein 2 INFAPE M31165 573.9 37.7 Eat BCL2-related protein A1 BCL2A1 V027467 565.9 754 Eat BCL2-related protein A1 BCL2A1 V027467 567.8 652.2 Eat Cyclobydralase I (dopa-responsive dystonia)		tumor necrosis factor, aloba induced protein 6	SCYB11	AF030514	655.1		7
BCL2-related protein A1	425 at	Interferon alpha-inducible protein 27	INFAIP6	M31165	573.9		75.1
The standard of the continuation of the cont		BCI 2-related protein A1	IF127	X67325	565.5		
Prostaglandin-endoper academic growth stimulating activity, alpha GRO1 oncogene (melanoma growth stimulating activity, alpha) GRO1 oncogene (melanoma growth stimulating activity) GRO1 oncogene (melanoma growth sti	37944 at	GTP cyclobydrolase 1 (dona responsing dustrain)	BCL2A1	U27467	547.8		
and cyclocxygenase)	1069 at	Drostaplandin-endoneroxide synthere 2 / /prostacional	GCH1	U19523	505.4		
GRO1 oncogene (melanoma growth stimulating activity, alpha) GRO1 X54489 486.7 11.5 at hexabrachion (tenascin C, cytotactin)	1	and cyclooxygenase)	PTGS2	U04636	495.3		
at hexabrachion (tenascin C, cytotactin) Addition (tenascin C, cytot	77706_at			0.00			
at hexabrachion (tenascin C, cytotactin) CHCI Edg91 X54489 (A8.7) 486.7 11.5 at interfeuchin 1, beta interferon, beta 1, fibroblast at interferon, beta 1, fibroblast 474.9 37.3 at interferon, beta 1, fibroblast at interferon, beta 1, fibroblast 1L1B M15330 468.5 30.5 at small inducible cytokine subfamily A (Cys-Cys), member 19 SCYA19 A8900887 394.2 25.2 at small inducible cytokine subfamily A (Cys-Cys), member 19 SCYA19 A8900887 394.2 25.2 at interferon stimulated gene (20kD) at aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde MT1G J03910 370.2 20.5 at aldehyde dehydrogenase, E3 isozyme) at aldehyde dehydrogenase, E3 isozyme) ALDH9 A127172 326.5 326.5 36.5 at S100 calcium-binding protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 145.5 at hypothetical protein A86.8602 296.2 145.5 at interferon, gamma Interferon, gamma Interferon, gamma Interferon, gamma Interferon, gamma Interferon, gamma Interferon, gamma Int	408_at			AA641972	493		7.8
at interferon, beta interferon, beta interferon, beta 1, fibroblast AF026941 484.1 612.9 1 at interferon, beta interferon, beta 1, fibroblast at interferon, beta 1, fibroblast at interferon, beta 1, fibroblast 30.5 at 37.3 at 37.5 at 37.5 at 37.5 at 37.5 at 37.5 at 37.5 at 37.2 at 37.2 <td>38549_at</td> <td></td> <td>GK01</td> <td>X54489</td> <td>486.7</td> <td>11</td> <td>7.1</td>	38549_at		GK01	X54489	486.7	11	7.1
at interfeukin 1, beta HXB X78565 474.9 37.3 at interferon, beta 1, fibroblast Interferon, beta 1, fibroblast Interferon, beta 1, fibroblast 428.5 30.5 at small inducible cytokine subfamily A (cys.Cys), member 19 SCYA19 AB000887 425 188.4 at interferon stimulated gene (20kD) MTIG J03910 370.2 0.5 at aldehyde a protein with tetratricopeptide repeats 2 IFIT2 M14660 327.2 200 at S100 calcium-binding protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 145.5 at hypothetical protein AP0 (calgranulin B) AR618602 296.2 15.3 at interferon, gamma Interferon, gamma IFING J00219 289.9 58.8 at interferon, gamma Interferon, gamma Interferon, gamma Interferon, gamma Interferon 278 99.5		hexabrachion (tenascin C. cytotactin)		AF026941	484.1		1149.5
at small inducible cytokine subfamily A (Cys-Cys), member 19 IFNBI M15330 468.5 30.5 at small inducible cytokine subfamily A (Cys-Cys), member 19 SCYA19 AB040831 425 188.4 at interferon stimulated gene (20kD) MTIG J03910 370.2 0.5 at aldehyde dehydrogenase, E3 isozyme) ALDH9 AI127172 327.2 200 at interferon-induced protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 3.6 at S100 calcium-binding protein A9 (calgranulin B) \$100A9 W72424 313.3 0.5 at hypothetical protein A hypothetical protein A hypothetical protein A hybothetical protein A hybothetical protein A hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein B hypothetical protein			HXB	X78565	474.9		1.5
at small inducible cytokine subfamily A (Cys-Cys), member 19 SCYA19 A8948319 425 188.4 at small inducible cytokine subfamily A (Cys-Cys), member 19 SCYA19 AB000887 394.2 25.2 at interferon stimulated gene (20kD) MTIG J03910 370.2 0.5 at aldehyde dehydrogenase, E3 isozyme) ALDH9 AI127172 326.5 3.6 at interferon-induced protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 3.6 at S100 calcium-binding protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 145.5 at hypothetical protein A9 (calgranulin B) AA618602 296.2 15.3 at hypothetical protein Interferon, gamma If ING J00219 278 99.5	1214 s at	14-	1118	M15330	468.5		
at small inducible cytokine subfamily A (Cys-Cys), member 19 SCYA19 AB000887 425 188.4 at interferon stimulated gene (20kD) at aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme) ISG20 U88964 327.2 200 at aldehydrogenase, E3 isozyme) at interferon-induced protein with tetratricopeptide repeats 2 at S100 calcium-binding protein A9 (calgranulin B) IFIT2 M14660 320.5 145.5 at hypothetical protein AM618602 296.2 15.3 at interferon, gamma IRPIG J00219 289.9 58.8 at interferon, labha IL15RA AF035279 278 99.5	52615 at	-1	IFNB1	V00535	433.9		540.3
metallothionein 1G 35.2 25.2 at interferon stimulated gene (20kD)	36067 at			AA948319	425	1	
at interferon stimulated gene (20kD) MTIG J03910 370.2 0.5 at aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde ISG20 U88964 327.2 200 10 at interferon-induced protein with tetratricopeptide repeats 2 IFIT2 M14660 326.5 3.6 3.6 at S100 calcium-binding protein A9 (calgranulin B) \$100A9 W72424 313.3 0.5 57 at hypothetical protein AA618602 296.2 15.3 1 1 1 1 at interferon, gamma Interferon, gamma IFING J00219 289.9 58.8 3 at interfeukin 15 receptor, alpha IL15RA AF035279 278 99.5 1	326 at		SCYA19	AB000887	394.2		2.8
Sidehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme) Sidehyde dehydrogenase, E3 isozyme) Sidehydrogenase, E3 isozyme, E3 isozyme) Sidehydrogenase, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isozyme, E3 isoz	33304 at	interferon stimulated gene (20kD)	M/1G	J03910	370.2		1.5
dehydrogenase, E3 isozyme) Stock of the protein with tetratricopeptide repeats 2 IFIT2 A127172 326.5 3.6 interferon-induced protein with tetratricopeptide repeats 2 IFIT2 M14660 320.5 145.5 5 \$100 calcium-binding protein A9 (calgranulin B) \$100A9 W72424 313.3 0.5 hypothetical protein AA618602 296.2 15.3 interferon, gamma Interferon, gamma 58.9 58.9 interferon, alpha Interferon, alpha 278 99.5	53579 at	aldehyde dehydrogenase 9 (gamma amingbutus) datu a	18G20	U88964	327.2		103.7
Interferon-Induced protein with tetratricopeptide repeats 2 FIT2 M14660 320.5 145.5 5 5 5 5 5 5 5 5 5		dehydrogenase, E3 isozyme)	ALDH9	A1127172	326.5		2.1
at hypothetical protein S100A9 W72424 313.3 0.5 at hypothetical protein AA618602 296.2 15.3 at interferon, gamma iFNG J00219 289.9 58.8 at interleukin 15 receptor, alpha IL15RA AF035279 278 99.5	11/71 2t	S100 21 Entering Line Line With tetratricopeptide repeats 2	IFIT2	M14660	320.5	145	5723
at Interferon, gamma AA618602 296.2 15.3 at interleukin 15 receptor, alpha IL15RA AF035279 278 99.5	13853 at	hypothatical protein A9 (calgranulin B)	S100A9	W72424	313.3		α ο
at interleukin 15 receptor, alpha 15 receptor, alpha 15 receptor, alpha 15 receptor, alpha 15 receptor, alpha 16 receptor, alpha 16 receptor, alpha 17 receptor, alpha 17 receptor, alpha 17 receptor, alpha 18 receptor, alph	021 at	interferon gamma		AA618602	296.2		981
		interlenting 15 recentor alaba	IFNG	J00219	6.682		36.2
		miterieumii 10 receptor, alpha		AF035279	278		1117

Figure 11A

41531_at		TM4SF1	A1445461	27R	α C	6.
1097_s_at	chemokine (C.C motif) receptor 7	CCR7	L	275 6	0.00	1.3
61818 at			1	0.0/2	100.0	88.3
35577_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member	SERPINB7	AF027866	265	32.3	2.5
)		1.04	0.0
37219_at	monokine induced by gamma interferon	MIG	X72755	2616	0 107	
34929_at	tumor necrosis factor receptor superfamily, member 8	TNEDCES	MOSEEA	201.0	7.40/	182.7
33955_at	interleukin 12A (natural killer cell stimulatory factor 1 cytotoxic	120	MEROOT	200.9	0	0.8
		W777	167C0W	720.7	18.4	14.6
41096_at	S100 calcium-binding protein A8 (calgranulin A)	\$10048	1106134	7 070		
41468_at	T cell receptor gamma locus	0 00 L	1	243.4	5	6.9
35000 at	tumor necrosis factor (ligand) superfamily, member o	SPOLINE STOTINE	1	745.1	5	1
33705 at	Inhosphodiesterase 4R cAMP, specific (dupos (Oxegophic)	INFOR	003398	232.3	2.9	3.1
	phosphodiesterase E4)	PDE4B	L20971	232.3	51.8	92.7
1403_s_at	small inducible cytokine A5 (RANTES)	E VOC	1011101			
48864 at	interferon, alpha-inducible protein 27	0.1.A.	171171	232.1	9.06	200.3
33965 at	small inducible cytokine A1 (1 200 home)	11-12/	A1991845	216.4	274.9	141.4
36116 at	thyroid hormone recently interest 10	SCYA1	M57506	216.3	0	7.8
1400	my out floringle receptor interactor 10	TRIP10	AJ000414	215.9	26.7	7
47855 at	corolly sufficient gractor z (granulocyte-macrophage)	CSF2	M13207	210.9	0.1	
£1371 2+	andia E bindia =	IL19	AA151656	205.5	0	0.5
1052 24			AA555023	204	148	479 5
22700 at	unior necrosis ractor (TNF superfamily, member 2)	TNF		201.2	47.5	57
T	Sitiati fituacible cytokine A5 (RANTES)	SCYA5	AF088219	191.5	64.1	1 2
T	13A24 DIOCEIII		W74027	189.7	74.5	32.5
49148 at			AI075407	185.9	169.1	121.9
38584 at	interferon indicate district district district described and production of the second district distric		AA947472	182.2	52	423.6
T	signaling lymphontic poting will telfalficopeptide repeats 4	IFIT4	AF026939	179.4	153.2	1486
T	Signature Dymphocytic activation molecule	SLAM	U33017	178.3	14.3	
Ţ			AA210892	176.1	24	34.8
	striati friductore cytokine B subtamily (Cys-X-Cys motif), member 13 (B. cell chemoattractant)	SCYB13	AF044197	171.2	0	2.3
1334_s_at	colony stimulating factor 3 (granulocyte)	COE3	XO3656	1,63	,	
57761_at			112000	10,	1:2	7.7
40159 r at	Inelitrophil extosolic factor 1 (47kD) chronic grapulomateus disease		AI313233	161	9.09	33.7
		NCFI	M55067	160.7	91	140.3

		MTIA	K01383	160.3	223	01/
T	CU38 antigen (p45)	CD38	D84276	160.1	102.8	18.6
7	ite I 3 aceta	PMAIP1	D90070	159.8	000	1000
J	interferon-stimulated protein, 15 kDa		M13755	159	0.00	408.2
at	similar to rat myomegalin		U51694	156	0 00	213.0
T	small inducible cytokine subfamily B (Cys. X.Cys), member 10	SCYB10	X02530	152	00%	6.2
T			A/807018	151 1	330	343.7
I	SGRF protein, Interleukin 23 p19 subunit		A1796983	1777		30.6
1	lung type-I cell membrane associated glycoprotein		AE030428	14071	5.0	2.5
Ī	superoxide dismutase 2, mitochondrial	SODS	X07834	143.7	5 6	1.2
- 1	metallothionein 2A	ACTAN	A1001001A	141.0	03.1	42.3
aţ	adenosine A2a receptor	4C 4 C C C C	701651	138	45.1	82.3
48919_at po	potassium inwardly-rectifying channel, subfamily 1 member 2	A CONTACA	240950	13/.9	31	27.9
		NCINDS	AA393850	130	11.2	13.1
	sorting nexin 10		AA521246	129.3	35.4	18
	PPAR(gamma) angionoietin related protoin		AI285531	127.4	55.8	74.2
ĺ	Service Protection College Protection		N57259	126	7.9	14.7
Γ	interleukin 7 recentor		AI247103	124.7	84.6	27.2
		IL7R	AI655781	123.1	41.5	20.9
	nterleukin 10		AI735586	122.3	4.7	0.2
L		1,10	U16720	121.9	4.3	3.2
			AI654525	120.3	174.3	127.2
1	Macrophage myristovlated alaning rich Ciging authority		AW014801	120.2	4	10.2
Ī			X70326	119.6	44.8	42
	Dutative secreted ligand homologous to fix 1		AA769482	117.4	12.2	9'9
Π		Ltix	AI338625	117.2	3.8	3.3
Γ		MT1B	M13485	116.3	11.1	20.1
at		USP18	AA143794	114.4	158.3	218
63066 at			AI498361	113.1	77.9	73.9
			AA001735	113	12.6	96
te	are an induced deniantential and protein 1 (9.27)	IFITM1	J04164	112.7	140.9	173.6
50827 at			AA251131	111.4	76.5	828
te	hynothetical protein El 190637		AW001213	109.2	52.4	6.6
, te			A1620475	108.9	42.7	28.3
	Marian Julian 1		AL049389	108.4	0	2.9
1		LAD1	1142408	0.00		

364544 at carbonic anth/calculating for transport regulator 6 FXVD6 AL043089 103.8 73.3 82795_at carbonic anth/calculating for transport regulator 6 CAIZ AF037355 10.27 10.3 10.2 82795_at carbonic anth/calculating for transport regulator 6 AL0780337 10.27 10.2 10.2 3120_at at metalethromating for transport 7 alpha bydroxylase). MTIF M10943 10.2 30.8 33055_at polyperbild at metalethromating for transportation 6 at monotone P450, subtamily VINIB (cxysterol 7 alpha-hydroxylase). CYP7B1 AF029403 99.5 17.5 70097_at polyperbild at monotone P450, subtamily XXVIIB (25-hydroxyntamin D.1 alpha-pydecase). Average at the carbonic polyperbild at the carbonic polyperbil polyperbild at the carbonic polyperbild at the carbonic polyperbild at the carbonic polyperbild at the carbonic polyperbil polyperbild at the carbonic polyperbil		1	2.5	0	25.3		6 1.2		39.	0 0	3 41.1	2.9			Ö		43.		12.9			94.1	5				3/./	11.3			7.7
Interleukin 7 receptor	73		8		30	13	17.	oc c	29.		63.	17.	6	100	300	388	200	62		4.)	1	3/.		111	0	36.0	20.5	50.6	15.1	5	
interleukin 7 receptor carbonic aniydrass XII interleukin 7 receptor metallothionein 1F (functional) cytochrome P450, subfamily VIIB (oxysterol 7 alpha-hydroxylase), cytochrome P450, subfamily VIIB (25-hydroxyvitamin D-1-alpha- cytochrome P450, subfamily XXVIIB (25-hydroxyvitamin D-1-alpha- AKAPE A Akinase (PRKA) anchor protein Z Akinase (PRKA) anchor protein Z Akinase (PRKA) anchor protein Z Akinase (PRKA) anchor protein Z Akinase (PRKA) anchor protein Z Akinase (PRKA) anchor protein Z Akinase (PRKA) anchor protein Z Akinase (PRKA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase (PRXA) anchor protein Z Akinase	103.8	103	102./	102.4		101.8	99.5	99 5	66	99.2	98.3	98.2	98.2	97.1	96.4	95.8	94.9	94 5	93.7	92.7	2 00	92.3	65	92	91.6	91.3	91	6.06	90.7	88.7	87.8
carbonic anhydrase XII interleukin 7 receptor metallothionein 18 (functional) cytochrome P450, subfamily VIIB (oxysterol 7 alpha-hydroxylase), polypeptide 1 indolearmine-pyrrole 2,3 dioxygenase indolearmine-pyrrole 2,3 dioxygenase cytochrome P450, subfamily XXVIIB (25-hydroxyvitamin D-1-alpha- Type receptor-associated factor 1 The receptor-associated factor 1 A kinase (PRKA) anchor protein 2 The receptor-associated factor 1 A kinase (PRKA) anchor protein 2 Cardiotrophin-like cytokine; neurotrophin-1/B-cell stimulating factor-3 metallothionein 2A cardiotrophin-like cytokine; neurotrophin-1/B-cell stimulating factor-3 metallothionein 2A cardiotrophin-like cytokine; neurotrophin-1/B-cell stimulating factor-3 metallothionein 1H indolearmine-pyrrole 2,3 dioxygenase E-phosphofructo-2 kinase-fructose-2 (6-biphosphatase 3) metallothionein 3 (growth inhibitory factor (neurotrophic)) E-phosphofructo-2 kinase-fructose-2 (6-biphosphatase 3) Similar to lysosome-associated membrane glycoprotein metallothionein 3 (growth inhibitory factor (neurotrophic)) Browth arrest and DNA-damage-inducible, alpha matrix mietalloproteinase 1 (interstitial collagenase) MI	1 1		20000774	- 1				1	AA932068	AA678425			Ш		AA059458	l	AL047300	AA873008	Al936516	AI040033	- 1	1	l	AA733119	1		AI765775	AB013924	M93311	M60974	M13509
carbonic anhydras interleukin 7 recept metallothionein 11 cytochrome P450, polypeptide 1 indolearnine-pyrro cytochrome P450, hydroxylase), polyty TNF receptor assoc A kinase (PRKA) an A kinase (PRKA) an metallothionein 2A chloride channel Kt Burkitt lymphoma r metallothionein 1H indolearnine-pyrrole 6-phosphofructo-2-, similar to Iysosome metallothionein 3 (6-phosphofructo-2-, similar to Iysosome metallothionein 3 (6-phosphofructo-2-, similar to Iysosome metallothionein 3 (8-phosphofructo-2-, similar to Iysosome metallothionein 16- growth arrest and D matrix metalloprote	FXYD(1	M-11		INDC			CVPOTE			TRAF1		AKAP2					MT2A	CLCNKB	BLR1		MT1H	ODNI	PFKFB3		MT3	GADD45A	MMP1
	se XII			interleukin / recep	metallothionein 1F	subfamily VIIB (oxysterol	0.0.0 diameter	υl			cytochrome P450, subfamily XXVIIB (25-hydroxyvitamin D-1-alpha	inyai oxyidse), polyp			ichor protein	1000			cardiotrophin like cytokine; neurotrophin 1/B cell stimulating factor 3			Burkitt Ivmohoma		$\overline{}$		6-phosphofructo-2-kinase/fructose-2-6-hiphosphoftage	Similar to lysosome associated membrane alygonatain	metallothionein 3 (growth inhibitory factor (neurotrophic))	growth arrest and DNA-damage-inducible, alpha	Imatrix metalloproteinase 1 (interstitial collagenase)	

Figure 11D

	7 T	0/0010	/0	17.5	/
DKFZP586G0522 protein		AW008790	85.4	4.8	52.3
pellino (Drosophila) homolog 1	PEL11	AL043980	85.4	6.2	54.5
superoxide dismutase 2, mitochondrial	SODZ	AA142976	84.4	32.6	17.7
major histocompatibility complex, class II, DO beta	HLA.DOB	X03066	84.2	55.5	30.1
		AA131041	84	77.5	157.1
		AI446168	83.4	119.5	160.2
		U50527	82.5	50.7	14.2
phospholipid scramblase 1	PLSCR1	AB006746	81.8	68.4	32.6
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4	SERPINB4	U19557	81.2	0.7	1.1
solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	SLC6A12	U27699	6.08	46.2	10.4
tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity,	TIMP1	D11139	79.8	1	6.0
collagenase inhibitor)					
		AI984197	79	0.2	6.0
metallothionein 1E (functional)	MT1E	R92331	78.7	4.6	8.6
KIAA0668 protein		AA009571	78.6	23.3	31.3
		AA576959	78.3	9.6	0.7
syndecan 4 (amphiglycan, ryudocan)	SDC4	D79206	77.4	5.8	20.7
		AL079435	76.5	7.7	0.0
KIAA0963 protein		AB023180	75.3	33.5	1.2
gap junction protein, alpha 4, 37kD (connexin 37)	GJA4	M96789	74	13.5	4.2
		W28501	73.5	28.6	16.2
		A1635522	72.4	7.8	8.6
hypothetical protein FLJ22318		AI250747	72.4	0	0
ir receptor superfamily, mem	TNFRSF9	U03397	72.27	7.8	19.5
guanylate binding protein 1, interferon inducible, 67kD	GBP1	M55542	72.1	49.4	49.8
		AI660377	71.6	38.3	4.8
interleukin-1 homolog 1		AI814314	71.5	4.1	23
KIAA0580 protein		AB011152	71.4	27.4	18
RNA helicase related protein		H68340	71.4	10.1	21.9
chondroitin sulfate proteoglycan 2 (versican)	CSPG2	X15998	71.2	4.1	27.4
similar to rat myomegalin		AI659612	71.1	8.6	11.8
		0.11004	;		

42204 at						
668_s_at	matrix metalloproteinase 7 (matrilysin utarias)		AI219461	70.7	4.8	Y
73455_f_at	1	MMP7	122524	70.6	1.3	
63675 at			H72723	70.4	82	T C
37643_at	tumor necrosis factor receptor superfamily, manual		AI680833	69.2	1	0.0
44513_at	o ladillati, tillatillati occasione occasione o	TNFRSF6	X63717	69	17.4	30
39114_at	decidual protein induced by progesterone		AI760613	8.89	81.5	36.6
37641_at	interferon induced, hepatitis Cassociated microtinkular acceptance		AB022718	9.89	26.6	286
	protein (44kD)		D28915	68.5	51.1	43.6
49438_at						
32026_s_at	PDZ domain containing guanine nucleotide exchange factor(GFF)1		A1535730	68.4	21	15.8
63769 at			AB002311	68.3	25.1	16.6
7117			AIZAGESE	0.50		
/11/4 r at	т		00000000	8./0	49	14.3
568/9_at	heparan sulfate (glucosamine) 3-0-sulfotransferase 3R1	1000	A1921158	67.8	81.9	115.6
1006_at	matrix metalloproteinase 10 (stromelysin 2)	19213201 19213201	AA/80067	67.6	2.5	34.8
47517_at		MMP10	X07820	67.5	2.4	3.6
1715_at	tumor necrosis factor (ligand) superfamily, mamber 10		AA639645	67.1	51.4	5 6
59185_at	OT Jack Training, Training, Training	TNFSF10	U37518	66.8	1797	0.0
41475_at	niniurin 1		AA926689	66.3	00	100.5
595 at	Pornosis factor alaba indire	NIN	U91512	65.2	7 35	
1036 at	Interleukin 15	TNFAIP3	M59465	65.1	11.7	10.7
77244 at	DHLH factor Hesd	IL15	U14407	64.7	16.6	22.0
286 at	١,		AI380603	64.7	0 4	1.77
38326 at	, membe	H2AF0	119779	64.6	15.4	23.6
51015 at	Paris Con Sales		M69199	64.6	20.8	1.70
75014 i at	KlAA1533 protein		AI655467	64.4	21.6	
Г"	tor alpha.indi.cod protein		AW006583	64.4	37.7	4.4
	NK homeobox (Drosophila) family 3 A	TNFAIP2	M92357	63.8	17.8	0.0
36227 at	A'C (alina), lating of A	NKX3A	AI557413	63.8	0000	10.4
1717 c at	backlowing IAB control		AF043129	62.7	0.7	12.5
78/82 ==	Dacuiovital IAP repeat containing 3	BIRC3	1145878	03.4	21.8	18.5
10407 dl		1	040040	03.1	47.7	20.2
51232_at	hypothetical protein FLJ20764		AA/05165	62.7	3.6	35.7
39221_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and		AI684508	62.7	4.1	2
	ITIM domains), member 2	רוראפל	AF004231	62.6	6.1	17.8
		_	_	_	_	_

1510 at			A1823649	63	2	
1019 at	vets avian erythroblastosis virus E26 oncogene homolog 2	FTS	1	013	01.0	48.7
51920 at	melanoma differentiation associated protein 5			01.0	3.6	4.4
45289_at	novel Ras family protein		MAI 34938	61.8	41.7	22.4
49140 at			AA133248	61.7	3.8	24.3
53201 at			A1244908	61.5	3.8	4.4
4 +	Constant of the state of the st		A/928513	61.2	144	
34974 at	disintegral protesses	MX2	M30818		61	T
	CD80 antion (CB38		Y13323	61	5 -	00
536 AD 24	COOV antiger (CDZS antigen ligand 1, B7.1 antigen)	CD80	1	5 6	1 00	C.1
33043 at	Stiali 1 (drosophila homolog), zinc finger protein	SNALI	1	000	0.07	15./
44250 41	Pos-induced protein PIGPC1		┺.	0.00	500	8.
44289_at	NY-REN-18 antigen		105000	39.9	0.0	0.5
44981_s_at			AA58/445	59.8	23.1	1.9
51474_at			AA115266	59.2	45	15.
38121 at	tryptophanyl:tRNA synthetase		≤	58.7	2.4	7.4
1914 at		WARS		58.2	45.4	45.6
48377 at		CCNA1	U66838	57.6	16	70.3
32606 at	brain acid soluble protein 1		AI347073	57.3	21	11.6
72660 p at		BASPI	AA135683	56.9	α / Ι	0.11
37163 at	DKF7P58601610 protois		AA776412	56.8	24.4	11
32700 at			AL050374	56.3	10	33.3
40300 04	Badinylare Diriging profess 2, interferon-inducible	GBP2	L	7 7 7	1000	10.0
72302 at				0.00	43.9	6.1
58391_at	testis zinc finger protein		A1002042	55.4	14.7	1.9
37954_at	annexin A8		AI/9814/	55.2	2.9	20
34582_at	Solute carrier family 1 (plial high affinity, glutamata trans-	ANXAB		55.1	0	C
	member 2	SLC1A2	U01824	55	0	1.2
186/_at	CASP8 and FADD-like apoptosis regulator	OEI AD	AE006775	1		
906 at	Signal transducer and activator of transcription 4	VEVE	ш	54.9	24.7	5.8
1377_at	nuclear factor of kappa light polypeptide gene enhancer in Broalls 1	NEVD1		54.6	10.3	5.9
01011	(p105)	NENBI	M58603	54.5	18.3	18
1200 at			710040014	1.		
89899 at	myxovirus (influenza) resistance 2, homolog of murine	CAVA		54.1	57.5	0
1891_at	mitogen activated protein kinase kinase kinase 8	ZVINI	۲Ι.	54	64.3	70.9
76762 at		MAPSK8	D14497	53.8	4.5	11.2
48757 at	EH domain containing 1		AI246590	53.8	8.9	10.2
	4 9	EHD1	AI986040	53.8	0	

64603 at			N47335	53.7	5.7	0.0
37014_at	myxovirus (influenza) resistance 1. homolog of murine (interferon-	M×I	M33880	53.6	3.00	2.03
	inducible protein p78)))	3	2.60
649_s_at	chemokine (C.X.C motif), receptor 4 (fusin)	CXCR4	106797	53.5	7.07	36
74633_at	tumor necrosis factor, alpha-induced protein 2	TNEAID2		200.0	10.7	30
63382 at	Interferon consensus sequence binding protein 1	100001	A10720430	0.00	10.0	0.1
47287 21		T IGOD!	A1073304	23.3	35.7	00
36027 24	The section of the se		AI4/54/3	53.5	2.5	6.9
30057 91	hypothetical protein, expressed in osteoplast		AB000115	53.4	60.4	83.5
486/6 at			AL046192	53.3	0	0
3/185_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	SERPINB2	Y00630	52.6	0	0
40670_at	kynureninase (L-kynurenine hydrolase)	KYNU	AI148772	52.5	13.6	7 0
37137_at	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine	GZMB	M17016	52.3		15.3
80773 at	(1.202.202.202.202.202.202.202.202.202.20					
1000	Ŀ		H15073	51.8	8.6	13.9
48025 at	Nok adaptor protein 2	NCK2	AI934552	51.7	5.9	6.9
63/80 at	hypothetical protein FLJ11259		AA814195	51.4	19.6	26.4
	exostoses (multiple) 1	EXT1	879639	50.9	22	80
3/451 at			AL109695	50.6	4.8	7.8
35143 at	KIAA1031 protein		AI138605	50.6	24 1	4.6
669_s_at	interferon regulatory factor 1	IRF1	L05072	50.6	35.4	27.2
34435_at		AQP9	AB008775	50.5	15.3	3.4
32814 at	Interferon induced protein with tetratricopeptide repeats 1	IFIT1	M24594	50.5	70.1	76.9
37716_at	111	MOX2	X05323	50.5	7	
1/36 at	insulin-like growth factor binding protein 6	IGFBP6	M62402	50.4	0	104.8
00901 at			AI016542	50.4	9.1	4.4
02332 at			AI821392	20	7	1.7
40000 at	=1		AI358871	49.8	6.0	0.4
41/45 at	interferon induced transmembrane protein 3 (1.8U)	IFITM3	X57352	49.6	74	6 69
510/5 at	pannexin 1	PANX1	AA115920	49.5	3.9	
3252/ at	adipose specific 2		AI381790	49.3	1.4	1.4
35412 s at	interieron regulato	IRF7.	U53831	49.2	41.5	54.1
35985 at	A kinase (PRKA) anchor protein 2	AKAP2	AB023137	49	20.1	24.6
/04b0_f_at			A1654525	48.9	206	757

Figure 11H

	antiproteinase, antitrypsin), member 1	SERPINAI	X01683	48.8	2.5	2.4
	ling prote					
	tumor necrosis factor receptor superfamily member 18	S100A12	U83664	48.3	0	9.9
Ī.,		INFRSF1B	M32315	48	3.4	3
60103 at			AI830607	47.1	3.3	
T	carbohydrate (N.acetylalisossanias 6.0) - 16.1		AI916948	46.9	13.9	44
	receptor interacting serine thropping Cinocal	CHST7	N64774	46.8	23.4	
Τ	regulator of C. protein signalling 16	RIPK2	AF117829	46.7	26.8	104 9
Ī	prostaglandin E susthans	RGS16	U70426	46.6	2	101
Τ	retinois acid indused 2	PTGES	T03380	46.5	200	4
ŧ		RAI3	A1990405	46.5	00	
54565 at			AI129310	45.7	0.8	2.0
51670 i at			AA149736	45.6	8.7	10.3
58667 at			A1161358	45.6	13.2	52
Г	dual specificity phosphatase 5		AA442239	45.4	0.4	7 7
Г	sphatasa	DUSP5	U15932	45	12.1	10.5
+		DUSP1	X68277	44.6	0.5	202
56561 at			AI590710	44.5	9.7	
	dual adaptor of phosphotyrosine and 3 phospholistical		W37880	43.8	0.1	
#	n FI 123375		AF150266	43.8	9.5	
			AI818808	43.4	18.3	62
246 s at s	75246_s_at_solute carrier family 1 (plial high affinity all tampts to		AA665185	43.3	3.1	-
	member 3	SLC1A3	W26838	43.1	7.2	4.8
T	erythrocyte membrane protein band 7.2 (stomatin)	FPB72	X85116	000		
46630 at p	plastin 3 (T. Isotorm)	PLS3	A1983923	42.0	13	21.6
_			AW005111	12.5	1.5	7.89
Τ	adelijiate kirase 3	AK3	X60673	2007	0.0	1
203/3_at	UDP-Gai:betaGicNAc beta 1,4. galactosyltransferase, polypeptide 5	B4GALT5	AA133969	42.2	9.3	9.5
	prostaglandin E synthase	i i				
		716EV	AF010316	42.1	0	1.2
43524_at K	KIAA1170 protein		N95225	42.1	4.1	808
88629 at			C14031	42.1	18.4	7
<u></u>	STAT induced STAT inhibitor 2		AI337136	42	18.5	15.7
	_		0000,			

Figure 11I

	metastasis Z	TIAM2	A1126294	416	25.5	0 9
serine (or cysteine) proteinase member 1	proteinase inhibitor, clade G (C1 inhibitor),	SERPING1	X54486	il 🗔	67.8	17.1
75868 <u>r_at</u>			00010214			
48822_s_at adenylate kinase 3			_1.	41.5	10.4	
mitogen-activated	Orotein kinase kinase Linase Linase	AK3	_1	41.5	6.1	0.5
KIAA0172 protein	o milase Milase Milase 4	MAP4K4	AB014587	41.4	2.7	9.0
			D79994	41.4	3.6	10.9
pre-B-cell colony.e			AB006624	41.3	5	2
Γ	101		U02020	41	8.3	16.3
		AIM2	AF024714	40.9	18.1	16
			AA194980	40.7	35.3	101
44640 at			N27438	40.2	2.4	4.3
64333 s at pyrophosphatase (inorganic)			W30985	40.2	11.6	8.4
adenosine deamin		dd	AW009649	39.9	10.9	5
		ADA	X02994	39.7	4.1	3.2
GRO3 oncogene			AL049963	39.4	1.8	
Γ		GRO3	M36821	39.3	1.9	1.4
48014 at			C14904	39.3	13	22.8
38388 at [2,5] olippadenylate synthetase	740.46 103		N54957	38.8	5.2	
inhibin, beta A (ac	fivin A activin AB sinhs not contides	OASI	M11810	38.7	54	103.7
at .	aprila polypeptide)	INHBA	J03634	38.6	4.9	5
54147 at pyruvate dehydrogenase kinase isoenzyme A	Some A		AI963642	38.5	33.4	11.9
transcription facto	+ 01116	PDK4	AI763378	38.3	4.5	9.0
			AI347001	38.2	44.7	11.3
68652_at			AF070570	38.1	14.3	8.7
67259_at			AI431778	38	3.8	9.0
51104_at			R56235	37.9	0	6.3
59283_at hypothetical protein FLJ20035			A1937446	37.7	10.5	22.6
62130 at 28kD interferon responsive protein	nie		AL042790	37.5	24.6	11.4
H2B histone family			AA651720	37.5	34	40
at JM5 protein		HZBFB	AJ223353	37.4	13.7	16.1
1			Z78315	37.4	27.2	1
41045 at secreted and transmembrane 1			AA580047	37.3	29.6	43.2
s at Inlastin 3 (T isoforn		SEC I M1	U77643	37.2	67.4	10.4
7		C C C	Moooo	1	,	

39070_at	singed (Drosophila)-like (sea urchin fascin homolog like)	SNL	U03057	36.9	23.6	31
34476_r_at	epiregulin	EREG	D30783	36.5	80	126
38389_at	2,5'-oligoadenylate synthetase 1 (40.46 kD)	OAS1	X04371	36.5	71.8	35
90421_at	conserved gene amplified in osteosarcoma		AA633203	36.5	35.1	8.6
1343_s_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3	SERPINB3	968998	36.4	0	0.3
48331_at			AL041454	36.4	3)	16.7
69876_at			AI825713	36.1	32.1	60.3
55634_at			AI040355	35.9	21	3.9
34916 s_at	tumor necrosis factor receptor superfamily, member 4	TNFRSF4	S76792	35.7	20.3	7.8
43456_at	serine/threonine protein kinase MASK		AI299952	35.5	2.6	0
62214_at	hypothetical protein FLJ11354		AI583960	35.5	28.7	23.8
52729_at	CD44 antigen (homing function and Indian blood group system)	CD44	AA037772	35.3	3.3	9.0
45256_at	pre-B-cell colony-enhancing factor		AI271460	35.1	7.1	33.4
54823_at			AI651594	35.1	30	5.8
56169_at			W55852	35	2.2	29.4
64170_at			AI609751	35	3.2	0.5
32686_at	prostaglandin E receptor 3 (subtype EP3)	PTGEP3	96098G	34.9	2.2	2.2
53261_at	- 1		AI337231	34.9	10.4	1.6
	hypothetical protein FLJ10307		AA747448	34.8	5.3	1.3
46133 at			W60263	34.8	34.9	12.6
33305_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	SERPINB1	M93056	34.7	9.2	0
33730_at	retinoic acid induced 3	RAI3	AF095448	34.7		4.6
40153_at	ATP binding cassette, sub-family B (MDR/TAP), member 2	ABCB2	X57522	34.3	33	40.6
37294 at	B-cell translocation gene 1, anti-proliferative	BTG1	X61123	34.3	15.2	0
36609_at	solute carrier family 1 (glial high affinity glutamate transporter). member 3	SLC1A3	D26443	34.2	5.8	3.4
51550_at			AI681179	34	13.3	22 5
Ţ,			AA203416	33.9	10.8	14.7
	collagen, type V, al	COL5A3	AI984221	33.9	2.1	3.9
37305 at	enhancer of zeste (Drosophila) homolog 2	EZH2	U61145	33.6	10.9	2.4
53983_at	hypothetical protein PR02714		AI139975	33.6	13.8	0.3
55353_at			AA760977	33.6	6.9	9
848_at	TNF receptor associated factor 1	TRAF1	U19261	33.5	6.6	5.5

52183 at			H38110	33.5	9.1	5.8
73972 at			AA243659	33.5	15.4	18
737.4_at			A1863446	33.1	173	0
			AA210833	33.1	210	3.05
	custerni (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	CLU	M25915	32.9	O.	8.7
59365_at			1000			
56922_at			U5963/	32.9	6.9	4.9
51026 at hypothetical protein PRO081	13		AA211158	32.7	18.2	35.
			N30257	32.6	3.3	
1445_at chemokine (C-C motif) recentor-like	ntor-like 2		H17489	32.5	22.9	8
36543_at coagulation factor III (thron	III (thrombonlastin tissue factor)	CCRL2	1	32.3	6.4	3.5
	ביים ביים ביים ביים ביים ביים ביים ביים	F.3.		32.3	6.6	4.2
1633 g at pim-2 oncogene				32.2	3.6	8.6
Γ	protein	FIMZ	┙	32	15.7	11.4
			-4	31.6	6.1	18.4
		hypoprotein	1	31.6	2.4	23.
47113 at Kruppel-like factor 5 (intestinal	(led		_1	31.5	0.1	1
FLN29 gene produ		KLF5	- 1	31.5	41.2	7
glutamate decarbo	brain 67kD)		AB007447	31.4	36.2	36.8
Г		GADI	AL042399	31.4	5	
36575_at regulator of G-protein signalling	ing 1		AI199418	31.2	19.8	24.4
glycoprotein lb (platelet)	alpha polypentide	KGS1	S59049	31	46.9	16.
Zinc finger protein 259	and dad for a second	GP1BA	J02940	30.9	9.1	7.6
		ZNF259	AF019767	30.5	2.7	
small inducible cvt	Okine A4 (homologous to mouse Min 15)		٨	30.5	5.2	0
	Compared to House INID-1D)	SCYA4		30.3	13.4	13.3
60835_at			R37337	30.1	6.4	3.6
47076 at			AI831561	30.1	6	5.6
31693 f at H2A histone family member			- 1	29.9	2.6	3.4
hypothetical profein	1 L	HZAFG		29.8	16.1	30.5
_	Ictase (6 AVD) cubucit		AA854113	29.8	3.8	
Γ	ESI 6. 4AD SUDUING		AI480328	29.8	8.6	8.6
ngnino il institutioni	C L C L V	UBEZLE	AA883502	29.7	38.7	20
, ,			1.0000			

47318 at	47318 at	RCN1	AI817760	29.7	11.9	9
84909 21			AI949175	29.7	5.4	
3000 at	ı		AA902134	7 97	5. 7.7.3	300
50594 at	STAL Induced STAL Inhibitor-2		AF037989	29.2	5.50	39.0
190 at			AI967984	29.2	4.3	22
מיים מון	iluciear receptor subtamily 4, group A, member 3	NR4A3	U12767	29.1	200	0.5.5
40362 at			AI989871	29.1	96.90	7.5
40302_al	inclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2		53	11.4	5.2
67764 r at						
44729_at	hypothetical protein FL 113855		AA0048/9	29	4.4	11.8
32863_at			AI027524	28.8	10.5	13.
53010_at			AL023754	28.7	7.3	1.6
36139_at	DKFZP586G0522 protein		AI809925	28.6	4.2	29.8
1953 at	vascular endothelial prowth factor		- 1	28.5	1.5	20.
56999_at	. 1	VEGF	-1	28.4	6.2	7
53799 at	hypothetical protein similar to maise Desist		AI625959	28.4	11	Č
89202 at	-1		AA628434	28.3	2	
40098 at	EH domain containing 1		AI347361	28.3	30.4	6
58941 at		EHD1	AF001434	28.1	9.0	3.9
42769 at	alphase Atalpha		AI765967	28.1	24.1	
81887 at			N46441	27.9	0.7	0
44825 at	RAD50 (S. cerevisiae) homolog		AI766826	27.8	10.9	33.8
51278 at		RAD50	AA126482	27.8	17.5	30.9
49670 at			Al139543	27.7	2.8	2.6
37442 at			W96225	27.7	2.1	
40268 at	FOS-like antigen 2		AL050378	27.6	5	11.8
47971_at	ferritin, heavy polypentide 1	FOSUS	X16706	27.6	1.7	2.1
54491 at		FTH1	T92243	27.6	6.3	80
41872 at	deafness, autosomal dominant E		AA043562	27.5	ĸ	3.1
48105 at	latexin protein	DFNA5	AF073308	27.4	24	1.3
63380_at	hypothetical protein DKF2p434P0531		AI672094	27.4	6.5	6.0
56500 at			AI732727	27.4	5.9	4.9
65628 at			AI241578	27.4	9.8	
38617 at	IM domain kinase 2		AW023171	27.4	1.6	3.4
		LIMK2	D45906	27.3	4.4	

38783 at	manufacture and a second a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and a second and a second and a second and a second and a	ADM	D14874	27.2	8.5	7
50072 24	יויסטווין אין עמוטוופוווטומוופ	MUC1	J05581	27.2	36.1	300
300/3 at	neuropiiin z	NRP2	AA778058	27.0	1001	3.0
49249 s at			44533079	2.7.2	10.0	
44115 at	hypothetical protein from EUROIMAGE 588495		6,000000	27.1	2.8	2.5
87497_f at			AA486504	27.1	3.1	3.8
56641 at	liver expressed antimicrobial poptido		AI832016	27	21.1	7.7
52905 at			AI937227	27	10.1	2.5
86581 r at			AI279898	26.9	14.5	
-} {			AA700110	26.8	2.7	35.6
T	2-3 Uligoadenyiate synthetase 2	OAS2	M87434	26.7	280	34.8
ij,	Crosterin (completifelit lysis infinition, SP-40,40, suifated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	CLU	AW008412	26.7	4	2
49117_at	interferon induced protein 75, 52kD	11	110000			
52958 at		171/5	AI/43445	26.5	24.4	7.1
38970 s at	Nef-associated factor 1		N63458	26.5	0.8	
			AJ011896	26.4	7.6	4.2
40496 at		H2BFL	AA557205	26.4	3.9	0.5
Τ	Tierrodi Income e 'T Tierrodi Income	C1S	J04080	26.3	5.6	7.9
Τ	insulin-like growth factor, binding protein 4		H16258	26.3	9.0	2.6
Τ	-10	IGFBP4	M62403	26.2	72	18.6
173 g at	The state of the s		AI807170	26.2	0.8	0
	H1 histone family member 2			26.2	15.6	19.2
	filmor necrosis factor alpha inducible collustrations	H1F2	AI189287	26.1	2.3	10.1
	tercine zipper domains, funtingtin interacting protein Containing factor IIIA-interacting protein L; transcrption factor IIIA-interacting protein		AF070533	56	45.9	21.1
64733_r_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9	SERPINB9	AA156247	26	12	6.4
			A A E 2 2 2 1 C	0		
56691_at			44322010	97	6	3.6
	H1 histone family member 0		AI935202	26	15.1	1.2
at	_i	H1F0	297630	25.9	19.3	1.4
56871 at			AI735440	25.9	12.1	6.5
7	mitochondrial colute carrier		AI953847	25.7	8.6	12.8
Τ				25.7	4.2	2.1
	design commercial support in a management of the prince	DVTE	00000			

18 OF 10 O			A1693688	25.6	16.7	
1			A1214996	25.5		
	B7-H1 protein		AAAAAAA	0.02	01	4.3
	serine/threonine kinase 19	OT7.10	MAZ92201	25.6	∞	6.1
Г		SINIS	75250	25.5	9.0	18.
† t		TFPI2	D29992	25.5	0	1
1	1:0000000000000000000000000000000000000		AI990212	25.3	8.3	4.9
Τ	- 1	APOL1	AA156784	25.2	182	17.0
T	an I	OASZ	AI340262	25.2	27.3	101
	Z-5 Oligoadenylate synthetase 3	OAS3	AA135525	25.2	0.00	10.
	myosin X	MVO10	AB018342	2.5.2	20.0	10.8
\neg	promyelocytic leukemia	IMG	M82027	7.62	5 6	
	ADP-ribosylation factor-like 4	VIOV	173050	1.62	20.3	8.8
t	KIAA1091 protein	1	000000	24.9	1.1	0.4
1586_at ins	insulin-like growth factor binding profein 3	0.00	AB029014	24.9	10.8	5.1
	tathionine gamma lyas	IGFBF3	M358/8	24.9	3	14.4
Γ	Odr42 effector protein 2	CTH	AI955061	24.8	2.8	
Π			AF001436	24.7	6.7	10.9
T	Sertim inducible kinase		AI653230	24.7	4	1.5
1			AF059617	24.6	0.2	19.4
58702 at			AI826091	24.6	1	
, ,	profein tyrosine phornhaters and a second		T55716	24.5	0	40
1.	ordin through a dase, non-receptor type z	PTPN2	M25393	24.4	6.4	1.2
1			AA568587	24.4	10.8	0.8
	interferon-induced protein 35	DYRK3	Y12735	24.3	0.2	1.9
		IF135	U72882	24.3	35.4	12.9
1742 s at tur	41742 s at Itumor necrosis factor alpha inducible collustration		AI983437	24.3	2.9	9.9
leu fac	leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA interacting protein	-	AF061034	24.3	28.1	8.7
36564_at			0177CW			
6175 s at hu	36175 s at human immunodeficiency virus type I enhancer kinding acceptance		W2/419	24.7	7.6	2
48964 at		HIVEP2	AL023584	24.2	7	5.7
59133 at			A1629027	24.2	17.2	9 1
Γ	hynothetical protein		AA131626	24.1	1.2	0.7
;	prostagiandia 12 (prostagia)		AI949434	24.1	7.5	19.9
		CHC	00.00			

35094_t_at	Ieukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	LILRA3	LILRA3 AF025527	23.9	oi ci	1.5
83874_at			AI024818	23.9	7.8	4.4
46266_at	serine (or cysteine) proteinase inhibitor, clade A (alpha-1	SERPINA8	AI208913	23.9	15.5	6.6
39422_at	KIAA0477 gene product		AB007923	23.8	11.2	7.1
47899_at			AA056755	23.8	16.9	13.4
62217_at			T81422	23.7	7.2	15.8
55334_at			AI249019	23.7	2.3	0
32186_at	solute carrier family 7 (cationic amino acid transporter, y+ system),	SLC7A5	M80244	23.6	3.5	2.3
	member 5					
44235_at			H82526	23.6	2	9.2
88550_at	hypothetical protein FLJ12929		AI468004	23.6	4.9	0
63017_at	pleckstrin homology domain containing, family A (phosphoinositide	PLEKHA4	AA521373	23.6	0.2	49.9
	binding specific) member 4		_		_	
54744_at			AA582287	23.5	8	3
37032_at	nicotinamide N-methyltransferase	LMNN	U08021	23.4	0	1.2
32156_at	poliovirus receptor-related 2 (herpesvirus entry mediator B)	PVRL2	AF044968	23.4	5.9	8.9
34481_at	vav 1 oncogene	VAV1	AF030227	23.3	0	0
37028_at	growth arrest and DNA-damage-inducible 34		U83981	23.2	1.9	8.6
41503 at	KIAA0854 protein		AB020661	23.1	10.5	8.6
54610_at			AI479815	23.1	4.1	9.5
39839_at	cold shock domain protein A	CSDA	M24069	23	1.1	0
41142_at		OXCT	U62961	23	3.7	4.5
35718_at	interferon-induced protein 41, 30kD	IF141	L22342	23	37.3	14.5
1779_s_at	pim-1 oncogene	PIMI	M16750	23	3.5	9.9
34770_at	mitogen-activated protein kinase kinase kinase 8	MAP3K8	Z14138	22.9	9.0	3.3
~ "	phorbolin-like protein MDS019		AL078641	22.9	41	25.5
87811_at			AA868517	22.9	1.1	18
47870 r at	hypothetical protein DKFZp761C169		AW003245	22.9	4	8.8
908_at	\neg	IFIT2	M14660	22.9	34	384.9
88906_at	KIAA1442 protein		AL110312	22.8	0	1.8
38281_at	caspase 7, apoptosis related cysteine protease	CASP7	067319	22.7	14.4	4.9
54782_at			AI281068	22.7	9	1.1
87415 at			W73083	22.7	4.8	17.3

Response of Deliantic Cens to a

Inventors:

Nir Hacohen, et al.

38582 2	serine protesse inhibitor Kazal tyne 1	LANGO	00013014	000	3 0	00.
10000		JANIA	A1901220	22.5	0	10.6
			AI916646	22.6	0.7	2.1
84601_at			AI469960	22.6	2.9	4
889_at	integrin, beta 8	ITGB8	M73780	22.5	2.1	1.2
36526_at	exostoses (multiple	EXTL2	AF000416	22.5	7.5	0
39119_s_at	natural killer cell transcript 4		AA631972	22.5	34.2	10.5
56979_at			AA133395	22.5	3.4	3.4
35036_at	complement component C1q receptor		U94333	22.4	1.2	6.0
41451_s_at	SAR1 protein		W28498	22.3	2.8	3.6
64930_at	FN5 protein		AA587944	22.3	15.6	3.9
35957_at	stannin	NNS	AF030196	22.2	16.3	1.1
68355_at			AI655376	22.2	0	0.7
49364_at			AL041551	22.2	1.7	2.7
946_at	t-complex-associated-testis-expressed 1-like 1	TCTEL1	D50663	22.1	20.3	12.3
47544_at			AA741324	22.1	4.8	5.3
80151_at			AA031832	22	0.7	0.3
46175 i_at			AA552969	22	8	0
36453_at	KIAA0711 gene product		AB018254	21.9	1.1	0.3
68002_at			AA503803	21.9	17.2	13.1
92145_at			AI703103	21.9	13.4	27.4
32529_at	transmembrane protein (63kD), endoplasmic reticulum/Golgi		×69910	21.7	23.9	6.8
38272_at	MKP-1 like protein tyrosine phosphatase		AF038844	21.7	2	0
62939_at			D12309	21.7	16.6	4
69197_r_at			AA508552	21.6	6.1	C
44087_at	HSPC018 protein		AI279029	21.5	20.8	2.1
58605_at	DNA segment on chromosome X (unique) 9928 expressed sequence	DXS9928E	A1697939	21.5	20.6	9.4
44092 at			AI862887	21.3	17.7	5.5
51016 s_at	_		AI971498		13.6	5.0
1508_at	integrin, alpha 9	ITGA9	D25303	21.2	0	0.4
	defensin, beta 1	DEFB1	AI309115		7.8	15.1
91587_at			AI554946	21.1	4	1.9
51092_at	putative zinc finger protein NY-REN-34 antigen		AI950095	21.1	14.6	8.5
53757 at			AA131524	21.1	1.8	3.6

		NDRG1	D87953	21	100	0
55843 at	Jun dimerization protein p21SNFT		A1359117	110	0.70	0.0
46152_at			VI760261	1300	4.0	0.1
51161_at	ras homolog gene family, member A	V 10 V	ı	20.9		9
1776_at	Ras-related associated with diabetes		- 1	20.9	5.2	20.3
39071 at	Integrin, alpha V (vitropentin receptor, slobs polymentids, and	RRAD	-[20.8	0	1.2
	(D51)	ITGAV	M14648	20.8	1.6	1.3
1237_at	immediate early response 3	IFB3	081017	0 00		
51637_at				6.00	4.7	٥
41242 at	UDP-N-actev/glucosamine pyronhosphorylase 1		666791	20.8	2.6	11.6
40852 at		UAPI	AB011004	20.7	1.9	1.2
61873 at	diversity kinasa			20.7	18.9	29.9
47500 at	2	GK		20.7	13.9	0.5
44370 at			AA805337	20.6	7.1	2.8
64247 at			AI589469	20.6	0.3	2.5
48311 at			H40631	20.6	4	3.1
	hypothetical protein 23851		AI458231	20.6	3.8	1.3
60857 at	chloride intracellular channel 4		AF035313	20.5	14.3	16.9
43901 at		CLIC4	AA142983	20.5	6.3	2.7
39623 at	Norrie disease (pseudoplioma)		AI435160	20.5	8.7	2
106 at	runt-related transcription factor 3	TON S	- 1	20.5	0.8	0.3
34699 at	CD2-associated protein	RUNX3	- 1	20.4	17	11.3
36560 at	KIAA0481 gene product	CUZAP	- 1	20.4	12.9	8
1729 at	TNERSE14-associated via death domain		AB007950	20.4	1.2	0
56409 at		TRADD	L41690	20.4	13.9	1.7
46567 at			W72194	20.3	0.3	1.5
'l ~	lipin 2		AI732347	20.3	1	0.1
33291 at	anyl releasi	LPINZ	D87436	20.2	47.2	18.2
33157 at	insulinoma associated 1	RASGRP1	AF081195	20.2	2.4	2.7
39143 at	nisumonia associated 1	INSM1	M93119	20.2	4.5	σ
35-01-00	indical ractor of activated 1-cells, cytopiasmic, calcineurin-dependent	NFATC1	008015	20.2	1.8	0
91350_at	71 - 71		AA989283	202	7 3	7.0
53855 at	cyclin K	CCNK	X84721	20.2		
52875 at			N36284	20.1	12.7	12.5
J20/ Jan			00000			

53/2/_at			00203710	100		
61130 at			AI/586U8	20	7.8	1.7
50296 i at	apolipoprofein 1 3		٩	20	3.3	1.9
. 1 "	TNE indirect protein	APOL3	- 1	20	24.4	12.1
30640 34	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		AF099935	19.9	2.6	0 /
48276 at	Blutailinie-fructose-b-phosphate transaminase 2	GFPT2	'	19.9	0	D: /
318 34	H1 histons famil:		AI275691	19.9	9.9	
259 at	2. E'oligondoniole anni y, member A	H1FX		19.8	7.9	1 6
63332 at	 Congoadenylate synthetase like 	OASL	L40387	19.8	6.9	1194
51155 at			AA127696	19.8	11.7	11 4
53995 at	hynothetical protein		AL043669	19.8	6.2	8.7
54310 at			Al346913	19.8	1.1	4
45785 at	DKFZP566B1346 profess		AA975511	19.7	1	2
74908 at				19.7	8.6	3.4
64449 at		IF135	~1	19.7	35.8	8.9
40388 at	discs. large (Drosophila) homolog-associated exetain 1		AI810399	19.7	5.7	3.4
84220 at	S. C. S. C.	DLGAP1	AB000277	19.6	2.1	0.1
32965 f at	heat shock 70kD protein 1R		AI373122	19.6	0.1	1.1
38010 at	BCI 2/adenovirus F18 19kD interacting society	HSPA1B	W28645	19.5	0	2.2
35463 at	homeo box (expressed in ES calls) 1	BNIP3	AF002697	19.5	5.8	0.2
71787 r at		HESX1	AF059734	19.4	20.3	40.2
34039 at	Nmphocyte antigen 94 (mouse) homolog (22thinsting)		- 1	19.4	14.4	0.5
	1946)	LY94	AJ001383	19.3	0	0.8
65738_at	TERA protein		7073670			
32640_at	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	M24283	19.3	10.8	4.1
88541_at						
91017_at	baculoviral IAP repeat-containing 3		AI800/35	19.2	0.2	0
63742 r at	duct	BIRC3	U54711	19.2	19.6	e
45602 at			AA910186	19.2	1.5	3.4
48018 at			AA195108	19.2	1.3	2
49283 at			AA700227	19.1	31.1	9.3
52696_at			AA158597	19.1	10.1	6.0
37615 at	prowth factor recentor hound protein 10		AW024937	19.1	14.9	1.8
51771 at		GRB10	D86962	19	3.9	60.3
			AA284560	σ	00	-

2. Response of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

		AAUSSBS6)	5	13.5	0.0
		AI312873	18.9	12	0.8
		AI291314	18.9	3.7	1.5
solute carrier family 12 (potassium/chloride transporters), member 7	SLC12A7	AI816843	18.9	1.9	0
CASP8 and FADD like apoptosis regulator	CFLAR	AI302459	18.9	11.6	1.6
dual specificity phosphatase 10	DUSP10	AB026436	18.8	7.8	11.2
plasminogen activator, urokinase receptor	PLAUR	U09937	18.8	3.3	5.3
novel retinal pigment epithelial gene		AI973108	18.7	5.4	4.1
myristoylated alanine-rich protein kinase C substrate (MARCKS, 80k·L)	MACS	AA131320	18.7	7.3	8.2
baculoviral IAP repeat containing 2	BIRC2	U37547	18.6	4.9	13.5
		AI554044	18.6	13.5	14.8
hypothetical protein DKFZp434F2322		AI632223	18.6	2.7	0.3
Alg5, S. cerevisiae, homolog of		AA425251	18.6	4.7	3.8
		AI982765	18.6	12.9	14
Nef associated factor 1		AJ011896	18.5	5.4	1.5
		AL050227	18.5	0	4.8
LR8 protein		AA152202	18.5	14.2	4
cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	AI989792	18.5	2.6	4.9
CD44 antigen (homing function and Indian blood group system)	CD44	L05424	18.5	0.6	
		AI422986	18.5	5.7	5
		AI674731	18.5	2.5	1.7
DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4		18.5	4.6	26.4
integrin, beta 8	ITGB8	AI129512	18.5	2	9.0
		A1652899	18.5	8.5	1.6
		AW014148	18.5	0.9	0.4
dual specificity phosphatase 2	DUSP2	L11329	18.4	2.6	4
methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	MTHFD2	X16396	18.4	21	0
interleukin 2 receptor, alpha	IL2RA	X01057	18.4	0.2	1.8
Janus kinase 1 (a protein tyrosine kinase)	JAK1	AL039831	18.4	13.2	2.9
		AW022213	18.4	8.8	00
plexin C1	PLXNC1	AF030339	18.3	38	0

82588_at 38555_at

55830_at 82933_at 54759_at 44744_at

36578_at

189_s_at | 48740_s_at | 48081_at |

73776_at 53831_at 49626_at 47533_at 38971_r_at 38971_r_at 39516_at 32222_at 1

62113_at 62561_at 53497_at 57733_at 61428_at 1292_at 40074_at

1125_s_at 44207_at

1702_at interleukin 34877_at Janus kinas 79520_at 32193_at plexin C1

	hunothotical protein El 192021		X82200	18.3	22.2	11
53489 at			AA011633	18.3	2.1	2
Τ	4410		A1928764	18.3	8.5	20.8
T	iylate Lyclase 1, soluble, alpha 3	GUCY1A3	Y15723	18.2	3.1	E C
64285 at			AI768334	18.2	0	O
T	hypothetical protein El 110164		AI050855	18.1	1.9	
T			AI431797	18.1	3.2	2
51510 r at			AA999894	18.1	2.5	9.9
1	institing ike growth factor 1 recented		T92882	18.1	10.1	4
1 10	Blown Jaciot I receptor	IGF1R	X04434	18	m	7.4
; 	promyelocytic laukamis		AI338290	18	2.2	2
, to	٦l	PML	X63131	17.9	49.4	18.9
			AA767436	17.9	3.4	2.6
1203 at			W70067	17.9	7.9	3.9
34965 at cvst	cystatin F (leukocystatin)		D17357	17.8	5.2	10.3
ŧ		CST7	AF031824	17.7	9.4	2.7
at		SAT	AL050290	17.7	12	9.
			AA502943	17.7	3.7	
42721 at			AA723927	17.6	23.2	15.8
at	KIAA0603 gene product		AI261490	17.5	4.3	5.9
			AI948512	17.5	18.7	12
35682 at			N24987	17.5	9.4	1.6
Τ	sterile alpha motif and leucipe gionographic		AI133727	17.4	1.4	32
at	Commence of the contract of th		N95341	17.4	0.5	
1	hypothetical protein El 120373		AI982723	17.4		0
	KIAA0942 protein		AW021103	17.4	9.0	5.5
37823 at smal	Small inducible cytokine subfamily 4 (Ove Ove) momber 6		AI073412	17.4	0.2	5.1
П	chemotactic protein 2)	SCYA8	Y16645	17.3	63.9	47.1
j j			AF070530	17.3	7 3	
T			AB015228	17.3	, i o	0.0
55441 r at 54M	SAM domain, SH3 domain and nuclear localisation signals, 1	SAMSN1	AI823872	17.3		0.4
			H15727	17.3	2	0.5
j t			AI991958	17.2	0.4	1.2
a a	iiyai oxysterola (11:Deta) denydrogenase 1	ומוונטו	MATCACE	,		

35153_at	e syndrome 1 (nibrin)	NBS1	AF058696	17.1	10.8	25
280.40 at	~I	ITPR3	U01062	17.1	0.0	5,4
30040 at	Splicing factor 30, survival of motor neuron-related		AF107463	171	0.0	5 6
39108_at	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	SST	1	17.1	116	3.1
50361_at			Ľ	17.1	0 7 7	t t
55588_at	hypothetical protein FLJ13868		20000010	1./1	24.5	11.4
167_at	eukaryotic translation initiation factor 5	L	1	1/.7	3.4	1.7
35238 at	Ciated factor 5	EIF5	- 1	17	4.3	0
1461 at	minchaer factor of Vanna light polymortide	IRAF5	۱۲	17	2	0
5	inhibitor, alpha	NFKBIA	M69043	17	4.9	6.3
76847_at			A10E1161			
54029_at			10110610	1/1	6.1	3.4
70591 at	hypothetical protein FL 121162		AA948385	17	6.2	4
56331 at	n FI 1206		AL046389	17	0.4	0.3
40082 at	fatty acid Communa A liman last		AA478923	17	3.7	1.4
30003 21	217	FACL2	D10040	16.9	11.5	A Tr
מבררר ה	priospiratoyii lositol glycan, class A (paroxysma) nocturnal hemoglobinuria)	PIGA	D11466	16.9	8.5	5.8
52786_at			A1266042	0.91	C	
48372_at			240004V	10.9	0.7	9
53773_at	tumor necrosis factor (ligand) superfamily member 13h	00.100	C/201047	16.9	6.3	3.8
64403 at		LINFOF 13B	AA682496	16.9	17.6	11.2
54063 at			AA195829	16.9	0.2	0.7
69573 at			AI801777	16.9	4.4	6.2
41386 i at	KIAAA346 protein		AI718148	16.9	7.1	3.6
40635 at	flotillin 1		AB002344	16.8	4.5	0.5
36671 at	asparagine everthetere	FLOT1	AF089750	16.8	13.6	12
	CD36 antiren (collacer time 1	ASNS	M27396	16.8	8.6	3.5
7000	2 (lysosomal integral membrane protein II)	CD36L2	D12676	16.8	30.9	9.5
55776 at			W20082	16.8	96.90	7 7 1
54769 at			N52761	16.8	10.4	14.1
32668 at	Signal ANA Location of an analysis o		AI298599	16.8	5.1	200
40960 at			AL080076	16.7	4.5	200
5-000	odi caricetaciono pera 1,4. galactosyltransterase, polypeptide 1	B4GALT1	D29805	16.7	4.9	3.9
196_s_at	caspase 5, apoptosis-related cysteine protease	CASP5	U28015	16.7	00	
			21222	1,.,,	0.4	4.6

67401_at			AI434675	16.7	16.1	6.4
55629_at			AL040635	16.7	9.7	9.5
38797_at	KIAA0062 protein		D31887	16.6	0	2.3
58242_at	solute carrier family 21 (organic anion transporter), member 11	SLC21A11	AA053855	16.6	2.5	0
54819_r_at			AI720898	16.6	6.1	1.3
46655_at	transcription factor (SMIF gene)		AA131327	16.6	8	14.5
39986_at	DKFZP586D0919 protein		AL050100	16.5	4.2	4.9
37933_at	retinoblastoma binding protein 6	RBBP6	X85133	16.5	2.8	61.5
81932_at			A1659966	16.5	8.6	0
79721_at			AI733197	16.5	11.6	56.6
52675_at			AI581142	16.5	7.4	3.6
50375_at			AI091460	16.5	4.1	1.2
37416_at	ras homolog gene family, member H	ARHH	235227	16.4	15.5	11.5
39064_at	5,10·methenyltetrahydrofolate synthetase (5·formyltetrahydrofolate cyclo-ligase)	MTHFS	L38928	16.4	2.4	16.3
35785_at	trinucleotide repeat containing 15	TNRC15	W28281	16.4	3.3	3.8
79053_at			AI962796	16.4	4.3	1.6
48556_at	HIV TAT specific factor 1	HTATSF1	AA581365	16.4	6.4	4.2
86536_at			AI740796	16.4	8.8	1.7
55692_at	hypothetical protein FLJ11656		W22924	16.4	4.3	2.7
35937_at	MHC class I polypeptide related sequence B	MICB	l. :	16.3	17.2	32.3
			AI079327	16.3	3.3	0.1
80084_at			AI889019	16.3	5.6	0.8
54990_at	hypothetical protein		AW009586	16.3	9	8.2
52062_f_at			H98105	16.3	22.9	6.4
35113_at	solute carrier family 22 (organic cation transporter), member 1	SLC22A1	X98332	16.2	1.8	10.1
31883_at	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	MTRR	AF025794	16.2	5.2	0
35275_at	adaptor-related protein complex 1, gamma 1 subunit	AP1G1	AL050025	16.2	9.0	0.3
53661_at			AL038450	16.2	2	5.2
36398 at			W28729	16.1	1.1	25.8
49353_at	hypothetical protein FLJ20216		AI927837	16.1	0.3	0
72808_at			AI640523	16.1	6.1	32.6
39723_at	culin 1	CULI	۹	16	6.5	4.8
296_at	tubulin, beta polypeptide	TUBB	X79535	16	12.7	5

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7	m	15.2	M83667	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	1052_s_at
11.4	4.8	15.3	T95101			42933_at
0	∞	15.3	A1990633	STAT5A	signal transducer and activator of transcription 5A	/5183_at
4.6	2.5	15.3	AL041566			63307_at
58	6.3	15.4	A1692445			56278_at
O	1.1	15.4	AA628024			70631_at
42.7	14.3	15.4	AI743005			69589_at
13.9	8	15.4	X92841	MICA	MHC class I polypeptide related sequence A	40755 at
9.6	21.6	15.4	M37766	CD48	CD48 antigen (B.cell membrane protein)	38006_at
7.8	12.3	15.5	AA017070			86261_at
1.2	3.2	0.01	10.04 UU		inhibitor)	
3.5	14.6	15.6	AI823982		nypotnetical protein FLJ11000	37.300 at
8.9	1.9	15.6	Al143121			45748_at
4.8	1.9	15.6	X72631	NRIDI		31637_s_at
8.5	9.9	15.6	X84373	NRIPI		40088 at
44.6	26.5	15.7	AI347618			82359_at
1.8	5.9	15.7	AW002763		porcupine	43391_at
18.8	2.1	15.7	293930	XBP1	X-box binding protein 1	39755_at
0	3.3	15.8	W46406		hypothetical protein bA395L14.2	55081_at
0.2	4.9	15.8	AA160973			45143_at
2.2	5.3	15.8	A1634355			85724_at
1.2	4.9	15.8	D50495	TCEA2	transcription elongation factor A (SII), 2	745_at
6.1	11.1	15.8	AI865431	TNFRSF5	tumor necrosis factor receptor superfamily, member 5	35149_at
1.6	6.3	15.9	D13146	. CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	344 s at
0.4	5.8	15.9	M84349	6500	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	39351_at
6.7	19.1	15.9	L07633	PSME1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	36600_at
e	8.5	15.9	M74447	ABCB3	ATP binding cassette, sub-family B (MDR/TAP), member 3	39988 at
-	9.6		0162000	200	associated antigen 1; alpha polypeptide)	
	5.11	0 1	4000010	E CH	integral olabol (antigon 0011A (a100) lumphonto function	40006 24
1.6	10.7	16	U36310	GFUZ	similar to mouse Xrn1 / Dhm2 protein	41021 s at
	107	2	136310	CDDS	41021 s at Iplycerol 3:phosphate dehydrogenase 2 (mitochondral)	41071 s at

3020/_dl	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)	PSMB9	PSMB9 AA808961	15.2	15.8	3
73800_at			7.000014			
80408_at	ribosomal protein L37a	A75 IQQ	AAAC1504		2.3	0.9
64879_at	heparan sulfate 6-0-sulfotransferase	TUC/7	AA901504	15.2	0.3	0
37732 at		- NOON	- 1	15.2	0.2	0
81726 at		КУВР	-1	15.1	4.6	5.3
63984 f at			AI885498	15.1	10.7	7.2
-} +-			AA535914	15	16.4	9.2
			AI440145	15	12.7	2.5
51842 at			A1634580	15	16.9	9.4
41237 at	- 1-		AI570531	15	2.9	7.3
63032 at	and a second parionity complex, class 1, A	HLA-A	D32129	14.9	9.7	5.6
81035 i at			AI653152	14.9	3.1	11
56850 at			AI573275	14.8	7.8	1.9
87002 ===			R08417	14.8	3.5	12
51022 at	in the second se		A1270476	14.8	28.7	63.7
71763 at	Ωlr	SPHK1	AI769914	14.8	c	1.5
77567 at	reticulocalbin 1, EF-nand calcium binding domain	RCN1	D42073	14.7	9.7	5.4
62266 at	Acoton Interior		AI694316	14.7	0.5	22
72553 at	ingpointed protein reactions		AI339505	14.7	6.1	17
52831 at			AI335361	14.7	4.2	3.4
			AI160811	14.7	0	29.8
4 -			AA005281	14.7	16.7	12.4
40957 at	KIAA0160 protein		AI161358	14.7	5.7	16.9
33804 at	profein tyrosine kinase 3 kata	KIAA0160	D63881	14.6	17.7	5
70634 at		PTK2B	U43522	14.6	13.4	5
44008 at			AW007125	14.6	1.3	1.3
53389 at			AI921877	14.6	3.1	1.3
34726 at	Calcium channel voltage dependent hets 2 subusit		H70631	14.6	1.9	3.7
32533 s at	Ίτ	CACNB3	U07139	14.5	0.1	3.3
78077 at	מומים מומים	VAMP5	AF054825	14.5	39.7	13.4
44728 at			AI125204	14.5	9	É
46699 at			AI819734	14.5	1.5	2.5
36980 at	nroline.rich protein with puclear tarracting gives		AIU52110	14.5	0.2	4.2
	Promission protein man marketing signal		003105	14.4	00	2.4

			2000			
51854_at	KIAA1128 protein		AI9224/0	14.4	7.2	1.1
34887 at			AA424126	14.4	6.3	5.6
62174 at	SWI/SNF related matrix associated actin dependent romitations		N92548	14.3	7.9	1.4
70507	- =1	SMARCBI	N63449	14.3	1.9	4.9
71000 at			AA281239	143	C C	6
31080_at	010000		M55630		2 10	0.0
300049 at	NIAAUS/U protein		AB023187	14.2		20.5
50992 at		NXL	AI653621	14.2	0	30.5
20002 at	udai specificity phosphatase 10	DUSP10	N36770	14.2	4 1	9.01
70516_at	leucine-rich protein mRNA		AI817736	14.2	4.1	10.0
79494 at			T77813	14.2	6:0	0.0
47782 at			N34516	14.2	10.1	9
54077 at	hynothetical protein FI 110430		R88823	14.2	2	
46526 at			W18181	14.2	6.0	9 4
40210 at	RAB13 member DAS concern from the		AI434025	14.2	13.4	13.9
59516 24	KIDDIO, HIGHIDEL NAS OHCOBERE TAMIN	RAB13	X75593	14.1	6.4	
1440 c at	Monte of profession		AA210695	14.1		10.5
32827 at	Oncogene TC21		X83490	14.1	2.6	28
34308 at	13		AI365215	14	800	57
36148 at	-1 .	HZAFL	U90551	14	4.9	13.2
32901 5 24	alliyloid Deta (A4	APLP1	U48437	14	10.7	2.5
35.001_3_al	increopriosifiii 1 (flucteolar phosphoprotein B23, numatrin) pseudogene 14	NPM1P14	AC005192	14	3.9	1.7
54064 i at			7000000	,		
72541_at			1020201	14	C	5.7
57833_s_at	NY.REN.45 antigen		A1002805	14	1.7	1.6
57579_at			AW001803	14	1.1	0
1876_at	V-ral simian leukemia viral oncogene homolog A (ras related)		A1580/21	14	4.6	4.6
36872_at	cyclic AMP phosphoprotein, 19 kD	KALA	M29893	13.9	4.1	2.2
60019_at	leucine-rich neuronal protein	-	AL120559		12.3	4.7
87957_r_at		LYIN	AA94/309	13.9	10.6	1.4
49302_at	HBV associated factor		AA513538	13.9	9.9	3.6
64124_at			A19/181/	13.9	9.1	5.4
47578_at			AA206408	13.9	3.2	0.5
		_	AA160156	ď	_	C

Ī	1	ZNF151	Y09723	13.8	5.4	4
1		LTA	M16441	13.8	000	
40339_at gamma-aminobuty	minobutyric acid (GABA) A receptor, pi	GABRP	L			
62314_at			L			n
48062_at			AA418490		0.7	4.0
51508 <u>i_</u> at			19282		7.0	
56832_at			192002	13.7	2./	9.
48099 at			A1071408	13./	6.9	12.3
74566 at insulin-like growth	e growth factor-hinding protein 4		AAUUSUZ3	13.7	14.8	4.6
ŧ		IGFBP4	A1440424	13.7	75.4	14.1
1-			AW008462	13.7	1.1	2.5
73035 at Gilanylate binding			AI968055	13.7	0.7	9.0
í	Silving protein 1, interferon-inducible, 6/KU	GBP1	٤	13.7	8.7	-
	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	L29277	13.6	6.9	2.2
37393 at hairy (Drosophila)	sophila) homolog	HRY	119314	136		
88283_at			41961740		5 6	9.0
734_at mucin 4, tracheobr	racheobronchial	VOLIM	01/10/14	13.0	Σ.1	0.5
45606_at		100%	M04394	13.6	1.7	7.8
38463 s at ladenosine mononh	mononhosnhate deaminase (isoform E)		AA846692	13.6	0	0.2
1		AMPUS		13.6	2.6	0.1
Т			AB014515	13.5	7.4	10
78072 at			AA939344	13.5	4.3	
57670 at phosphoprotein as	rotein associated with CEMs		AI743607	13.5	1.1	11.7
i to	didil associated with GEINS		AI860212	13.5	4.8	1.2
56671 at linase endothelial			AA151346	13.5	12.1	11.7
7		LIPG	N29319	13.5	1.1	1.6
	A construction of the cons		AW009767	13.5	1.1	3.6
te te	orneriyigididiyi. Qoelizyine A synthase I (soluble)	HMGCS1	AL048840	13.5	2	
37360 at Ivmphocyte antiger	Pantigen 6 complex logic E		AW006742	13.4	6.4	12.4
1	-1	LY6E	U66711	13.4	13.6	8.3
44795 at STAT included STA	Cad STAT inhibitor 2		A1983632	13.4	8.3	3.1
te	- 1		A1129818	13.4	1.1	2.8
42362 at CCAAT/enhancer h	honcer binding profess // // // // // boncer binding		T62969	13.4	1.2	3.4
T	=1	CEBPD	A1633245	13.4	3.1	3.4
T	= :	KIF2	Y08319	13.3	24.6	7.3
329 at Involuetical protei	Drotein F JVXXX		100000			

51024_at			AI400509	13.3	17.3	7.2
51030_at			AA843962	13.3	6.1	200
46238_at			A1193110	13.3	1.4	Õ
32150_at	golgi autoantigen, golgin subfamily a, 4	GOLGA4	X82834	13.2	4.8	2.2
36776_at	lymphocyte-activation gene 3	LAG3	X51985	13.2	148.7	69.7
33106_at	nuclear receptor subfamily 1, group H, member 3	NR1H3	U22662	13.2	18.1	18
66903_r_at			AI002222	13.2	2.2	2.6
42803_at	E2F transcription factor 5, p130-binding	E2F5	AI377305	13.2	3.2	2.2
48097_at	transmembrane protein with EGF-like and two follistatin-like domains 1	TMEFF1	AA001144	13.2		0
46712_at			W63773	13.2	2.4	7 6
32684_at			AF038174	13.1	15.5	2.9
1170_at	colony stimulating factor 1 (macrophage)	CSF1	M37435	13.1	6.9	3.2
36103_at	small inducible cytokine A3 (homologous to mouse Mip-1a)	SCYA3	D90144	13.1	6.1	7.6
62367_at			AI220446	13.1	0.3	2.6
45583_at			AA602585	13.1	6.0	5.9
64189_at	DKFZP564J0863 protein		W60080	13.1	4.1	0
51220_at		SERF1A	W67895	13.1	4.7	3.6
53102_s_at	CGI-22 protein		AA627551	13.1	2.6	0
55518_at	tachykinin 3 (neuromedin K, neurokinin beta)	TAC3	AA004764	13.1	4.2	14.6
56080_at			AI703473	13.1	12.8	8.3
37324_at	transferrin receptor (p90, CD71)	TFRC	X01060	13	7.7	1.3
83568_at			R06436	13	9.0	5.1
60504_at			AI859849	13	3.8	4.5
63785_at	Mitochondrial Acyl-CoA Thioesterase		A1074605	13	15.4	3.2
44838_at	hypothetical protein FLJ12752		AI271348	13	4	3.1
65895_at	DKFZP564A2416 protein		AL040007	13	17	1.2
41469 at	protease inhibitor 3, skin-derived (SKALP)	PI3	L10343	12.9	0.4	5.4
40061_at	pleiomorphic adenoma gene-like 2	PLAGL2	D83784	12.9	61	5 6
40137_at	protein tyrosine phosphatase, non-receptor type 1	PTPN1	M31724	12.9	5.3	5.2
36484_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	GALNT3	AI935146	12.9	5.5	8 4
	acetylgalactosaminyltransferase 3 (GalNAc·T3)					
35992_at	musculin (activated B cell factor 1)	MSC	AF087036	12.9	80	
37951_at	deleted in liver cancer 1	DLC1	AF035119	12.9	0	2.6
39120_at	metallothionein 1L	MT1	AA224832	12.9	0 1	0.3

38349_at			AF038564	12.9	10.8	0.5
50745_at			AI143457		4.2	
65147_at			AI818579	12.9	0.2	4.1
61489_at			AI718763	12.9	3.7	3.4
65281_f_at			H22954	12.9	0.7	12
44853_s_at	CGI-34 protein		AA528059	12.9	10	7.4
73146_at	_	VEGF	1	12.9	5.5	1.6
44376_at	KIAA0582 protein			12.9	5.4	7.3
1573_at	platelet derived growth factor beta polypeptide (simian sarcoma viral	PDGFB	M12783	12.8	0	0.5
	(v·sis) oncogene homolog)				,)
39628_at	RAB9, member RAS oncogene family	RAB9	AI671547	12.8	7.4	3.5
33260_at	son of sevenless (Drosophila) homolog 1	SOS1	L13857	12.8	11.2	20.00
72558_at			AI858718	12.8	1.1	0.7
52850_at	KIAA1151 protein		AA128296	12.8	6.0	4 7
41409 at	basement membrane-induced gene		AF044896	12.7	8.3	Ċ
39857_at	syntaxin 11	STX11	AF044309	12.7	5.6	12.9
32240_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	PSMD5	D31889	12.7	0.8	1.5
37352_at	nuclear antigen Sp100	SP100	M60618	12.7	10	I.C.
57094_at	transmembrane protein 2	TMEM2	AI189381	12.7	1.9	2.1
44920_at			AI914925.	12.7	4.8	7.6
41385_at	differentially expressed in adenocarcinoma of the lung		AB023204	12.6	1.1	1.9
39032_at	transforming growth factor beta-stimulated protein TSC-22		AJ222700	12.6	1.1	3.1
38160_at	lymphocyte antigen 75	LY75	AF011333	12.6	13.5	0
32217_at			AF052105	12.6	6.3	7.6
473 g at	signal transducer and activator of transcription 5B	STAT5B	∪48730	12.6	4.6	1.9
45721_at	endothelin converting enzyme 1	ECE1	AL039866	12.6	4.3	5.7
63662_at			A1126468	12.6	4.9	4.5
52327 s at			A1989346	12.6	6.0	5.7
39211_at	hypothetical protein FLJ10374		AF091080	12.5	7.7	5.7
32593_at	KIAA0084 protein		D42043	12.5	6.3	0.5
75796_at			AI028528	12.5	1.3	9.0
76037_at			W86659	12.5	2.5	0
76688_at			AI312606	12.5	0	1.3
79145_at			W72060	12.5	8.0	8
86629_at			AA614137	12.5	10.6	3.2

Figure 11CC

56435_at	hypothetical protein FLJ20625		44573770	2		
39695_at	decay accelerating factor for complement (CD55, Cromer blood group	DAF	1	7 9	5.9	χ Ω
	ĺ	ì))	7:1	7.0
39710_at	P311 protein		1120501			
39749 at	proteasome (prosome macronain) 268 subunit non Attanto A	000	12000			8./
32697 at	A) monophocopy	PSMD4	021007	9.9	5.5	0
40803 24	ייינינינינינינינינינינינינינינינינינינ	IMPA1	AF042729	9.9	3.8	-
20202 at	CHO		1	9.9	3.6	4.5
32723 at	BH3 interacting domain death agonist	BID	AF042083	9.9	4.2	6
40901 at			017989	9	1	90
32/84_at	serine/threonine-protein kinase PRP4 homolog		AB011108	9.9	3.0	0.4
950 at	translocation protein 1	TI OC 1	D87127	9 9		5 6
38119_at	glycophorin C (Gerbich blood group)	GYPC	X12496	0 4	2.7	0 0
39134_at	target of myb1 (chicken) homolog	TOM1	AJ006973	9	7 6	2.5
37078_at	CD3Z antigen, zeta polypeptide (TiT3 complex)	CD37	104132	9 9	7.7	
48484_at	CGI-111 protein		41972302	0.0	7.7	24.5
90975_i_at			2007CN	0 0	7.0	2.2
62371 g at	hypothetical protein FI 113153		C0977N	0.0	4.8	6.0
59000 at	x 010 protein		AI221377	9.9	2.9	5.6
44718 at		× 010	AA629304	9.9	4.8	4
671/13t			AA577672	9.9	5.7	7.9
			AI267607	9.9	1.1	3.7
72/58 at			AA262084	9.9	2.9	5.5
10537 at			AI638014	9.9	8.5	
F0371 24	7,1901 301 301		W18190	9.9	0.8	0 6
58523 at	אוטומון דאניאאן		AI743689	9.9	4.1	0
54007 24			AA614814	9.9	2.6	3.5
17551 at	purative transcription regulation nuclear protein; KIAA1689 protein		AW051603	9.9	9	0.5
81066 24			AA226241	9.9	2.8	3.9
53607 24			AI285898	9.9	2.3	3.9
53666 at			C14838	9.9	1.4	9
23552 f at			AA114900	9.9	3.8	6.4
22777 24	thrombourh A martin		AA703100	9.9	1.9	16.2
22//2	unomboxane A synthase 1 (platelet, cytochrome P450, subfamily V)	TBXAS1	D34625	9.9	6.5	6.3
51251_at			AI189200	v.	0	α v
806_at	cytokine-inducible kinase	CNIK	1156000		3 0	0 0
		5	026000	0.0	0.0	2.5

Figure 11EEE

320/3 at	butyrophilin, subramily 2, member A1	BTN2A1	U90543	6.5	2.5	Δ.
32313_at		TPM2	M12125			
41349_at	presentlin 2 (Alzheimer disease 4)	POFNO	1			
34808_at	KIAA0999 protein	7		0.0	4 ,	
599 at	H2.0 (Drosophila) like homen hox 1	=======================================	ABU23210	0.5		3.
36179 at	Drotoin Pinaco activated activity	HLAI		6.5	2.4	
37625 at	interferon regulation factor 4	MAPKAPK2		6.5	2.4	0.0
63316 24		IRF4	1	6.5	9.7	1.7
03310 at	עואה טוונטווון וווטנוו סוסיפות אני	RBM8B	AL047586	6.5	5	
400339 at			AI439092	6.5	0.4	9.9
40929 at			AA521311	6.5	10	3.7
030/2 at			AI351753	6.5	1.5	
40202 at			W93382	6.5	1.2	26
8628U at			AI916767	6.5	32	0
/ 52 / 6_at	nypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A	A1983856	6.5		6.0
70210_at			AI798924	6	1.3	,
/0/53 g at			A1829840		0.10	2.1
49132_at			A145907E		1.70	
45491_s_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila)	MIITE		0.0	0 0	5.2
	homolog); translocated to, 6			0.0	7.0	υ. <u> </u>
49510_at	mitogen-activated protein kinase 8	MAPKR	A1681315	2 2	C	
68856_r_at			T79833		2.3	1.4
74456_r_at			A1970474		7.7	1
92130_r_at			TO1117H	0.0	0.0	
65794_f_at			01010	0.0	Σ.Τ	4.2
55103_at	TIG.1		AL042362	6.5	1.7	0.8
68885_r_at			A1031000	0.0	2.3	2
51089 at	KIAA1140 protein		AA394332	0.5	7	3.9
148 at	FLI-REI ATED RNA POI YMERASE II ELONGATION EACTOR		AL042799	6.5	4.5	5.4
33326 at	- 1		U88629	6.4	1.4	5.3
920 at	natural killer tumor recognition common		D42087	6.4	2.9	1.8
32563 at	ATPase Nat/K+ transmitting hets 3 - 1	NKTR	L04288	6.4	0	14.7
56350 at	act, ractor dailspoining, pera 3 polypeptide	ATP1B3	U51478	6.4	3.6	3.8
15370 11			AI928492	6.4	5.5	1.5
403/9 at			AI659019	6.4	5.8	9.6
10204 at			AA643507	6.4	17.1	23.3

Figure 11FFF

62288 at			AI336854	6.4	3.1	102
52007 at			AI190755	6.4	2.9	2.1
	hypothetical protein SBBI48		AA521293	6.4	2.6	3.4
77716 of	Divizi 30401003 protein		AI738434	6.4	1.3	e e
70200 24			AW006759	6.4	0	11.7
12307 g 2+	4 - 4 - 4 - 4 - 4 - 4 - 4 - 4 - 4 - 4 -		AI761629	6.4	1.3	7
72507 5 4	liypottietical protein FLJ131/1		AW001604	6.4	13.8	66
64106 at			AI984040	6.4	1	0.7
47655 at	Lo. associated serine arginine protein 1		AI916676	6.4	0.8	1.1
51249 at	neural polynomial no tract binding		AI022328	6.4	6.5	8.6
62684 at	diffe tract billding		- 1	6.4	2.8	3.2
	secondic denyal offenase complex, subunit A, mayoprotein (Fp)	SDHA	~	6.4	m	5.9
51588 21			AI762208	6.4	2.2	5.1
82806 24			2933319	6.4	0.2	5.7
1 205			AI476732	6.4	0.3	
1385 at	transforming growth factor, beta-induced, 68kD	TGFBI	M77349	6.4	3 2	2 0
32034 at	1-box and wb-40 domain protein 1B	FBXW1B	AB014596	6.4		5 1
45/31_at	HSPC003 protein		AA581878		7	7.7
58954_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH.	ADHIEN			0 0	y .
				4.0	5.3	6.5
1228_s_at	meningioma expressed antigen 6 (coiled coil proline rich)	MGFAG	1173682	6 9		
32961_at	c-myc promoter-binding protein		L		3.6	0
34951_at	putative chemokine receptor; GTP binding protein		70341/			2.1
41768 at	Drotein kinase, cAMP-dependent regulation, type I alaka (tiggina		⅃	6.3	3.2	4.6
	specific extinguisher 1)	7 X X X X X X	M33336	6.3	1.2	0
1/46 s at		TRAF2	112597	6.3	7.0	
39219 at	CCAA1/enhancer binding protein (C/EBP), gamma	CEBPG	1			7
38332 at	purinergic receptor P2X, ligand-gated ion channel, 4	P2RX4	(183993	200	t C	
35978_at	proline-rich Gla (G-carboxyglutamic acid) polypeptide 1	PRRG1	1	0 0		0.0
	RAB27A, member RAS oncogene family	RAB27A	1	0 0	0.1	4 7
'4	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	X66435		2	9.0
	KIAAUS82 protein		A1761647	0 0		
40/18 at	cathepsin W (lymphopain)	CTSW	1 -	9	100	5
41015_at		PRKAA1	1	6.3	0.3	7.0
34056 g at	34056 g at Jactivin A receptor, type IB	ACVR1B		8 9) (7
			1	2.5	١	5

50101			AA431258	6.3	2.3	11.2
30131 at			AI806586	6.3	3.2	3.9
498/5 at			AI733353	6.3	5.9	16.6
			AI217191	6.3	0.1	C
g	hypothetical protein DKFZp762N2316		T92186	6.3	2	
44840 s at			N59198	6.3	1.1	4
65364 at			W56309	6.3	9.5	8.1
الم			AA923345	6.3	0.8	0
/2851_r_at			A1990894	6.3	2.6	1.1
- 11			AI198946	6.3		4.6
54804 r at			T40707	6.3	3.1	2
53128_at	hypothetical protein FLJ10494		AI678076	6.3	140	3.2
65148_at	hypothetical protein FLJ20139		AI860687	6.3	C	
84858 at	hypothetical protein DKFZp547G183		AI082794	6.3	α-	- 1
52694 at	-		AW044663	93	000	30
43519_s_at	CGI-107 protein		AA442417	6.3	2.4	
658/6_at			R45447	6.3	2.1	0
61115_at	hypothetical protein, estradiol induced		AA442301	6.3	1.9	46
60215_at			AA278413	6.3	2.8	0
4/0/4_at	disrupter of silencing 10		AI125866	6.3	2.2	3.5
315//_at	collagen, type XIX, alpha I	COL19A1	D38466	6.3	C	2 5
46326 g at			AA044197	6.3	6.3	
39112_at	upstream transcription factor 2, c-fos interacting	USF2		6.3	2.1	5.3
44080 at			W68180	6.3	5.2	1 17
3/524_at	serine/threonine kinase 17b (apoptosis inducing)	STK17B	AB011421	6.2		
32210_at	phosphoglucomutase 1	PGM1	M83088	6.2	4.2	1.2
33/U/ at		PLA2G4C		6.2	1	1
33331_dl	translation factor sull nomolog		AF064607	6.2	89	C
35015_at	cortistatin	CORT	N30625	6.2	2.1	
35328 at	- 1		AF055023	6.2	3.4	7.9
35097_at	Immediate early protein		M62831	6.2	1.6	15.2
37572 at	uridine phosphorylase	UP	X90858	6.2	5.4	0.2
3/0/3 at	Ē,	NSMAF	X96586	6.2	6.1	0
30003 at	LO-IIITETACTITIS TACTOR (TALE TAMILY NOMEODOX)	TGIF	X89750	6.2	4.4	9.9
Segun at			AI797146	6.2	0.4	4.2

48021_at	kinesin heavy chain member 2	KIF2	AI652174	6.2	7.3	2.8
90428_at			AI355272	6.2	6.1	3.4
78954_at			AA420590	62	0	9.0
68619_at			AI204439	62	3.7	1.0
66092_at			AI951574	6.2	6.3	1 4
59293_at	poly(A)-binding protein, cytoplasmic 1-like		AI962727	6.2	0.5	4.5
68996_f_at			AI681967	6.2	20	50
58398_at			AA829521	6.2	2.2	10.0
64099_at	hypothetical protein FLJ10700		W81185	6.2	5.9	1.2
44650_at			AI307750	6.2		3.2
51962_at	hypothetical protein FLJ12484		W45523	6.2	2.7	3.6
47087_at			AI310524	6.2	2.5	i m
48300_at			AA713522	6.2	2.4	4.3
63013 at			AL120446	6.2	7.7	4.2
1361_at	telomeric repeat binding factor (NIMA-interacting) 1	TERF1	U40705	6.2	3.9	2 6
55525_at			AI972498	6.2	5.5	9
3/114_at	AT-binding transcription factor 1	ATBF1	L32832	6.1		6.3
35086_at	fis485		AB024705	6.1	C	000
39082_at	annexin A6	ANXA6	Y00097	6.1	2.4	0.0
. ~'I		RFP	J03407	6		
		CDYL	AL050164	9	000	0.4
40570_at	forkhead box 01A	FOX01A	AF032885	6.1	8	4.5
32168_s_at	Down syndrome	DSCR1	U85267	6 1	1 4	300
39218_at	zinc finger protein 23 (KOX 16)	ZNF23	1~	2		0.0
34773 at	tubulin specific chaperone a	TBCA		6.1	27	1:5
33905_at	methyl-CpG binding domain protein 2	MBD2	AF072242	6.1	7 6	, C
35625_at	CD97 antigen	CD97	X94630	6.1	4 5	0 0
36515_at	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase		AJ238764	6.1		0
35739_at	myotubularin related protein 3	MTMR3	AB002369	9	å c	C
37610_at	hypothetical protein FLJ10803		AI765280	1.0	0,10	
35017_f_at		HLA.J	M80469	1.09	2 000	
566_at	ikemia	PML	M79462	9	9 9	0.1
	hypothetical protein FLJ20639		A1749464	6.1	,	t C
58201_at	hypothetical protein FLJ20511		AI796121	6.1	3.4	18

45298 at			N66638	9	2.8	7 7
T			AI760126	9		4 6
	uncharacterized hematopoietic stem/progenitor cells protein MDS030		AI357582	9	3.6	2.4
65665_at			AA699970	9	1 7	0.
67989 at			AA825836	9	7 2	1 5
79858 at			AI693951	9	5.2	3.7
T			AI810528	9	4.3	2.0
	lucosyltransterase 4 (alpna (1,3) tucosyltransferase, myeloid-specific)	FUT4	AI970292	9	14.7	13.8
\vdash	complement component 2	C2	802607	9	α 4	7 1
44839_s_at			AW006891	9	200	1
<u>,,</u>			AA513397	9	1 5	23.4
T	chromosome 11 open reading frame 1	C150RF4	W60695	9	0.0	
70150 at			AA083860	9	1.1	
53310 at			AA447177	9	3.5	2.4
5000 at			AW003235	9	1	3.2
T	0000140		AL047045	9	4	0
T	r NOVI49 protein		- 1	9	3.2	4.2
T	ucieoprotein poly	SNRPG	- 1	9	0.8	0.5
Į,	hypothetical protein El 112426	ATP2B1	AI337321	9	1.3	0
46323 at	ypomiencai protein ruu 2438		AI979240	9	6.0	0
†	inoma HMOIC fucion partner		- 1	9	0.7	0.1
+	pointa rimaro lusion parmer	LHFP		9	0	1.3
T	dedicator of outo-kinesis 2		AA987596	9	1.9	3.4
Τ		DOCK2	D86964	9	2.6	5.6
T	karyonharin (importin) bota 2		AB028965	9	9	6.4
ŧ	מיזיטקייניין (יויייקטייניון) טפים כ	KPNB2	AI653355	9	2.7	3.5
+	imminoglobilin besing constant same 2002		AW002183	9	5.2	9.9
+-	and the second recard constant gaining of Gooth marker)	IGHG3	AF067420	5.9	3.8	17.1
†	tumor suppressing subtransferable candidate 2	9		5.9	1.1	10.5
1	omologous to yeast nitrogen permoses (sendidate a	18803	-1	5.9	2.6	4.2
	Suppressor)		AF040708	5.9	1.4	2.7
38516_at sc	sodium channel, voltage gated, type I, beta polypeptide	SCN1B	L10338	5.9	0	8
	ļ.					

894 g at	ubiquitin carrier protein		M91670	0 4	10 1	
38552 f at	B-cell receptor associated protein RAP29		1001010		χ.	5.4
41183 at	Cleavage etimulation factor 2' pro DNA minist 2 77.0	1	A1984/86	5.9	4.7	0.4
2000	MANAGE SUMMINISTING TO DIE-RINA, SUBURIL 3, 1/KD	CSTF3	U15782	5.9	4.6	6.3
32224 at			AB018312	5.9	7.2	5 0
39008_at		d0	M13699		0	11.0
35936 g at	carnitine palmitoy	CPT1B	Y08683		187	7. 9
1797_at	cyclin-dependent l	CDKN2D	1140343	0.0	10.	0 0
34392_s_at	RAB1, member RA	PARI	A1050268		1.1	200
35990_at	KIAA0478 gene product	TOWN	APO07047	0.0	7.7	7
36634 at	BTG family, member 2	DTCO	AB00/34/	υ [υ [T.I	8.8
37048_at	٦	0192	072049	ν. Σ. (6.0	0.3
48026 at			0.00970	U 1	4.2	3.5
56479 at	hynothetical protein El 120419		A1984814	5.9	3.2	1
57364 at			7/8377	5.9	2.8	0.8
82018 7 24	hypothetical protein El 191909		AA031731	5.9	0.8	0.8
80771 24			AI733306	5.9	1.1	1.8
50000 of			R73518	5.9	9.6	2.4
33902 at			AI279954	5.9	0.5	2.1
3/035 L at	ppzt nomolog		A1934584	5.9	1.8	1.6
42044 at			AA777406	5.9	0	000
31043 at			AL036254	5.9	3.9	6.5
46006 at			AI863033	5.9	11.6	4.7
40330 S at			AI057283	5.9	1.1	0.1
65351 r ot			R38041	5.9	2.6	1.1
47350 at			AA146979	5.9	3.2	5.1
913/1 24			AI798960	5.9	3.2	2.7
46889 at			AI291659	5.9	4.5	3.8
46089 at			N74444	5.9	1.4	3.9
17856 at			N90525	5.9	2.8	4.3
10100 t at			AA999846	5.9	9.0	2.1
40105			T91299	5.9	0	88
22EFO 2 24	Gill protein		AL041780	5.9	2.9	7.4
1705 at	condition of the second second	CEBPA	Y11525	5.9	4.9	4.6
1/00 at	Iteliiobiastorna pinging protein Z	RBBP2	S66431	5.9	2.4	7.5
45005_at	INADA deliyurdgenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)	NDUFB10	AA195976	5.9	5.8	5.9

Figure 11LLL

	6.9	0	7 0		000	59.5	3./		7.1	3.5	0.5	25.7		7.17	0.0	, c	4.6	9.9	1.2	2.1	3.1	1	Ó	9	0	21.3	2.6		35.2	5	3.8	5.9	6.7	
AA976857 5		C) r	1.1	5.1		0.1	0 0			T a	0.6	0.8	4.1	1.7	6.5	6.1	4.7	0.1	2.5	2.1	19.9		1.7	4.1	7.9		2	0	
notein kinase-activated protein kinase 3 MAPKAPK3				28.6	α	0 0	0 0	0 0	υ. Σ	2.8						5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	
not reading frame 18 In re	AA976857	AF052169	AB029343	W27949	AI557322	A1192108	ABOUTOTA	0404040	004209	AL0091/9	AF010312	U65093	MOSOBO	AASREGE	AI952982	AI435076	AA399389	H73401	AI340002	AA602921	AI308862	AI435586	AI872476	N55264	AI423056	AA429326	H15157	AI694367	T54916	AW006123	T70214	U09578	AB011083	0.000.
HCR (a-helix coiled-coil rod homologue) putative heme-binding protein hypothetical protein chromosome 21 open reading frame 18 microfibrillar-associated protein 1 H2A histone family, member C LPS-induced Tamily, electin L (lymphocyte adhesion molecule 1) growth arrest and DNA-damage-inducible, gamma hypothetical protein mitogen-activated protein kinase-activated protein kinase 3 adenylate cyclase 3 AH-type solicing regulatory protein files biodizer activity and the cyclase 3 AH-type solicing regulatory protein files biodizer							COLOBETS	MEADI		חבאור	VEN	CITED2	SFI		GADD45G																	MAPKAPK3	ADCY3	000
at the state of th				putative heme-binding protein		hypothetical protein			H2A histone family, member C			Cbp/p300 interacting transactivator, with Glu/Asp-rich carboxy terminal domain, 2	selectin L (lymphocyte adhesion molecule 1)		growth arrest and DNA-damage-inducible, gamma													hymothochical protein	האסמופונים המשנה של המשנה של המשנה של המשנה של המשנה של המשנה של המשנה של המשנה של המשנה של המשנה של המשנה של ה			rotein kinase-activated protein kinase	מתבוואומוב הארומאב א	(KH:tvoe solicing regulatory protein /FIIOF bipding protein 0)

17 0777	E 1/170 at	CFL1	AI500557	αc	3.6	, 61
4419 al			AA214559		0 0	15.6
54152 at	eukaryotic translation initiation factor 4E binding protein 1	FIEAEDD1	VIJICOLV		0.9	
46304_at	hypothetical protein, clone 2746033	LII 41.07 L	AIUZODOS	X	5.2	5.8
39378 at	heclin 1 (noiled not myosin like DOI 2 interests		AA126461	5.8	8.7	9.3
7795 at	anden latace D	BECN1		5.7	3.3	c
35606 24	a yisullatase D	ARSB	M32373	5.7	4 3	
3000 at	nistidine decarboxylase	HDC	ı	5.7	2.5	1.60
58/_at	endotnelial differentiation, sphingolipid G-protein-coupled receptor, 1	EDG1	M31210	5.7	1 1	1.2
40408 at	Cysteinyl-tRNA synthetasa					!
41126 at	solite cerrier family 1 (alithamata (CARS	L06845	5.7	5.7	
15-C-11	member 4	SLC1A4	AA978353	5.7	7.9	4.7
41399_at	KIAA1111 protein					
1452 at	LIM domain only 4		AB029034	5.7	3.1	0.7
34857 at		LM04	U24576	5.7	1.5	6
36066 at	KIAA0828 profein		224724	5.7	4.5	0.2
38038 at	lumican		AB020635	5.7	2.4	7.6
35414 s at	jagged 1 (Alagilla syndroms)	LUM	U21128	5.7	0	0.7
39136 at		JAG1	U77914	5.7	1.9	23
59314 at	retinoic acid induced 1	OSR1	AB017642	5.7	3.1	1
56469 at	hypothetical protein	RA11	AI926671	5.7	4.5	3.2
80994 i at			W44483	5.7	1.7	
			T70600	5.7	3.6	0.5
66745 i at			AI694530	5.7	1.9	0.7
60417 r at			AA969889	5.7	0.3	4.5
50377 at			AI081821	5.7	3.3	7
79389 at			AI081607	5.7	1.7	2.7
47144 at	ASB:1 protein		AI026951	5.7	1.2	0.4
82601 at	Bicell CLI /lymphoma 6 (zipc finger protoin 51)		AI018173	5.7	4.1	4.5
42829 at	State migel protein 31)	BCL6	AA778666	5.7	3.1	0
85100 at			N58166	5.7	2.8	3.9
68048 at			AI567916	5.7	m	3.8
70124 at			AA701259	5.7	0	0.5
80894 at	histone acetyltransferase		AI770116	5.7	2.6	0.1
43395 s at	Dna I (Hsp40) hom		AA553554	5.7	1.9	4.4
			CA COCCATA TOTAL			

Nir Hacohen, *et al.* Inventors:

71040_at			A1026365	14.3		
46.368 at			0000000	0.7	1.4	1.4
51 702 at			H80286	5.7	1.5	3.5
51792 at			68020M	5.7	2.1	
46153 at			R02594	5.7	62	
4/602 at			AA393223	5.7		7
57968_r_at			AA431469	5.7	8.0	1.0
37214 g at	deoxyribonuclease I-like 1	DNASF111	X90392	7.7		0 0
1357_at	lubiquitin specific protease 4 (proto-oncogene)	VOSI	1	7.7		5.6
39105_at	vasodilator-stimulated phosphoprotein	000	1	7.0	3.4	8.3
53155 at		L ANDL		5.7	2.6	5.9
46664 at	anontosis, associated speck like protein containing a Othor		AA608559	5.7	4.4	7.1
37506 at	Historical association appear the protein containing a CARD		AI148558	5.7	5.1	6.3
40773 at	models light solves at 1		_	5.6	1.7	1.2
40//3 at		MYL5	ı	5.6	5.9	0
33/10 24	DAD2 CTD222 ACTIVATING BESTEIN	POLR2A	X63564	5.6	3.1	4.2
35137 of	TABLE GITASE ACTIVATING PROTEIN		AL096752	5.6	7.2	5.2
33137 at		MYOM1	06069X	5.6	0.7	2.9
35150 at	hypothetical protein from clone 24/96		AF070596	5.6	4.6	2.4
3231 at	numan Immunodeficiency virus type I enhancer binding protein 1	HIVEP1	X51435	5.6		12.2
1000 at		REL	X75042	5.6		5 7
9201 at	Kno guanine exchange factor (GEF) 11	ARHGEF11	AB002378	5.6	3.2	0
33320 <u>_</u> d1	solute carrier lamily 1.1 (proton-coupled divalent metal ion transporters), member 2	SLC11A2	AB004857	5.6		0
35787_at	dynein, cytoplasmic, intermediate polypeptide 2	CIONCIO	AIGRESON	5 6	2 2	
37177_at	CD58 antigen, (lymphocyte function associated antigen 3)	CD58	1	2 4	0.0	
39562_at	CGG triplet repeat binding protein 1	CGGRP1	4	0 4		0.0
40757_at	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterace 3)	GZMA	M18737	5.6	1.3	23.9
46771_at			101004			
0840 r at	neurexonhilin 4		W69383	5.6	2.3	2.8
65150 at	CG1.18 protein	NXPH4	AI498771	5.6	2	3.3
73901 at			AI073484	5.6	1.8	0
			AI984965	5.6	6.0	1.4
62914 at			AI765590	5.6	0.7	1.4
84232 at			AI363275	5.6	6.0	1.2
60837 7 24			AI806926	5.6	1.2	3.9
1004-1-al			AI765718	5.6	-	C

42881 at	7647171 1000 10 1000 10		W81045	9.6	3.6	
			R88708	5.6	1.6	
46060 24			AI148006	5.6	4.2	
45337 at			AI743903	5.6)
63251 s at			W72338	5.6	5.9	
91623 at			AA904828	5.6		O
51185 at	PAN2 protein		AI185207	5.6	2	0
53302 r at			AI309334	5.6	4.2	3
46727 at			AI741209	5.6	4.3	10.
			A1146850	5.6	6.0	
53689 at			AL120562	5.6	1.5	
57000 f at	meningioma expressed antigen 5 (hyalimagidada)		[5.6	2.2	
46660 at	ein El 110074	MGEAS	_1	5.6	0.1	
46670 at			AA018399	5.6	3.7	O
44136 at			AI921097	5.6	2.9	0
78784 at	stannin		_1	5.6	2.8	4
69458 f at		SNN	_1	5.6	2.7	0
40045 g at	Chromosome 18 open reading frame 1		AI693465	5.6	2.1	15.
56225 at		C180RF1	AF009425	5.6	4.5	er.
64028 s at			AI744466	5.6	3.3	4
49390 at			AI886403	5.6	4.4	5.9
52261 at			AA999858	5.6	5.6	5.6
38614 s at	O-linked N-acetylaticosamine /GlaNAs/ tages		AI970054	5.6	4.7	6.4
11 420	acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	06T	U77413	5.5	1.1	1.8
	ribosomal protein 56 kinase, 90kD, polypeptide 5	RPS6KA5	AF090421	7	3.3	C
30006 4 ct	I ANT Dinging protein 2; KIAAU/33 protein		AB018276			o -
30061 0+	Hypothetical protein		W29115) LC		1.0
210 - 41	porte marrow stromal cell antigen 2	BST2	1	2 4	0.0	
1310_at	proteasome (prosome, macropain) subunit, beta type, 2	PSMB2) L		0.
40219 at	TIMBA:Inducible		AI 796944) r	\ C	4.0
0100 at	MARADUS gene product		D13630			4.2
3266U at	KIAAU342 gene product		AB002340		3.2	0.9
3// g at	sema domain, immunoglobulin domain (Ig), short basic domain	CEMASO	VECCOOD A		3.6	3.
	secreted, (semaphorin) 3C	SEIVIASC	SEIMASC ABOUUZZU	5.5	8.1	
			_	_		

Figure 11PPP

32307_s_at	collagen, type I, a	COL1A2	V00503	5.5	С	1.3
33362_at	Cdc42 effector protein 3		AF094521	5.5	2.1	66
۱,۰	KIAA1128 protein		U90912	5.5	25	20
	hypothetical protein FLJ10849		W25874	5.5	0	0.3
39149_at	papillary renal cell carcinoma (translocation associated)	PRCC		5.5	1.5	1 7
422/2 at			AA743565	5.5	1.3	9
58524 at			W03029	5.5	4.1	
54492 s at			AW001883	5.5	0.9	3.2
74006 at			AI984623	5.5	0.7	
00//4 at			AA978204	5.5	3.3	2.1
76375 T at	Zinc ringer protein 1/3	ZNF173	AW009746	5.5	5.5	14.1
7420 at			AI203222	5.5	1.3	0
4/409 at			AI452516	5.5	2.9	1.5
75201 r at			AI688900	5.5	11	7
32200 at	putative No-DIVA-methyltransferase		AI016585	5.5	5.1	10.4
82806 at			AA993487	5.5	5	26
41153 T at	catenin (cadherin-associated protein), alpha 1 (102kD)	CTNNA1	AF102803	5.5	3.7	0.1
29008 at			AA176289	5.5	2.6	0.3
/3601_at			AI885677	5.5	0	0.0
03950 at			R22212	5.5	0.8	4 6
43838 s at	nypotnetical protein PR01068		AA100948	5.5	0.4	3.4
5468U s at			A1660022	5.5	1.2	0.6
00320 at			AI475514	5.5	10.2	32.1
45590_at			AI769269	5.5	7.2	0
57470 at			H24422	5.5	1.7	1.6
90470 at			AI091581	5.5	2	2.7
50187 24			AI199443	5.5	0.5	2.5
72576 at	CN1 (monaco monaco	H46074	5.5	9.0	6.1	
55773 at	down (Keniela) control of arritio acid synthesis 1, yeast) like 1	GCN1L1	A1939557	5.5	0.5	1.2
55856 r at			AI457965	5.5	1.7	6.0
71516 r at			AA993791		1.4	2.8
69622 24			240202	5.5	0.3	2.1
35247 24			AI669987	5.5	6.1	4
3324/ at			AI557062	5.5	2.9	5
60061_at	arachidonate 5-lipoxygenase-activating protein	ALOX5AP		5.5	5 1	2 2

455/8_s_at			N26243	5.5	1.8	6.7
44693_at	hypothetical protein FLJ11937		9869EN	5.5	4.2	5.8
52107 g at	CGI-90 protein		AI800674	5.5	6.2	7.6
39748_at			AL050021	5.4	2.5	0
40788_at	adenylate kinase 2	AK2	U84371	5.4	2.7	0
31522 f at	H2B histone family, member G	H2BFG	Z80779	5.4	2.5	8.5
35879_at	galanin	GAL	M77140	5.4	8.3	0.4
33713_at	transiocase of inner mitochondrial membrane 17 (yeast) homolog B		AJ005895	5.4	2.2	3.1
41234_at	DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	AI540318	5.4	6.0	6.2
31633 g at	zinc finger protein 259, pseudogene	ZNF259P	295118	5.4	0	0.2
39209_r_at	pro-platelet basic	PPBP	M54995	5.4	0.4	4.2
	thromboglobulin, connective tissue activating peptide III, neutrophil					
	activating peptide-2)					
41275 at	E2F transcription factor 5, p130-binding	E2F5	U31556	5.4	0	0.7
33480_at	motilin	MLN	X15393	5.4	1.8	5
38016_at	transcriptional activator of the c-fos promoter		M94630	5.4	2.7	6.0
34376_at	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	DINA	AB019517	5.4	2.2	9.6
34892_at	tumor necrosis factor receptor superfamily, member 10b	TNFRSF10B	AF016266	5.4	0.3	3.5
35284_f_at	hypothetical protein FLJ10738		W28620	5.4	0	3.6
36554_at	acetylserotonin O-methyltransferase-like	PIWSY	Y15521	5.4	1.8	2
36991_at	splicing factor, arginine/serine-rich 4	SFRS4	L14076	5.4	5.3	4.2
2045_s_at	hemopoietic cell kinase	HCK	M16592	5.4	0.8	0.6
48436_at			AI922968	5.4	0.1	2.4
91799_at			AA586814	5.4	5.2	0
65158_at			AI741328	5.4	3.8	1.2
56548_at	angiotensin II, type I receptor associated protein		AI858573	5.4	1.2	0.1
87038_at	skb1 (S. pombe) homolog	SKB1	AA932371	5.4	1.7	2.5
78538_at			AI023295	5.4	7.5	2
75064_at	NOD2 protein		AA910520	5.4	2.0	1.1
87105_at	protein kinase Chk2		N24330	5.4	1	1.7
58246_at	hypothetical protein FLJ12903		A1807668	5.4	2.5	5.1
91400_at			AI309016	5.4	3.6	3.2
44780 s_at	44780_s_at collagen, type IX, alpha 1	COL9A1	N66408	5.4	2.2	5.2
81442_at			AI916887	5.4	1.7	0.1

59341_at			A1311017			
47951_at			AA52114E	D.4	4.7	D. C.
47878_f_at	KIAA0117 protein		A1656512	4.C	2.0	5.2
43488_at	transporter-like protein		A1768065	4.0.7	2.8	٦
87391_at			AA707322	7 6	10	100
87617_at	hypothetical protein FLJ13385		AA639580	5.4		0.5
68909_at			AI091231	5.4	0.7	1
69715_at			AI743419	5.4	0.5	800
72052_at			N71632	5.4	0.3	4.4
54/99 at	glutaminase	STS		5.4	0	C
58825 at		PTMA	AI701911	5.4	6.9	7.3
5/042 at	Similar to Caenorhabditis elegans protein C42C1.9		W74749	5.4	1.6	C
4905/ g at			AA521489	5.4	11.9	0
5/0/4 s at			AW021642	5.4	1.5	m
50943_at			W87422	5.4	0.8	5 7
45655 at	tumor antigen SLP-8p		AL045849	5.4	5.7	2.4
46105 at			AA149641	5.4	5.4	C
55009_at			AI359000	5.4	2.2	C
			W29045	5.4	0.5	, r.
39341 at	thyroid hormone receptor interactor 6	TRIP6	AJ001902	5.4	000	
37759_at	Lysosomal associated multispanning membrane protein 5		U51240	5.4	200	7
39163_at	likely homolog of rat kinase D interacting substance of 220 kDa. KIAA1250 protein		W27233	5.4	0.2	6.4
45521_s_at	_		A1967955	2	u	1
63793_at			AI797479			0.7
45736_at	two-pore channel 1, homolog		AL048491	5.4	5.0	100
36495_at	fructose-1,6-bisphosphatase 1	FBP1	U21931	5.4		7.0
31996_at	brefeldin A inhibited guanine nucleotide exchange protein 2		AI798834	5.3	12	4.0
41634 at	KIAAU256 gene product		D87445	5.3	4.6	2.4
3//98_at	chromosome 8 open reading frame 2	C80RF2	AB018790	5.3	0.3	000
41134 at			AB023181	5.3	3.4	
1383_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	PPP2R2A	M64929	5.3		12.4
41170 at	KIAA0663 gene product		AB014563	5.3	27	ır.
37575_at			AL050192	2 2	3.6	0.0

Figure 11SSS

П	KIAA1046 protein		AB028969	5.3	4.8	3.3
	modulator recognition factor I		M62324	5.3		7.7
			AA034067	5.3	- 1	2.1
T	ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	A1922486		3	0.4
			AW021968		0.6	0 0
. 4			AA128061	5.3	1.7	899
81911_at			AW051492	5.3	2	0.4
81/63 t at			AI393033	5.3	2.1	12
_			AI674428	5.3	1.4	0.4
s at	catenin (cadherin-associated protein), delta 1	CTNND1	A1863000	5.3	4.5	6.6
Ī			A1800640	5.3	6.2	23.2
ai	nypotnetical protein FLJ20093		W87653	5.3	2.3	3.4
1			AI989354	5.3	5.6	6 1
at	nypotnetical protein FLJ11058		N63911	5.3	2.1	α τ
91891_at			AL045717	5.3	1.6	1.2
85939 at			A!694139	5.3	0.4	
86004 at			AA767895	5.3	0.5	7.0
/10/4_at			AI912203	5.3	1.7	4
/3112_at			R35404	5.3	1.6	
/3811_at			AI972618	5.3	12	
/5063_at			AI732791	5.3	m	7.4
Ţ	- [AI872409	5.3	1 9	0
ä	hypothetical protein FLJ11136		AI497781	5.3	2.5	11
1	oothetical protein FLJ20831		AA131537	5.3	o c	101
_	F-box only protein 4	FBXO4	AI961240	5.3	1.3	0.5
	n rLJ102/6		AA219406	5.3	1.1	0.1
=	protein kinase, CAMP-dependent, regulatory, type II, beta	PRKAR2B	AI792179	5.3	9.7	2
677730 at			R68222	5.3	3.1	8.1
T			AW005511	5.3	m	e
T	lax interaction protein 1		U90913	5.3	3.7	5.3
Т	aidenyde denydrogenase 10 (fatty aldenyde denydrogenase)	ALDH10	U46689	5.3	3.9	5.1
35336 at KIA	KIAAUU63 gene product		AL021707	5.3	3.6	6.2
Ħ		MTCP1	Z24459	5.3	2.6	4.3
a	phosphatidylserine synthase 1	PTDSS1	D14694	5.3	2.2	5.7
38011_at KPt	KPB5-mediating protein		AB006572	5.3	2	4.9

Figure 11TTT

52936 at						
55567 24			T65761	5.3	1.5	5.1
2000/ at	C		AA147933	5.3	5.3	5.2
38684 at		ATP2C1	AJ010953	5.2	9	2.0
32183_at	splicing factor, arginine/serine-rich 11	SFRS11	M74002		1 9	0.0
39407_at	bone morphogenetic protein 1	BMP1	M22488		2.6	3 4
39742_at	TRAF family member associated NFKB activator	TANK				٥
31856_at	glycoprotein A repetitions predominant	GARP	224680		3.9	5.3
319/5 at			X55503			0 -
33869_at			AI 080218		0.0	0.0
39342_at	methionine-tRNA synthetase	MARS	X94754	5.5		0.0
830_at	Tax1 (human T-cell leukemia virus type I) binding protein 1	TAX1BP2	1125801	7.0		0 0
1105 s at	T cell receptor beta locus	TRB®	1	100	0 -	3.0
39950_at				10.5	<u> </u>	11.7
984 g at	mitogen activated protein kinase 12	MAPK12	X79483		700	0.0
37299_at	glycogen synthase 1 (muscle)	GYS1	104501			0.0
1119_at	replication protein A2 (32kD)	RPA2			2 0	
38384_at	phosphoribosylglycinamide formyltransferase.	FOVE	Τ	2.0	0.0	0.0
	phosphoribosylglycinamide synthetase.	5	724193	5.2	7.7	0.1
	phosphoribosylaminoimidazole synthetase					
38397_at	اخا	POI DA	100106	2 2	-	
38437_at	MLN51 protein		X80100		100	0 .
277_at	myeloid cell leukemia sequence 1 (BCI 2 related)	1 (1)	2000		7.0	1./
56371_at		MCLI	L08246	5.5	3.9	10
48873 at	Gene 33/Mig-6		06245650	2.5	70	0
53777 at	hynothetical protein El 192693		AI5/1452	5.2	3.4	25.2
74423 at			AI672353	5.2	3.8	2.2
82222 at			AI / 93024	5.2	2.2	2.6
50080 at			T64664	5.2	0.1	0.3
51715 at	in the form of the second seco		AI097194	5.2	3.3	3.2
00000 ot	iung type i ceit itterribrane associated glycoprotein		AA149854	5.2	3.5	6.4
50505 at			AA210905	5.2	4	3.4
39300 at			AA705681	5.2	1.5	4.5
4854/_at	pieckstrin nomology domain-containing, family A (phosphoinositide binding specific) member 1	PLEKHA1	AA875839	5.2	1.9	3.5
84960_at			A1004417	5.2	<u>u</u>	0
45272_at			AAOSRSEG	5.0	2 4	7.0

70053_r_at			AI734928	5.2	9.0	2.2
70170_f_at			AI251913	5.2	2.5	1.8
50205_at	leptin receptor	LEPR	N46838	5.2	5.1	15
80421_s_at	solute carrier family 21 (organic anion transporter), member 12	SLC21A12	AI347130	5.2	3.1	0
43535_at			N37020	5.2	2.2	0
87493_at			AL042667	5.2	0.4	0
47430_at			T65857	5.2	ō	O
66512_at			AI970258	5.2	1.6	2
45624_at	core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3		A1967968	5.2	6.9	4
	galactosyltransferase					
62306_at	hypothetical protein		T97347	5.2	2.3	2.8
55915 r at	hypothetical protein LOC54149		AI922520	5.2	13.7	15.9
46612 at	KIAA1624 protein		R39794	5.2	10.2	1.6
64740_at			AA470369	5.2	3.5	2.2
55800_at	hypothetical protein AL133206		W72766	5.2	2.2	0
61299_at	_	CCT6A	R43952	5.2	2.8	1.6
55650_at			W22914	5.2	1.7	2.5
51599_at			2945576	5.2	2.2	6.4
31816_at	glucosidase, alpha; acid (Pompe disease, glycogen storage disease	GAA	X55079	5.2	1.3	5.9
	(type II)					
40955_at	prostate tumor over expressed gene 1	PTOV1	U79287	5.2	2.6	4.6
41540_at	protein phosphatase 1, regulatory subunit 7	PPP1R7	250749	رة د ن	5.9	5.2
34811_at	⊑	ATP5G3	U09813	5.2	3.2	6.2
	(subunit 9) isoform 3					
36601_at	vinculin	VCL	M33308	5.2	4.6	5.1
37002_at	biliverdin reductase B (flavin reductase (NADPH))	BLVRB	D32143	5.2	3.8	5.3
48750_at	class I cytokine receptor		AI983115	5.2	4.6	4.9
44638_at	insulin-degrading enzyme	IDE	AA573292	5.2	2.6	4.2
59136_at			AA779895	5.2	5.1	5.2
48811_at	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase		AW007594	5.2	4	ວ
54912_at	translocase of inner mitochondrial membrane 13 (yeast) homolog B	TIMM13B	AL035821	5.2	3.4	5.4
51123 at			H11724	5.2	5	4.9
52012 at		;	AI659020	5.2	3.5	5.3

Figure 11VVV

53120_at	hypothetical protein FLJ20442		AIRS1916	5.0	C V	
487 g at	caspase 9, apoptosis-related cysteine protease	Odovo	L	2.5	t.	0.4
40491 at	DEAD/H (Asp.Glu-Ala-Asp/His) hox polyneptide 21	CACC	000321	0.1	7.7	2.4
32735 at	KIAA0931 protein	DOVE	W64331	5.1	1.3	2.3
24710 24	41.15		- 1	5.1	1	0.7
24710 at	Biutailillase	GLS	AB020645	5.1	0	0
39320_at	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	CASPI	U13697	5.1	6.9	1.1
35227_at	retinoblastoma binding protein 8	RBBPR	1172066	7-1	0	2
34378_at	adipose differentiation-related protein	ADEP	L	7 1		0.0
35845_at	SEC24 (S. cerevisiae) related gene family, member B	SFC24R	╚	† -	10.51	0. F
36888_at	KIAA0841 protein	1010		1 4	7.7	4 0
38027_at	fibulin 1	FBINI	X53742	7.1	0.0	9 0
32792_at	GCIP-interacting protein p29		AL 031/132	7.74	0.0	0.0
38369 at	myeloid differentiation primary response gene (88)	MVDOO	170451	1.0	3.6	4.1
38824 at	Tat-interacting protein (30kD)	M 1000	070451	1.0	15	18.4
37082 24	KINACASE COMP.		AF039103	5.1	5.8	12.6
27002 at	Nichotato gene product		AB007886	5.1	9.0	2.3
04/4/ 21	endosumne aibna	ENSA	AA167734	5.1	5.2	C
6502/_r_at			AA532470	5.1	2.1	2 1
84981_r_at	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	COL3A1	T54146	5.1	8.6	5.6
42564_at			C2210W	i,		
78014 at			/00+0M	3.1	6.3	4.6
47832 at			AA3/1513	5.1	2.7	0.7
، ا			AA100654	5.1	0	1
15000 s at			AI978590	5.1	1.9	104
50/63_at	NAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2		AA779863	5.1	9	3.4
42631_at			AI984505	5.1	18	100
8416/ at			AI742722	5.1	2.7	40
88155 at	HZB histone family, member B	H2BFB	AI125923	5.1	c	90
483/4 at			W87470	5.1	1.4	0 1
/4131_at			A1989784	5.1	2	4
58901 at			AW021543	5.1	0	4.4
01/45 r at			N76044	5.1	2.7	8
4439/ at			H11252	5.1	4.3	4.4
520/2_at	Inypothetical protein FLJ10/18		AA873182	5.1	0.8	4.1

Figure 11WWW

	adenyiate Kinase 3 alpha like		N32441	5.1	3.1	7 0
5861/at			AA149312	5.1	3.4	
	histidyi-tRNA synthetase	HARS	1 ~	, L	t m	-
				1 - 4	j <	1.0
54410_at			NZOZN	9 4	1 0	0.4
80825 at			21.001.4	7 .	7.7	
40279 at	KIAA0121 gene product		A1590115	5.1	9.0)
1630 c at	coloon tyroning kinds		D50911	5.1	3.4	3.7
33833 24	spiceri (ylusine Airiase	SYK		5.1	3.9	4.9
33033 at	spectrin, alpha, non-erythrocytic I (alpha-todrin)	SPTAN1	J05243	5.1	3.8	5.7
32334 at	chaperonin containing ICP1, subunit 4 (delta)	CCT4	AF026291	5.1	2.5	
48110 at	hypothetical protein FLJ11271		N91279	5.1	3.3	4 6
51179 at	prefeigin A-innibited guanine nucleotide exchange protein 2		AI741843	5.1	2.9	7.9
66339 at	transforming growth factor, beta-induced, 68kD	TGFBI	A1624028	5.1	2.2	5.1
61067 at	Clone FLB4/39		6069EN	5.1	4.5	5.2
01033 at			AA773816	5.1	5.1	7 7
49569 at	in FLJ20281		A1690893	5.1	4.2	4.5
65603 at	baculoviral IAP repeat containing 6	BIRC6	AA886981	5.1	2.9	5.4
45293 at	hypothetical protein from EUROIMAGE 363668		AA631902	5.1	4 4	7
56418_at	uncharacterized hematopoletic stem/progenitor cells protein MDS027		N25128	5.1	3.7	5.8
45224_at			0.0030000			
57714_at			AA001112	0.1	3.2	3.5
36908 at	mannose receptor. C type 1	1001	MA429113	5.I	3.6	5.1
55695 at	-i>	MKCI	- 1	5.1	4.2	4.6
38134 at	Deiomorphic adenoma gene 1	HSOS I	1	5.1	4.5	4.2
31898 at	KIAA0212 gene product	PLAGI	- 1	2	0.7	1.4
32142 at	Serine/threonine kinase 3 (Ste20) yeart homology	NIABUZIZ	796980	Û	3.7	2.3
1948 f at	nitric oxide synthace 24 (inducible henotomites)	51173	UZ6424	5	4.1	3.6
32233 at	forein family 1 member B (forein B)	NOSZA	U31511	5	0.4	2.7
32662 at	KIAAA170 gapa product	TORIB	AF007872	5	6.9	13
3/373 24	Manager of the product		AL041663	5	0.1	
1280 24	distriction of transfer the production of the protein 1		297054	5	1.1	0
1022 at	RIDITATIONE STRANSFERSE MS	GSTM5	L02321	5	1.1	4 8
10/2 K at	data eninging protein z	GATA2	M77810	S	1.5	89
30004 al	inajor vauit protein	MVP	X79882	5	11.8	6.0
391/0_at			AL049957	T.	-	

Title: Response of Dendritic Cells to a...

Inventors: Nir Hacohen, et al.

82798 g at	chromosome 6 open reading frame 32	C60RF32	AW016644	ı		3 6
48488_at	hypothetical prote			7 4		6.7
89829 at	hypothetical protein FLJ10521		A1003439	n L	0	0
66361 21			A1913026	ñ	0.0	0.6
72712 24	DAD mambar of DAS conserved from 1.1.1.1.1.0.0		AA009699	5	4.3	0.8
13/13 at	RAB, member of RAS oncogene family like 2A	RABL2A	AI051621	വ	0.4	2.5
53828 at			AI929168	5	1.1	3.6
624/2_at			H49102	5	1.5	2.3
83036 at			AI271559	5	0.5	m
			AA913354	2	0.8	2.5
83224 r at			AI053582	5	1.6	
66108 s_at			AI915696	5	2.9	
/9105_at			AA830599	5	5.6	2.2
69388 at			AI299040	5	0	2.6
49516 at			AA531016	5	9.9	i K
61354_at			AA218990	5	1.3	1 5
70495 at			AI453095	5	4.2	28
5/608_at			AA523335	2	1 7	
46169_at			AI745624	5	4.5	12.3
la,			R38647	2	2.9	C
			AL043875	2	3.5	5.1
51991 at			AI884621	Ω.		0.5
45204 s at			AI378647	2	10.2	5.2
45/87 at			N29695	5	2.3	5.6
5365/ r at	5365/_r_at non-kinase Cdc42 effector protein SPEC2		AI825880	5	2.2	2.4
58339_at	in FLJ1		R52747	5	2.7	i
73128_at	dihydropyrimidinase like 3	DPYSL3	AI983251	2	7.2	0
462// at	0,000		AI031551	5	10.2	1.6
20000 at	RABAS, member RAS oncogene tamily	RAB23	AI742498	2	1.4	1.6
25455 at			AA187437	5	0	0.5
F2257 : 21	lensin	SNL	AL046979	5	3.9	Ó
54167 at			2963428	5	1.7	1
20001 of			3162292	5	1.8	1.5
35001 at	proceinagenilysine, z-oxogiutarate 5-dioxygenase 3	PLOD3	AF046889	ည	2.1	5.9
40302 at	corricorropin releasing normone	CRH	V00571	5	4.7	3.8
48059_at			R61448	5	4.4	3.5

39340_at	hexosaminidase A (alpha polypeptide)	HEXA	M16424	2	1.5	5.1
65737_r_at			AI701293	5	2.7	5.7
58780_s_at	hypothetical protein FLJ10357		R42449	5	2.6	4.6
45255_at	CGI-69 protein		AI354351	5	3.5	5.2
45808_at	anaphase-promoting complex subunit 7		AA131793	5	2.4	5.2
34427 g_at	major histocompatibility complex, class lilike sequence	HLALS	U22963	4.9	3.7	6.0
38892_at	KIAA0240 protein		D87077	4.9	2.5	1.2
33437_at	homolog of yeast SPB1		AJ005892	4.9	1.3	0.7
36270_at	CD86 antigen (CD28 antigen ligand 2, B7.2 antigen)	98GO	U04343	4.9	13.2	3.9
35720_at	KIAA0893 protein		AB020700	4.9	2.2	10.8
31590 g at	gamma-aminobutyric acid (GABA) B receptor, 1	GABBR1	AL031983	4.9	6.0	10.3
41592_at	JAK binding proteir		AB000734	4.9	9	7.7
35293_at	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS	SSA2	J04137	4.9	2.3	1.4
35363 at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 17 (72kD)	DDX17	AL080113	4.9	2.7	0
36550_at	ras association (RalGDS/AF-6) domain containing protein JC265		AL049538	4.9	2.9	3
40347_at			AA913812	4.9	3.5	0.7
40668_s_at	CD6 antigen	9DO	U34624	4.9	2.5	12.2
40712_at	a disintegrin and metalloproteinase domain 8	ADAM8	D26579	6.4	7.2	1.2
75743_at			AA668789	4.9	3.4	1.6
78468_at			F26341	4.9	1	2.7
90341_at			H04388	4.9	4.3	0.2
91905_s_at			AI609998	4.9	0.7	1.3
47215_r_at			AA129058	4.9	2.9	8.4
49237_at	RNA binding motif protein, X chromosome	RBMX	AI971694	4.9	2.5	12.8
63242_i_at			AI809894	4.9	2	4.7
54658_at	hypothetical protein FLJ10955		A1961496	4.9	3.3	1.5
44731_at			AI807804	4.9	3.6	2.2
84588_at			AI691077	4.9	2.9	4.3
56965_at	HSPC056 protein		N51105	4.9	6.4	1
74935_at	hypothetical protein FLJ11274		W04760	4.9	0.3	2.6
43690_at			AA019641	4.9	0.2	0.4
75820_r_at			AI679201	4.9	1.6	2.5
65936_at			AA034414	4.9	3.3	4.7
69763_r_at			AI865825	4.9	6.0	3.8

44170 at			H53031	4.9	0.8	28
72092_t_at			AA677864	4.9	3.4	
			T91504		90	6.6
	papillomavirus regulatory factor PRF.1		N25612	4.9	2.5	
	SPY-like	TSPYL	AI972301	4.9	1.5	13
51941_at			AA442900	4.9	2.5	1.5
61063 at			AI248920	4.9	1.3	0.2
45012 at			AI744560	4.9	3.7	5.9
40000 at			AA479835	4.9	0.8	6.0
22300 at	0.0000		AW003215	4.9	1.8	2.6
65944 at	hypotnetical protein FLJ2U312		AA524056	4.9	1.2	2.8
22023 at	hypothetical protein FLJ11307		AI820049	4.9	2	1.6
22228 at	COV		AA524361	4.9	4.8	3.6
29313 at	KAD-ob protein		AI458521	4.9	3.5	2
03319 Lat			AI075909	4.9	1.1	3.4
84963_r_at	- 1		R42423	4.9	60	α
39131_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	SMARCAS	N36842	4.9		4.2
34406_at	KIAA0602 protein		AR011174	0	7.0	
34864_at	hypothetical protein		AE070639		2.7	0,1
31722_at	ribosomal protein L3	E Ida	1		0.0	0.0
36628_at	ralA binding protein 1	RAI RP1				2)(2)
56546_at	KIAA1545 protein		H17730			2.4
53884_at			AA312905		0.0	20.8
43306_at			AA126841		9.0	4.7
43038_r_at	43038_r_at KIAA1363 protein		A1769531	V 4	2.3	5.6
43053 g at			AW025012		0.0	1.0
49488_at	DKFZP434F1735 protein		AW005775		3.2	4.6
65501_s_at			79301810		3.0	4
51239_at	hypothetical protein FLJ23239		W67828		7.7	5.3
49633_at	hypothetical protein HES6		N21131	1 0		4.4
54878_at			AI 048421		0.0	δ.4
31895_at	BTB and CNC homology 1, basic leucine zipper transcription factor 1	BACH1	AB002803		1.3	4.0
1711 at	tumor protein n53.hinding protein 1	10000	1			
	taller place programs process, a	1 P 5 3 B F 1	0094/7	4	 	7 7

Figure 11AAAA

32940_at	Alport syndrome, mental retardation, midface hypoplasia and	AMMECR1	AJ007014	4.8	1.1	80
	elliptocytosis chromosomal region, gene 1					
39302_at	desmocollin 2	DSC2	X56807	4.8	0.5	2.2
33894_at	neuroepithelial cell transforming gene 1	NET1	AJ010046	4.8	1.7	0.5
35145 at	1 ==	ĽΖ	X96401	4.8	5	0
39604_at	pleckstrin homology, Sec7 and coiled/coil domains, binding protein	PSCDBP	AF068836	4.8	2.4	2.2
36971 at	KIAA0257 protein		D87446	4.8	5.4	2
	vinexin beta (SH3-containing adaptor molecule-1)		AF037261	4.8	2	8.7
35303_at	insulin induced gene 1	INSIG1	928960	4.8	2.6	0
35838_at	clones 23667 and 23775 zinc finger protein		090919	4.8	2.4	2.4
32530_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	YWHAQ	X56468	4.8	2.9	7.4
37358_at	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	UBE2E1	AI039880	8.4	1.7	4.6
231_at	transglutaminase 2 (C polypeptide, protein glutamine gamma- glutamyltransferase)	TGM2	M55153	4.8	2.5	0
39182 at	epithelial membrane protein 3	EMP3	U87947	4.8	3.8	5
75627_at			AA703201	4.8	4	1
52929_at			AL044396	4.8	1.5	4.6
50829_at			AA706818	4.8	10.8	10.5
64448_at	DKFZP727G051 protein		AA203321	4.8	0.8	1.6
89166_at			A1953998	4.8	4.6	0.7
67240_at			AI377910	4.8	9.0	0.4
51628_at			AA009692	4.8	2.8	0
85526_at			R64696	4.8	3.2	0
85530_at			AI732798	4.8	6.0	1.4
63817_at	DKFZP434B203 protein		AA099904	4.8	2.6	6.3
58926_r_at	hypothetical protein		A1979070	4.8	1.1	3.3
73656_r_at			AI719644	4.8	1.2	6.1
64152_at			AA703523	4.8	0	0.4
59698_at			H11817	4.8	0.1	9.2
76989_at			AI333655	4.8	0	0.3
48635_r_at			T95654	4.8	2.1	2.6
69001 at			AA831691	4.8	2.4	2.1

Figure 11BBBB

50134_at			R66534	4.8	1.5	5.8
73439_at	hypothetical protein MGC3156		AA349855	4.8	2	2.8
63373_at			AA194033	4.8	4.8	2.2
73574_at			AI290214	4.8	3.7	8.1
64577_at			H60064	4.8	2.1	2.9
44066 s_at	G protein-coupled receptor kinase-interactor 1	GIT1	AI887641	4.8	2.8	5.5
53546_at			A1168683	4.8	3.7	6.7
62165_at	x 006 protein		W72231	4.8	3.2	5.9
45580_s_at			A1983200	4.8	3.6	1.8
53680_at			AI130786	4.8	0	1.3
51813 at			AI797095	8.4	7.1	1.8
46237_at			AW001342	4.8	2.5	6.7
58682_at	DEAD/H (Asp.Glu-Ala-Asp/His) box binding protein 1	DDXBP1	AI348378	4.8	6.2	0
52347_at	CGI-60 protein		A1985204	4.8	0.3	1.4
54989_at			H43374	4.8	4.9	1.2
51697_r_at			AA649308	4.8	8	4
55601_at			AI742770	4.8	2.9	0
47608_at			AI697401	4.8	1.1	1.2
47330_at			W81697	4.8	1.5	9.3
70054_i_at			199829	4.8	1.7	3.5
73569_r_at			AI708856	4.8	6:0	2.7
75232_at			N31820	4.8	1.1	1.3
80059_at			H79244	4.8	1.1	3.4
84212_i_at			AI203819	4.8	0	2.6
38716_at	calcium/calmodulin-dependent protein kinase kinase 2, beta	CAMKK2	AB018330	4.8	0	2.4
41603_at	transducin (beta)-like 3	TBL3	002609	4.8	3.8	5
39866_at	ubiquitin specific protease 22	USP22	AB028986	4.8	2.6	5.9
40113_at	GS3955 protein		D87119	4.8	3.1	4.1
40824_at	RAN binding protein 16	RANBP16	AB018288	4.8	2.5	5.3
38943_at	holocytochrome c synthase (cytochrome c heme lyase)	SOOH	136787	4.8	2.9	4.4
38733_at	X-ray repair complementing defective repair in Chinese hamster cells 5 Individue strand-break rejoining. Kit autoantigen ROED)	XRCC5	M30938	4.8	1	4.3
33198_at	binder of Arl Two		AA206524	4.8	2.3	6.8
56520 at	nudix (nucleoside diphosphate linked moiety X) type motif 5	NUDTS	AI188576	4.8	3.3	4.3
45307 at			A1921204	4.8	1.6	5.9

50244 at	Inucleotide binding protein 2 (E.coli MinD like)	NUBP2	AA552351	4.8	5.6	6.4
45878 at			W21966	4.8	3.9	4.6
39971_at	lymphoblastic leukemia derived sequence 1	LYL1	M22637	4.8	3.5	4.8
	tetraspan 3		M69023	4.7	3.5	0.9
38630 at			AL080192	4.7	4.6	1.8
39486 s at	KIAA1237 protein		W28968	4.7	1.1	9.0
1713_s_at	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	U26727	4.7	0	5.6
39410 at	development and differentiation enhancing factor 2	DDEF2	AB007860	4.7	0.2	6.1
40202 at	basic transcription element binding protein 1	BTEB1	D31716	4.7	1.5	3.5
40064_at		ALS2CR3	AB011121	4.7	0.8	1.5
40470 at	oxoglutarate dehydrogenase (lipoamide)	НОВО	D10523	4.7	3.6	0.3
32820 at		CNOT4	U71267	4.7	4	10.4
39310 at	bradykinin receptor B2	BDKRB2	X86163	4.7	0.2	4.6
610_at	adrenergic, beta-2-, receptor, surface	ADRB2	L_:	4.7	6.0	2
33492 at			AI624840	4.7	1.8	7.1
35285_at	solute carrier family 4, sodium bicarbonate cotransporter, member 4	SLC4A4	AF007216	4.7	0.1	1.8
40310_at	toll-like receptor 2	TLR2	AF051152	4.7	3.5	0
35190_at	KIAA0469 gene product	KIAA0469	AL031447	4.7	1.3	2
37977_at	KIAA1528 protein		AI138834	4.7	2.4	0.4
39141_at	ATP-binding cassette, sub-family F (GCN20), member 1	ABCF1	AF027302	4.7	4.1	0
467_at	osteoclast stimulating factor 1	OSTF1	U63717	4.7	2.5	0
42270_at			W24320	4.7	1.5	6.1
56991_at			A1927199	4.7	1.2	6.5
57016_at	hypothetical protein FLJ11264		A1692513	4.7	6.4	10
52287_at	long-chain fatty acid coenzyme A ligase 5		AA514342	4.7	0.8	0
76152_s_at	┢		A1634548	4.7	0	0.7
81262_at			AI280818	4.7.	9.0	0.2
89955_at			AW020975	4.7	1[0
66849_at			AI160370	4.7	1.4	1.8
58452_at	sperm associated antigen 9	SPAG9	AL079765	4.7	2.4	11.1
75150 at			AI631846	4.7	3.8	1.1
83391_at			AI638800	4.7	1.1	2.8

Figure 11DDDD

	IIYpomencal protein rujzzyyo		D20046	4.7	10.6	29
7			AI962194	4.7	3.1	4 8
SUODOS r at putative brain nucl	n nuclearly-targeted protein		AI792919	4.7	- C	7 7
6/639 at			AL048402	4.7	3.1	5.5
6/363 at			AA436007	4.7	4.7	2.5
66160 at			AI874267	4.7	4.2	
8//8/ at			T83663	4.7	1	0
			T69727	4.7	4.4	0.00
56911 r at			N66563	4.7		0.5
86833 r at			Н68862	4.7	3.1	7.3
44202 dt			AA417797	4.7	38	2 9
72072 at			AI765157	4.7	8	7.0
22204_dt			AA894564	4.7	2	4.3
82391 at			AA630392	4.7	2.3	0
44588 at			AA160048	4.7	0.1	1.9
72514 at			AA604268	4.7	3.1	2.4
54387 at			N42884	4.7	1.2	0.3
46610 at			AI762856	4.7	4.8	1.4
60174 at			AL043934	4.7	0.8	0
74680 r at 151 N29 gene produ	product		N36861	4.7	2.1	5.5
Т			AW002527	4.7	7	6.3
49683 at			N93263	4.7	3.4	0
53670 at			AA027059	4.7	2.2	1.7
52855 at			AA664156	4.7	17.4	9.1
43752 at			AI885781	4.7	11.3	14.6
ŧ	Cytochrome c oxidase subunit Vh	-	AA191495	4.7	1.4	0.5
T	646 profein	COX5B	M19961	4.7	2.3	5.7
T		-+	AL050084	4.7	2.3	3.8
T		LSP1	M33552	4.7	1.1	8.8
T	Itanslocase of inner mitochondrial mambrass 10 (AA193416	4.7	4.1	4.6
T	n modern de mentione de la Cyeast, nomolog	TIMM10	W02499	4.7	4.6	4.9
Τ			Al342336	4.7	2.7	6.4
44705 at hynothetical protei	nrotein		AA789332	4.7	2.9	2.6
T			AA133356	4.7	3.9	4.9
3 2			00110014	. 1	6 0	

Figure 11EEEE

at			AI201843	17		
at				•	10 4	
at at			AWOO220E			1
at			00570044	4.7	Ω	4.
at			AA5214/6	4.7	4.4	3.4
at			AA225263	4.7	4.6	4.4
at			AI701480	4.7	2.3	3.4
at			W15284	4.7	1.9	3.6
at	nypotnetical protein MGC4368		AL121013	4.7	~	19
at	glutathione. S. transferase like; glutathione transferase omega		U90313	4 6	2 4	
at			AB007874			
	ADP-ribosylation factor GTPase activating protein 1	ARFGAP1	AA402332		1.1	1.0
1	protease		AB002134		7 6	15.7
	≥	KLRA1	AF047445		13	5.6
T	CUX1 / (yeast) homolog, cytochrome c oxidase assembly protein	COX17	AA149486	4.6	0	
	NAUH dehydrogenase (ubiquinone) Fe-S protein 2 (49kD) (NADH. coenzyme Q reductase)	NDUFSZ	AF050640		1.3	
38904_at v.src av	v.src avian sarcoma (Schmidt-Ruppin A.2) viral oncogene homolog	SRC	AF077754	4.6	1.9	12.7
33760_at peroxis	peroxisomal biogenesis factor 14	DEY14	ABO17546	,		
35166_at Down s	Down syndrome critical region gene 3	1000	ABO1 / 340	4.0	3.4	0.2
	KIAA1117 protein	באטפט	00/343	4.6	7.1	5.7
427 f at interfer	interferon alpha 10		ABU23040	4.6	9.9	3.6
	4	FNAIO	V00551	4.6	0.5	25.4
37493 at			AL042599	4.6	2.9	27.9
Τ			H04668	4.6	4.7	3.3
T.		TP53BP2	U58334	4.6	9.9	0.5
Τ	MAD (mothers against 4	FCER1G	M33195	4.6	1.2	1.8
	MADS (Highliers against decapentaplegic, Drosophila) homolog 4	MADH4	U44378	4.6	3.1	3.4
	who s box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	S57212	4.6	0.7	8.7
56131_at			10000			
64966_at			A114683/	4.6	1.8	2.4
	RNA polymerase transcription factor RRN3		Albb8641	4.6	5.2	6.1
	JŒ		N22730	4.6	3.9	1.6
	in carluggaing anzyme CZD 3 (mornologous to yeast UBC4/5)	UBE2D3	R81146	4.6	4.3	2.1
90289_at			AI827330	4 6	4	

Figure 11FFFF

73715 at			A1126206	4.6	1.9	12.3
51234 at			H92909	4.6	0.5	0.1
44050 st			T71614	4.6	0	1.5
44000 at	Seienoprotein W, 1	SEPW1	AA625451	4.6	1.9	17.2
19020 at			AA962105	4.6	2.3	0
4045/ at	splicing factor (CC1.3)		A1400626	4.6	m	13
62400			AI202885	4.6	2	2.2
83402 at			AA700080	4.6	3.4	m
84383 at			AI949708	4.6	2.2	6.2
03460 at			AA166751	4.6	4.5	1.7
4/4/1 at			AA916868	4.6	0.4	60
44/49 at			T66226	4.6	2.6	
8/408_at			AI221305	4.6	0.3	3.5
43131 at			T87150	4.6	0.3	3.7
53446 at			AA862900	4.6	4.5	27
77935 at			AI939620	4.6	2.5	8
87284 at			AA044789	4.6	3.8	0.6
4294/ at			AA042952	4.6	1.3	4.3
010/4 g at	7		N49836	4.6	4.1	4.0
72122 at	periin		AL046918	4.6	2	0
75575 at	2CC044171		W90634	4.6	2.1	0.3
7 3323 at	MANAGES Bene product		R34331	4.6	6.7	2.1
74643 at			AI823999	4.6	5.2	3.5
44043 at	- 1		AI633734	4.6	0	0
91750 of	_		H88129	4.6	2.8	2.9
16112 r 2+	ineparari surrate (glucosamine) 3.0 surrotransferase 3A1	HS3ST3A1	N71828	4.6	3.3	2.2
55264 24	hynothatical protein CBDIG7		AI700523	4.6	2	0
6277 24			W79937	4.6	0.5	0
17350 34	squarrious ceri carcinoma antigen recognized by I cell		W81246	4.6	1.3	0
47.333 at	1111111		AA887112	4.6	0	0.9
80770	hypothetical protein up.141E15.2		A1190033	4.6	2.6	1.6
55262 at			AA179496	4.6	0	0.1
73205 at			AI653767	4.6	18.2	19.8
45233 at			AA033783	4.6	3.3	0
40014 at			H46965	4.6	0.5	2.5

Figure 11GGGG

36444 s at	36444 s at Ismall inducible cytokine A5 (RANTES)	SCYAS	AF088219	4.6	3.7[4 5
41749_at	ES1 (zebrafish) protein, human homolog of	C210RF33	U53003	4.6	8	
41727_at	KIAA1007 protein		AB023224	4.6	2.9	5.2
41562_at	murine leukemia viral (bmi-1) oncogene homolog	BMI1	L13689	4.6	3.5	4.3
32562_at	endoglin (Osler-Rendu-Weber syndrome 1)	ENG	X72012	4.6	4.7	9
38041_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	GALNT1	U41514	4.6	3.3	3.5
	acetylgalactosaminyltransferase 1 (GalNAc.T1)					
38789_at	transketolase (Wernicke-Korsakoff syndrome)	TKT	L12711	4.6	3.3	6.4
48810_at	hypothetical protein DKFZp761H221		AI547243	4.6	3.7	6.5
43824_at			AI952129	4.6	2.5	5.3
44632_at			AA007697	4.6	2.4	4.7
45758_at			AA034095	4.6	m	5.9
65620_at	hypothetical protein FLJ14005		W52855	4.6	4.4	4.7
50036_at			A(189011	4.6	3.9	4.4
53935_at			W74486	4.6	2.4	4
55571_at			W58459	4.6	1.5	3.1
37119_at	vesicle-associated membrane protein 4	VAMP4	AL035296	4.5	2	6.0
34530_at			W73822	4.5	7.6	1.2
33019_at	Parkinson disease (autosomal recessive, juvenile) 2, parkin	PARK2	AB009973	4.5	2.3	10.5
33283_at	arrestin, beta 2	ARRB2	AF106941	4.5	0.8	0
31524_f_at	H2B histone family, member K	H2BFK	1	4.5	1.4	7.4
33665_s_at	33665_s_at colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-	CSF2RA	1	4.5	2.3	0.4
	[macrophage]					
34312_at	nuclear receptor coactivator 2	NCOAZ	AI040324	4.5	Č	7.6
33773_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila)		U13948	4.5	0	2.6
33504 at	neurexophilin 2	NXPH2	AF043467	4.5	14	œ C
37828_at	hypothetical protein FLJ11220		AL050064		12	4 4
36703_at	small inducible cytokine subfamily A (Cys.Cys), member 25	SCYA25	U86358	4.5	-	2.9
36452_at	synaptopodin		AB028952	4.5	1.6	3.6
35826_at	suppressor of Ty (S.cerevisiae) 5 homolog	SUPT5H	AF040253	4.5	3.1	3.6
36897_at	KIAA0027 protein		D25217	4.5	-	1.3
37941_at	myosin binding protein C, fast type	MYBPC2	X73113	4.5	1.3	6.7
38355_at	DEAD/H (Asp Glu-Ala Asp/His) box polypeptide, Y chromosome	YBO	AF000984	4.5	2.3	0.7
56367_at			7660£91A	4.5	1.8	1.1

Figure 11HHHH

65139_at	hypothetical protein FLJ12150		AI925240	4.5	8.6	0.8
76305_at			AA764974	4.5	1.4	0.5
76356_at			AA203497	4.5	1.6	1.6
59043_at			AI243147	4.5	0	0.4
82499_at			AI925051	4.5	1.1	0
56803_at	wingless type MMTV integration site family, member 5A	WNT5A	AI968085	4.5	1.3	0
67164_at			AI367020	4.5	2.1	0.1
65478_at			AI744031	4.5	3.9	1.2
43273_at			AI655806	4.5	0.8	1.4
68245_at			H48278	4.5	2.5	1.7
79480_i_at			N49201	4.5	1.7	1.7
56269_at	hypothetical protein FLJ12701		AI338045	4.5	2.5	1.4
49469_at			AI871490	4.5	1.4	1.4
73771_at			AI632232	4.5	2.5	3.7
57270 f at	glutaminase	STS	AI968420	4.5	4.8	0.3
86475_f_at			AI337926	4.5	3.1	3.1
63849_at	karyopherin beta 2b, transportin		AI885873	4.5	0	9.0
86015_at			AI652445	4.5	9.0	0.4
87673_at			AI982610	4.5	9.0	0.2
84407_r_at			A1032906	4.5	9.0	1
85125 g at			AI074707	4.5	2	3.6
53978_at			AW024692	4.5	1.2	11.3
45918_at			N53560	4.5	1.6	3.9
43356 s at	D-type cyclin-interacting protein 1		A1970622	4.5	1.4	0
62261_s_at	62261_s_at LIM domains containing 1	LIMD1	A1933287	4.5	3.7	1.7
45661_at			N90348	4.5	5.5	6.7
60188_at			AA629050	4.5	8.1	3.1
65892_at	fatty acid binding protein 1, liver	FABP1	AA001405	4.5	2.7	0
53997_at	seven transmembrane domain orphan receptor		AA622413	4.5	1.7	0.7
54521 g_at	_		A1084224	4.5	4.3	1.4
46234_at	CGI-148 protein		AA043242	4.5	4	4.9
54067_at			A1982669	4.5	0.3	0
48633_at	KIAA1254 protein		A1770067	4.5	3.3	0.7
62971_at	hypothetical protein FLJ12428		AI799804	4.5	2.9	2.3
61005_at			AA009648	4.5	ĸ	4.1

Figure 11IIII

57423 at			AA433928	4.5	0.5	C
87232_at			AA487296			5.3
33308_at		GUSB	M15182	4.5	0.8	4.8
32317_s_at		SULTIA2	U34804	4.5	3.1	4.1
39135_at	KIAA0767 protein		AB018310	4.5	3.7	4.3
47714_at			AA018412	4.5	2.4	2.7
33689_s_at	D-dopachrome tautomerase	TOO	AF012434	4.5	1.8	4.7
55301_at			AI634118	4.5	2.6	4.3
57497_at			AA419263	4.5	3.9	4.1
58468_at			C17704	4.5	4.5	4.3
58647_at	glutathione S-transferase M1	GSTM1	AA203289	4.5	8	3.2
46594_at	hypothetical protein FLJ20186		AW014780	4.5	4.3	4.6
44079_at	general transcription factor IIIA	GTF3A	AA166851	4.5	3.9	4.9
43485_s_at	hypothetical protein FLJ21343		A1633875	4.5		m
47104_at			A1760368	4.5	3.4	4
47561_at			AA877614	4.5	3.5	5.7
39385_at	alanyl (membrane) aminopeptidase (aminopeptidase N,	ANPER	M22324	77		0.1
	aminopeptidase M, microsomal aminopeptidase, CD13, p150)					
36347_f_at	H2B histone family, member D	H2BFD	AA873858	4.4	1.4	6.4
40407_at	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	KPNA2	U28386	4.4	2	2
31342_at	UDP-N-acetyl-alpha-D-galactosamine.polypeptide N-	GALNT2	X85019	4.4	1.3	8
			-		!	1
32635_at	transcriptional intermediary factor 1 gamma		AB029036	4.4	3.7	6.1
32693_at	KIAA1040 protein		AB028963	4.4	0.7	13.5
33219_at	KIAA1097 protein		AB029020	4.4	3.7	17
41770_at	monoamine oxidase A	MAOA	AA420624	4.4	0	0
34655_at	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	MPP2	AI951832	4.4	0.2	10.4
38982_at	TRF2-interacting telomeric RAP1 protein		W28865	4.4	1 6	4.3
35213_at	WW domain binding protein 4 (formin binding protein 21)	WBP4	AF071185	4.4	6.1	2.6
41584_at	nudix (nucleoside diphosphate linked moiety X) type motif 3	NUDT3	AF062529	4.4	6.0	6.4
35007_at			AC004940	4.4	0.5	0.8
37403_at	annexin A1	ANXAI	X05908	4.4	2.6	4.1
37088_at	serine/threonine kinase 13 (aurora/IPL1-like)	STK13	AF059681	4.4	2.6	3.9
56940 g at			AI963304	4.4	3.6	4.3

18118 24	CG 07 protein				
40110 at	Ι.	AA044743	4.4	1.5	1.8
26456 at	hypothetical protein dJ1181N3.1	AI632926	4.4	2.2	0
81567_at		AI190905	4.4	1.7	0
47459 at		AI290653	4.4	23	4 1
76717_at		AI375865	4.4	0.5	000
66616_at		AA285069	4.4	2.2	5 4
64991_at		AI762686	4.4	1	
64346_r_at	nuclear factor (erythroid-derived 2)-like 2	NFE2L2 AW023229	4 4	200	
82372_at			4 4	0.0	0.7
84765_at		AI446030	4.4	7.1	
49312_at		AA747303	4 4	3.2	7 4
63398_at	similar to Bos taurus P14 protein	AA130220	4.4	6.9	2
6/890_at		AI613399	4.4	3.2	
8/942_at		AA936705	4.4	2.7	1 6
45280_at		AA703316	4.4	1.5	
4/565_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog)	MLL W55861	4.4	1.4	2.9
70379_at		AI744361	4 4	-10	7.0
44328 at	hypothetical protein MGC5487	AA905113	4.4	2	9
62495 t at		AI433785	4.4	17.4	280
4336/ at		AI979164	4.4	1.5	0.4
43489 at	hairy/enhancer-of-split related with YRPW motif-like	HEYL AL040197	4.4	3.2	5.1
	hypothetical protein FLJ11269	AI741524	4.4	1.9	6.9
36384 at		R17914	4.4	1.3	0.5
48090 at		H48142	4.4	0	0
30204 at			4.4	1	2.9
69969 at	ribosomai protein 515a	RPS15A AW003898	4.4	2.9	0
03000 r at		AI031837	4.4	0	0.8
72020 21		AA063087	4.4	0.2	1.2
12320 at		A1638648	4.4	1.9	3
60537 24		AA536137	4.4	9.0	2.1
60137 at		AL038866	4.4	1.3	0.3
74302 24		H61529	4.4	3.1	3.6
74302 at		AA028209	4.4	1	2.6
41928_at		AA029647	4 4	3.5	4

Figure 11KKKK

35253 at	GRB2-associated binding protein 2	GAB2	AB011143	4.3	-1	
2007E at	Huclear ractor 1/B	NFIB			2.7	
39975_at	NIAALUSU protein; Golgi-associated, gamma-adaptin ear containing. ARF-binding protein 2		Æ	4.3	6.0	0.4
40332_at	7-60 protein		0.00			
36899_at	Special AT-rich sequence binding protein 1 (binds to publicar	i di	AF109134	4.3	4.2	5.3
1, 00,170	matrix/scaffold-associating DNA's)	SAIBI	M9/28/	6.3	8.4	9.9
3/188 at	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	PCK2	X92720	4.3	C L	
30309 at	dystroglycan 1 (dystrophin associated glycoprotein 1)	DAG1			3.6	S
38/96 at	complement component 1, q subcomponent, beta polypeptide	CIOB	X03084	0.4	2.7	1.9
2003/_at	globotriaosylceramide/CD77 synthase; Gb3/CD77 synthase; alpha1,4. galactosyltransferase; 4.N-acetylglucosaminyltransferase		AA769110	6.4	1.4	0.4
56927 at						
91181 at	Uncharacterized hematonoletic stem (prognation and		W49628	4.3	4.5	7.8
	The state of the s		AW044698	4.3	0	0
57414 at						_
58260 at			AA878480	4.3	1.3	c
87639 at	eukaryotic translation initiation factor of		AA806364	4.3	2	4 5
89954 at		EIF2C1	AI971316	4.3	3.1	0
49278 g at	200000000000000000000000000000000000000	CARS	AA908890	4.3	2.7	r α
85068 at			AA534436	4.3	6.0	0
80554 s at			AI032972	4.3	0	C
85293 at			AW004040	4.3	6.0	
90699 at			AI468014	4.3	0	
43708 at			AA434032	4.3	2.5	40
68195 at			R10307	4.3	0	4 1
68496 at			AI627334	4.3	6.0	2.5
86306 r at			A1653006	4.3	1.3	33
70302 at			AI656897	4.3	1.5	000
56319 at	Cofactor required for Sp1 transcriptional patients		AI222295	4.3	1.6	10
	(//kD)	CRSP6	C05931	4.3	2.7	4.8
49539 at	tryptophanyl tRNA synthetase 2 (mitochondrial)	WARSZ	R40635	7.3		
- 11	Hypothetical protein FLJ10415		AA524061	0.0	7.7	
65484_f_at	glutaminase	ਹ ਹ	A1768354	5.0	0.7	٦
		2	100000	4.5	3.3	0.4

Figure 11MMMM

40300 at			A1926365	5.7	1.2	-
51792_at			H80286	5.7	1.5	
46153 at			W07089	5.7	2.1	
47602_at			R02594	5.7	6.2	
57968_r_at			AA393223	5.7		8
37214 g at	deoxyribonuclease I-like 1		AA431469	5.7	2.8	0
1357_at	ubiquitin specific protease 4 (proto-opcogene)	DNASE1L1	- 1	5.7	1.6	2000
39105_at	vasodilator-stimulated phosphoprofein	USP4	- 1	5.7	3.4	α
53155_at		VASP	- 1	5.7	2.6	Ö
46664_at	apoptosis-associated speck-like protein containing a CABD		AA608559	5.7	4.4	7.1
37506_at	Huntingtin interacting protein A		A1148558	5.7	5.1	9
40773_at	myosin, light polypeptide 5, regulatory		- 1	5.6	1.7	-
40791_at		MYL5	- 1	5.6	5.9	
33418_at		POLR2A	X63564	5.6	3.1	42
35137_at	myomesin 1 (skelemin) (185kD)		AL096752	5.6	7.2	5.7
35198_at	hypothetical protein from clone 24796	MYOM1	06069X	5.6	0.7	00
35251_at	human immunodeficiency virus type I enhancer hinding arateis 1		AF070596	5.6	4.6	20
1856_at	V-rel avian reticuloendotheliosis viral oncogene homolog	HIVEP1	X51435	5.6	6.4	12.
39281_at	Rho guanine exchange factor (GEF) 11	REL	X75042	5.6	4.1	5.7
35320_at	solute carrier family 11 (proton counled division)	ARHGEF11	AB002378	5.6	3.2	
	transporters), member 2	SLC11A2	AB004857	5.6		N C
at	dynein, cytoplasmic, intermediate polypeptide 2					,
at	CD58 antigen, (lymphocyte function associated antigen 3)	UNCIS	AI986201	5.6	5.6	
39562_at	CGG triplet repeat binding protein 1	CD58	Y00636	5.6	6.5	0.6
40757_at	A (granz	CGGBP1	AF094481	5.6	2.4	
7	esterase 3)	AINIA SCINIA	M18/3/	5.6	1.3	23.9
je j			14/60505			
Ę	neurexophilin 4	VIGNIV	1409393		2.3	2.8
	CGI-18 protein	444	AI498//1	5.6	2	33
73901_at			AI073484	5.6	8.1	
72649_at			AI984965		0.9	1 4
62914_at			AI765590	5.6	0.7	1 4
84232_at			AI363275	5.6	6.0	1.2
69834_r_at			AI806926	5.6	1.2	3.9

42881 at			W81045	5.6	3.6	
			R88708	5.6	1.6	
46960 at			AI148006	5.6	,	100
			AI743903	5.6		C I
63251 s at			W72338	5.6		
			AA904828	5.6		
Г	PAN2 protein		AI185207	5.6		
1 =			AI309334	5.6	4	C.
46727 at			AI741209	5.6		101
46808 at			AI146850	5.6		
53689 at			AL120562	5.6		
57000_f_at mer	meningioma expressed antigen 5 (hyalingandasa)		_1	5.6		
_	ein Fl 110074	MGEA5	_	5.6	0.1	
Г	hypothetical profein FI 120038		AA018399	5.6		C
	Ę		AI921097	5.6		0
	stannin			5.6		4
1 =		NNS		5.6	2.	0.4
at	chromosome 18 open reading frame 1		AI693465	5.6	2.1	15.9
56225_at		CIBORFI	AF009425	5.6	4.5	3
64028_s_at			AI744466	5.6	3.3	4.6
49390_at			AI886403	5.6	4.4	5.6
52261 at			AA999858	5.6	5.6	5.6
	nked N-acetylglucosamine (GloNAc) transferace (1108 N		AI970054	5.6	4.7	6.4
acet	acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	061	U77413	5.5	1.1	1.8
	TAK1 hinding profess 2 Kingse, 90kD, polypeptide 5	RPS6KA5	AF090421	5.5	8.8	c
1.	hypothetical gotain 2, NIMAU 33 protein		AB018276		0.00	Ö
T	hone marrow stromal call cations o		W29115		8.0	1.8
Т	7	BST2	D28137		7.6	9
	HMBA inducible	PSMB2	D26599	5.5		4.6
Γ	KIAA0005 gene product		AI796944	5.5	C	0.4
Γ	KIAA0342 gene product		D13630	5.5	3.2	0.0
77 g at semi	Sema domain, immunoplobulin domain (In) short basis domain.		AB002340	5.5	3.6	3.2
	the state of the s	SEMASCI	SEMA3CI ABDDD220	u		

Change Change	COLIAZ	00000	5.5	0	-
		AF094521	5.5	2.1	9.2
T		U90912	5.5	3.5	2.5
nypotnetical protei		W25874	5.5		
331+3_at papillaly relial cell carcinoma (translocation-associated)	PRCC		5.5	1.5	17
722.7 2 at 585.0 at		AA743565	5.5	1.3	9
50057_ut		W03029	5.5	4.1	
74006 at		AW001883	5.5	6.0	3.2
66774 at		AI984623	5.5	0.7	
74975 f at zinc finger protein 172		AA978204	5.5	3.3	2.1
בווים ווופטרו היווים	ZNF173	AW009746	5.5	5.5	14.1
47489 at		AI203222	5.5	1.3	0
75201 f at		AI452516	5.5	2.9	1.5
55280 at Initative N6-DNA-methyltransferase		A1688900	5.5	11	7
		AI016585	5.5	5.1	10.4
41153 f at Toatenin (cadherin-associated protein) sloke 1 (100kg)		AA993487	5.5	5	2.6
Т	CINNAI	AF102803	5.5	3.7	0.1
73601 at		AA176289	5.5	2.6	0.3
		AI885677	5.5	0	0.2
43838 s at Invoothetical protein PROTOGR		R22212	5.5	0.8	4.6
		AA100948	5.5	0.4	3.4
68328 at		AI660022	5.5	1.2	0.6
45390 at		AI475514	5.5	10.2	32.1
42965 at		AI769269	5.5	7.2	0
57470 at		H24422	5.5	1.7	1.6
		AI091581	5.5	2	2.7
50187 at		Al199443	5.5	0.5	2.5
GCN1 (general control of amigo acid curthodic		H46074	5.5	9.0	6.1
DO IN INCIDENT	GCN1L1	AI939557	5.5	0.5	1.2
66856 r at		AI457965	5.5	1.7	6.0
71516 r at		AA993791	5.5	1.4	2.8
69622 at		Z40202	5.5	0.3	2.1
Small nuclear RNA		AI669987	5.5	6.1	4
Т		AI557062	5.5	5.9	5
3,	(\ L > C - \				

44693 at	100,000		N26243	S)	<u>∞</u>	6.7
	┪		N36986		4.2	5.8
5210/ g at	t CGI-90 protein		A1800674		2 9	2.0
39748_at			AI 050001	5 4	0.0	0./
40788 at	adenylate kinase 2	CAY	T		6.2	٥
31522 f at	H2B histone fam	ANA ANA	70043/1			0
35879 at	palanin	HZBFG	6//087	5.4	2.5	8.5
33713 24	Construction of the contraction	GAL	M//140	5.4	8.3	0.4
20/10-at	translocase of filler mitochondrial memorane 17 (yeast) homolog B		AJ005895	5.4	2.2	3.1
41234_at	DnaJ (Hsp40) homolog, subfamily B, member 6	DNA IRE	A15A0319	V		
31633 g at	zinc finger proteir	7NF250D	L	4.0	ر د د	6.2
39209 r at	pro-platelet basic	7507	1	0.4	0	0.2
	thromboglobulin, activating peptide			ი 4.	4.0	4.2
		F2F5	1131556	2		1
33480_at		Z		1 5		> i
38016 at	transcriptional activator of the c.fos promoter	1	00000		Σ.Τ	5
34376_at	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	DIXIG	AB010617		2.7	
34892_at	tumor necrosis factor receptor superfamily, member 10h	TNEBCETOD			7.7	9.6
35284 f at		100	ALO10200	0.4	0.3	3.5
36554 at	П	1	WZ862U	5.4	0	3.6
36991 at	Splicing factor, argining/sering-rich 4	ASMIL	Y15521	5.4	1.8	2
2045 s at		VTR04	L140/6	5.4	5.3	4.2
48436 at		TCK	M16592	5.4	0.8	9.0
91799 at			AI922968	5.4	0.1	2.4
65158 at			AA586814	5.4	5.2	0
56548 24	promote I the Later and a control of I have a		AI741328	5.4	3.8	1.2
87038 24			A1858573	5.4	1.2	0.1
70530 24	and (a. politica) normaliage	SKB1	AA932371	5.4	1.7	2.5
75054 at			AI023295	5.4	7.5	2
73004 at	INCUZ protein		AA910520	5.4	0.7	1.1
67103 at	protein Kirlase CriKZ		N24330	5.4		17
30240 at	ingpounencial protein FLUIZ903		A1807668	5.4	2.5	5.1
74780 s at	Yi advit nancillo		AI309016	5.4	3.6	3.2
914700 S at	collagali, typa IV, alplia 1	COL9A1	N66408	5.4	2.2	5.2
81442 at			AI916887	5.4	1.7	-

Figure 11RRR

		A	AI311917	5.4	2.4	0 9
4/951_at		Ą	AA521145	5.4		
47878_f_at	KIAA0117 protein	A	A1656542	7 4		3.6
	transporter-like protein	A	AI768065	5.4	4.2	
		À	AA707322		2.7	100
87617_at	hypothetical protein FLJ13385	4	AA639580	5.4	7.1	0.5
68909_at		A	A1091231	5.4	7.0	0.1
		A	AI743419	5.4	, C	4. T
/2052_at			N71632	5.4	0.00	0.7
54/99_at		GLS V	W72090	5.4	200	† C
28825 at		PTMA	AI701911	5.4	0 4	2 7
	similar to Caenorhabditis elegans protein C42C1.9		W74749	5.4	0 -	0
49057 g at		A	AA521489	5.4	11.9	
5/0/4_s_at		AV	AW021642	5.4	1.5	0 0
50943_at			W87422	5.4	2 00	0 7
45655 at	tumor antigen SLP-8p	A	AL045849	5.4	0,10	0.7
46105 at		A	AA149641			4.4
55009_at		7	359000	t c	4.0	5 0
32007_at			WOODAE	1 .	7.7	0
39341_at	thyroid hormone receptor interactor 6		1001000	0.4	6.0	5.5
	1.0	A CALL	AJUU1902	5.4	0.5	4
39163 at	,, ,		U51240	5.4	2.2	4.9
5	KIAA1250 protein	>	W27233	5.4	0.2	6.4
45521_s_at	KIAA0100 gene product	٩	A1967955	- -	L.	ľ
63793_at	DNA polymerase epsilon p12 subunit	A	A1797479	t V	0.0	0.7
45736_at	two-pore channel 1, homolog	A	AI 048491	י ע	3.7	4 P
36495_at	fructose-1,6-bisphosphatase 1	FBP1	U21931	5 4	3.5	J.C.
31996_at	brefeldin A-inhibited guanine nucleotide exchange protein 2	A	A1798834	2 2	F 14	t c
41634 at	KIAA0256 gene product		187445		2.7	4.0
37798_at	chromosome 8 open reading frame 2	CRORF2 AF	AR018790		0.4	4.0
41134_at	KIAA0964 protein		AB023181			2.3
1383_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	PPP2R2A N	M64929		7.5	12.4
41170 at	KIAA0663 gene product	AE	AB014563	5 3	7 6	C U
37575_at		Ī	AI 050100	2.5	2.7	9.0
		7	1 761000	5.3	3.6	2.1

38778_at	KIAA1046 protein		AB028969	5.3	0 <	C
382/8 at	modulator recognition factor I		M62324	22.0	000	5.5
58064_at	· ·		AA034067	200	11.7	7:7
45639 at	ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	A1922486	5.3) F	7.7
49290 at			AW021968	5.3	0.6	
3000/ at			AA128061	5.3	1.7	899
."1 ~			AW051492	5.3	2	0.4
			A1393033	5.3	2.1	12
61840 c at	atopio (cadbaria		AI674428	5.3	1.4	0.4
59451 at	-	CTNND1	AI863000	5.3	4.5	6.6
45323 at	hypothetical protein El 120002		AI800640	5.3	6.2	23.2
85691 at	יין איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן איניינימן		W87653	5.3	2.3	3.4
45247 at	hypothetical protein Cl 1110co		AI989354	5.3	5.6	6.1
91891 at	The first of the f		N63911	5.3	2.1	5.8
85030 24			AL045717	5.3	1.6	1.2
86004			AI694139	5.3	0.4	1 3
71074 24			AA767895	5.3	0.5	20
73110 24			AI912203	5.3	1.7	4 9
73811 34			R35404	5.3	1.6	
75062 24			AI972618	5.3	12	10
87/31 21			AI732791	5.3	m	7 4
49736 9 24	otory levitodtomyd		AI872409	5.3	1.9	0
1306A 24	hisportierical protein		AI497781	5.3	2.5	
45504 at			AA131537	5.3	60	1.1
43405 s at	hypothatical protein 4	FBX04	A1961240	5.3	1.3	0.5
70228 r at	profession kings of AMD description		AA219406	5.3		C
69705 at	process knigge, calvir dependent, regulatory, type II, beta	PRKAR2B	AI792179	5.3	9.7	1
67220 at			R68222	5.3	3.1	18
39416 at	Tay interaction protein 1		AW005511	5.3	e	m
40409 at	aldehyde dehydrogenase 10 (fatti aldah 11 11 11 11 11 11 11 11 11 11 11 11 11		U90913	5.3	3.7	2
35336 at	KIAA0063 gene product	ALDH10	U46689	5.3	3.9	5.1
35688 g at	mature T-cell prof		AL021707	5.3	3.6	6.2
37320 at	Inhosphatidylsering	MTCP1	Z24459	5.3	2.6	4.3
38011 at	RPRS-mediating protein	PTDSS1	D14694	5.3	2.2	5.7
			AB006572	5.3	2	4.9

Figure 11TTT

52936_at			165761	5.3	1.5	5.1
55567_at			AA147933	5.3	5.3	5.2
38684_at	ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	AJ010953	5.2	9	2.2
32183_at	splicing factor, arginine/serine-rich 11	SFRS11	M74002	5.2	1.9	0.2
39407_at	bone morphogenetic protein 1	BMPI	M22488	5.2	2.4	5
39742_at	TRAF family member associated NFKB activator	TANK	U59863	5.2	4	3.1
31856_at	glycoprotein A repetitions predominant	GARP	224680	5.2	3.9	5.3
31975_at			X55503	5.2	1.5	1.9
33869_at			AL080218	5.2	3.2	3.8
39342_at	methionine tRNA synthetase	MARS	X94754	5.2	1.9	0
830_at	Tax1 (human T cell leukemia virus type I) binding protein 1	TAX1BP2	U25801	5.2	0.8	3.6
1105_s_at		TRB®	M12886	5.2	1.3	11.7
39950_at			Y08136	5.2	0	6.0
984_g_at	mitogen activated protein kinase 12	MAPK12	X79483	5.2	5.9	8.8
37299_at	glycogen synthase 1 (muscle)	GYS1	104501	5.2	2	0
1119_at	replication protein A2 (32kD)	RPA2	J05249	5.2	0.5	9.0
38384_at	phosphoribosylglycinamide formyltransferase,	GART	X54199	5.2	2.7	0.1
	phosphoribosylglycinamide synthetase,					
	phosphoribosylaminoimidazole synthetase					
38397_at	polymerase (DNA-directed), delta 4	POLD4	009196	5.2		C
38437_at	MLN51 protein		X80199	5.2	2.6	1.7
277_at	myeloid cell leukemia sequence 1 (BCL2 related)	MCL1	L08246	5.2	3.9	10
56371_at			AA534298	5.2	3	0
48873_at	Gene 33/Mig-6		AI571452	5.2	3.4	25.2
53777_at	hypothetical protein FLJ22693		AI672353	5.2	3.8	2.2
74423_at			AI793024	5.2	2.2	2.6
82222_at			T64664	5.2	0.1	0.3
50080_at			AI097194	5.2	3.3	3.2
51715 at	lung type-I cell membrane associated glycoprotein		AA149854	5.2	3.5	6.4
80829_at			AA210905	5.2	4	3.4
59566_at			AA705681	5.2	1.5	4.5
48547_at	pleckstrin homology domain containing, family A (phosphoinositide	PLEKHA1	AA875839	5.2	1.9	3.5
0,000	Diriging specific, member 1					
84500 at			AI004417	5.2	0.5	0.2
45272_at			AA058569	5.2	5.6	2.4

	01 (2)		A1251913	5.0		
at at at at at at at at at at at at at a	11: 21 /			,	2.5	
at at at at at at at at at at at at at a		LEPR	N46838	5.2	5.1	
at at at at at at at at at at at at at a	ier iailiiy 41 (organic anion transporter), member 12	SLC21A12	AI347130	5.2	3.1	
at at at at at at at at at at at at at a			N37020	5.2	2.2	
			AL042667	5.2	0.4	
			T65857	5.2	0	
			AI970258		1.6	
	··galactose:N·acetylgalactosamine·alpha·R beta 1,3. transferase		AI967968	5.2	6.9	4
ᇣᆝᆝᆝ	al protein		T97347	C		
	hypothetical protein LOC54149		V.000500	3.6	2.3	2.8
	protein		0262261A	2.5	13.7	15.9
П			AAAAAAA	2.6	10.2	1.6
Ī	hypothetical protein AL133206		MA470369	5.2	3.5	2.2
61299_at chaperonin contai	containing TCP1, subunit 6A (zeta 1)	COTEA	PA30E2	7.0	2.2	0
55650 at		5	743332	2.6	7.8	1.6
51599 at			W22914	5.2	1.7	2.5
	alpha. acid (Domoo dicesson alpha al		29455/6	5.2	2.2	6.4
	Special action of the disease, glycogen storage disease type II)	GAA	X55079	5.2	1.3	5.9
40955 at prostate tumor ov	imor over expressed gene 1	PTOV1	1170287	C		
	osphatase 1, regulatory subunit 7	DPD107	750740	3.5	4.5	4.6
34811_at ATP synthase, H+	ase, H+ transporting, mitochondrial F0 complex, subunit c	ATP5G3	1,09813	7.0	2.9	5.2
) isoform 3)	2	j N	2.0	7.9
T		NCI	M33308	5.2	3 /	- 4
	eductase B (flavin reductase (NADPH))	BLVRB	D32143	5.2	0.00	0.1
			A1983115		0 4	0.0
44638_at insulin-degrading	rading enzyme	JOE	AA573292	10.0	0.0	4.4
			AA779895			4.2
48811_at N.acetyiglu	N-acety/glucosamine-1-phosphodiester alpha-N-acety/glucosaminidase		AW007594		4	5.0
54912_at translocase	translocase of inner mitochondrial membrane 13 (yeast) homolog B	TIMM13B	AL035821	5.2	3.4	5.4
51123 at			H11724	5.2	ıc	0 1
52012_at			AIRSONON		2	1.0

53120_at	hypothetical protein FLJ20442	All	AI681916	5.2	4.3	4.8
487 g at	caspase 9, apoptosis related cysteine protease	CASP9 U	U60521	5.1	4.2	2.4
40491_at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 21	L	W84531	5.1	1.3	2.3
	KIAA0931 protein	AB	AB023148	5.1	1	0.7
34719_at	glutaminase	GLS AB	AB020645	5.1	0	0
39320_at	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	CASP1 U	U13697	5.1	6.9	1.1
35227_at	retinoblastoma binding protein 8	RBBP8 U	U72066	5.1	6.0	5,3
34378_at	adipose differentiation-related protein	ADFP X	X97324	5.1	13.3	0.1
35845_at	SEC24 (S. cerevisiae) related gene family, member B	SEC24B AJ	AJ131245	5.1	1.2	3.4
36888_at	KIAA0841 protein	AB	AB020648	5.1	0.8	6.9
38027_at		FBLN1	X53742	5.1	6.0	0.5
32792_at	GCIP interacting protein p29	AL	AL031432	5.1	3.2	4.1
38369_at	myeloid differentiation primary response gene (88)	MYD88	U70451	5.1	15	18.4
38824_at	Tat-interacting protein (30kD)	AF	AF039103	5.1	5.8	12.6
37082_at	KIAA0426 gene product	AB	AB007886	5.1	9.0	2.3
54747_at	endosulfine alpha	ENSA AA	AA167734	5.1	5.2	0
65027_r_at		AA	AA532470	5.1	2.1	2.1
84981_r_at	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	COL3A1 T	T54146	5.1	8.6	5.6
42564_at		5	W84667	5.1	2.9	4.6
78014_at		AA	AA371513	5.1	2.7	0.7
47832_at		AA	AA100654	5.1	0	
43363_s_at		A	AI978590	5.1	1.9	10.4
50763_at	KIAA1080 protein; Golgi associated, gamma adaptin ear containing. ARF-binding protein 2	AA	AA779863	5.1	9	3.4
42631_at		A	AI984505	5.1	1.8	2.1
84167_at		A	AI742722	5.1	2.7	0.4
88155_at	H2B histone family, member B	H2BFB AI	AI125923	5.1	0	9.0
48374_at		8	W87470	5.1	1.4	9.1
74131_at		A	AI989784	5.1	2	4
ď		AW	AW021543	5.1	0	4.4
61745_r_at		_	N76044	5.1	2.7	∞
44397 at		1.	H11252	5.1	4.3	4.4
52072_at	hypothetical protein FLJ10718	AA	AA873182	5.1	0.8	4.1

Figure 11WWW

10057	adominate Vinace 2 alaba like					
10001 at	accilyiate hillage 3 alpha like		N32441	5.1	3.1	0.4
2001/at			AA149312	5.1	3.4	0
/4823_f_at	histidyl tRNA synthetase	HARS	1	5 1	0.0	5 -
64847_at				7	?;	0.1
54410_at			00140200	o l	4.4	3.4
80825 at			N/0443	5.1	2.7	0
10270	VIAA0101 2000 1000		A1590115	5.1	9.0	0
1000			D50911	5.1	3.4	3.7
1630 s at	spleen tyrosine kinase	SYK	Z29630	5.1	3.9	4 9
33833 at	Spectrin, alpha, non-erythrocytic 1 (alpha fodrin)	SPTANI	J05243	7.	a c	7.7
32594_at	chaperonin containing TCP1, subunit 4 (delta)	CCT4]~	7 2	0.0	7.7
48110_at	hypothetical protein FLJ11271		Ι.	1 4	5.4	7.7
51179_at	brefeldin A-inhibited guanine nucleotide exchange protein 2		A1741843	, r	0.0	0.4
68339_at	transforming growth factor, beta-induced, 68kD	TGFRI	L	1 -	0.7	y. '
65171_at	clone FLB4739	5	┸	7	7.7	1.6
61853 at			50805VI	2.1	4.5	5.2
10560 21	hypothotical protain El 100001		AA//3816	5.1	5.1	5.1
45005 at	hypothetical protein rejector		AI690893	5.1	4.2	4.5
00003 41	Daculoviral IAP repeat-containing 6	BIRC6		5.1	2.9	5.4
45293 at	hypothetical protein from EURUIMAGE 363668		AA631902	5.1	4.4	4
30410_dl	uncharacterized nematopoletic stem/progenitor cells protein MDS027		N25128	5.1	3.7	5.8
45224 at						
57714 at			AAU23862	5.1	3.2	3.5
36908 at	mannose receptor C type 1			5.1	3.6	5.1
55505 at	alminose receptor, o type 1	MRC1	1	5.1	4.2	4.6
20100	Blycuite cleavage system protein H (aminomethyl carrier)	GCSH	AI890917	5.1	4.5	4.2
31800 at	Dielomorphic agenoma gene 1	PLAG1	1	2	0.7	1.4
22140 at	Mindoziz gene product	kiaa0212	D86967	5	3.7	23
32142 at	serine/threonine kinase 3 (Ste20, yeast homolog)	STK3		5	4.1	3.6
22722 ct	illuric oxide synthase ZA (Inducible, hepatocytes)	NOSZA	U31511	5	0.4	27
32233 at	TOTAL BY THEMPER BY (TOTSIN BY)	TORIB	AF007872	2	6.9	13
32002 at	NIAAU1/U gene product		AL041663	ιĊ	0	2
343/3 at	upstream regulatory element binding protein 1		297054	0 4	1	1
1289_at	glutathione S-transferase M5	GSTM5	102321) LC	-	
1072 g at	GATA-binding protein 2	GATA2	M77810	2	7 6	0.4
38064 at	major vault protein	MVP	1) (α [.	0.0
39170_at			A1 0.4005.7	2 4	2	0.0

Title: Response of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

Inventors:	Nir Hacohen, et a	l.

- 1						
82798_g_at	chromosome 6 open reading frame 32	C60RF32	AW016644	5	0	2.5
at	hypothetical protein		AI889499	2	0	0
89829_at	hypothetical protein FLJ10521		A1913628	5	9.0	9.0
66361_at			AA009699	2	4.3	0.8
73713_at	RAB, member of RAS oncogene family-like 2A	RABL2A	AI051621	2	0.4	2.5
53828_at			AI929168	2	1.1	3.6
62472_at			H49102	5	1.5	2.3
83036_at			AI271559	5	0.5	3
82768 g at			AA913354	5	0.8	2.5
83224_r_at			AI053582	2	1.6	0.5
66108_s_at			AI915696	5	2.9	1.6
79105_at			AA830599	5	5.6	2.2
69388_at			AI299040	5	O	2.6
49516_at			AA531016	2	9.9	3.5
61354_at			AA218990	2	1.3	1.5
70495_at			AI453095	5	4.2	2.8
57608_at			AA523335	5	1.7	0
46169_at			AI745624	C)	4.5	12.3
46514_at			R38647	5	2.9	0
53321_r_at			AL043875	5	3.5	5.1
51991_at			AI884621	c)		0.5
45204_s_at			AI378647	5	10.2	5.2
45787_at	cyclin L ania-6a		N29695	2	2.3	5.4
53657_r_at	53657_r_at non-kinase Cdc42 effector protein SPEC2		AI825880	Ŋ	2.2	2.4
58339_at	hypothetical protein FLJ13222		R52747	5	2.7	m
73128_at	dihydropyrimidinase-like 3	DPYSL3	AI983251	2	7.2	0
46277_at			AI031551	5	10.2	1.6
58688_at	RAB23, member RAS oncogene family	RAB23	AI742498	2	1.4	1.6
55495_at			AA187437	5	0	0.5
46724_at	tensin	TNS	AL046979	2	3.9	0
52252_i_at			2963428	S	1.7	
54167_at			3162292	5	1.8	1.5
39801_at	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	PLOD3	AF046889	2	2.1	5.9
40382 at	corticotropin releasing hormone	CRH	V00571	5	4.7	3.8
48059_at			R61448	5	4.4	3.5

58780 s at 45255 at		HEXA	M16424	വ	1.5	ď
58780_s_a 45255_at			AI701293	2	2.7	i.c
45255 at	_		R42449	2	2.6	4.6
	CGI-69 protein		AI354351	ıc		0 4
g	anaphase promoti		AA131793) (2.0	41.0
34427 g a	at major histocompatibility complex, class I-like sequence	HIAIS	1	0 7	7.5	9:0
38892_at	KIAA0240 protein				0.0	0.0
33437_at	homolog of yeast SPB1		A 1005800	U. 4	6.7	7.1
36270_at	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	2800	1		2.7	0.
35720_at		000			13.2	3.9
31590 g at	_	10000	AD020700			10.8
o l	JAK binding prote	GABBRI	ALU31983	6.4	6.0	10.3
35293_at	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS	6422	AB000/34	6.4	9 0	7.7
	A/Ro)	7000		4. v.	2.3	1.4
35363_at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 17 (72kD)	DDX17	AL080113	6 7	27	
36550 at	ras association (RalGDS/AF.6) domain containing protein JC265		AL049538		000	
4034 / at	_		AA913812	4.9	200	,
40668 s at	CD6 antigen	9QO	U34624	4 9	25.0	10.7
40/12 at	a disintegrin and metalloproteinase domain 8	ADAM8	D26579	4.9	7.2	1.2
/5/43 at			AA668789	4 9	3.4	-
			F26341	4 9	;	7.0
90341_at			H04388	4 9	, r	7.7
91905_s_at			AI609998	4.9	5.0	0.0
4/215_r_at			AA129058	4.9	000	ς α
4923/ at	KNA binding motif protein, X chromosome	RBMX	AI971694	4.9	2.5	128
03242 at			AI809894	4.9	2	7 4
34030 at	liypotrietical protein FLJ10955		A1961496	4.9	3.3	1.5
04 E00 24			AI807804	4.9	3.6	2.2
56065 at	HCDCORG protein		AI691077	4.9	2.9	4.3
7/035 at	- 1::		N51105	4.9	6.4	
13690 at	=1		W04760	4.9	0.3	2.6
75820 r at			AA019641	4.9	0.2	0.4
65026 24			AI679201	4.9	1.6	2.5
0250 at			AA034414	4.9	3.3	4.7
69/63 r at			AI865825	4.9	6.0	88

441/0_at			11000011			
72092 f at			H53031	4.9	0.8	2.8
07/16 , 04			AA677864	4.9	3.4	7.5
64071 21			T91504	4.9	9.0	99
1040/1_at	Dapillornavirus regulatory factor PRF-1		N25612	4.9	2.5	-
49104 S at	LOT THIKE	TSPYL	AI972301	4.9	1.5	1.3
01000			AA442900	4.9	2.5	ا ح
01003 at			AI248920	4.9		0.2
45012 at			AI744560	4.9	3.7	5.9
40000 at			AA479835	4.9	0.8	6.0
55944 at	C. 100.17 - 1.1. 1.00.14		AW003215	4.9	1.8	2.6
55052 at	hypothetical protein FLJZ031Z		AA524056	4.9	1.2	2.8
55559 at	riypotrieticai protein FLJ11307		AI820049	4.9	2	1.6
50515 at	DAD Sh protein		AA524361	4.9	4.8	3.6
23310 f at	manora pintelli		AI458521	4.9	3.5	2
00013 - at			AI075909	4.9	1.1	3.4
20121	- 1		R42423	4.9	2.9	α.
39131_41	SWI/ SINF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	SMARCA5	N36842	6.4	3.2	4.2
34406_at	KIAA0602 protein		AB011174	0	,	
34864_at	hypothetical protein		AE070620		7.7	4.6
31722_at	ribosomal protein L3	0 100	000000		0.0	5.6
36628 at		N LS	ALUZZ320		y.	6
56546 at	KIAA1545 protein	KALBFI	L42542		2	4.3
53884 at			H17730	4.9	5.9	5.8
43306 at			AA312905	4.9	3.9	4.7
43038 r at	KIAA1363 protein		AA126841	4.9	2.3	5.6
43053 g at			AI769531	4.9	9.0	5.1
49488 at	DKF7P434F1735 protein		AW025012	4.9	3.2	4.6
65501 s at			AW005775	4.9	3.5	2
51239 at	hynothetical protein El 193930		Ai810687	4.9	2.7	5.3
49633 at	hypothetical protein FESS		W67828	4.9	3.8	4.4
54878 at	=		N21131	4.9	4.9	4.8
31895 at	BTR and CNC homology 1 hogis languages		AL048421	4.9	3.8	4.8
	or and cromoving to basic redcine zipper transcription factor 1	BACH1	AB002803	4.8	1.3	2
1711_at	tumor protein p53-binding protein, 1	TP53BP1	U09477	4.8	3.1	4 1

Figure 11AAAA

78-0+0-20	Albort syndrone, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene I	AMMECR1	AJ007014	8.4	1:1	8
39302_at	desmocollin 2	DSC2	X56807	4 8	C	00
33894_at	neuroepithelial cell transforming gene 1	NET1	1		0.0	2.2
35145_at	MAX binding protein	MNT	X96401	4 8	7	
39604_at	pleckstrin homology, Sec7 and coiled/coil domains, binding protein	PSCDBP	1	8.4	2.4	2.2
36971_at	KIAA0257 protein		DR7446	a v		
35675_at	vinexin beta (SH3-containing adaptor molecule.1)		AF037261		4.0	0
35303_at	insulin induced gene 1	INSIG1	1196876	ν ν	7 0	0.7
35838_at	clones 23667 and 23775 zinc finger protein		(190919		0.7	
32530_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	YWHAQ	X56468		2.9	7.4
37358_at	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	UBE2E1	AI039880	4.8	1.7	4.6
231_at	transglutaminase 2 (C polypeptide, protein glutamine gamma. glutamyltransferase)	TGM2	M55153	4.8	2.5	0
39182_at	epithelial membrane protein 3	EMP3	U87947	4.8	o c	
/562/_at			AA703201	4.8	4	
52929 at			AL044396	4.8	1.5	4.6
50829 at			AA706818	8.4	10.8	10.5
80166 2t	UNTZF/Z/GUSI protein		AA203321	4.8	0.8	1.6
09100 at			AI953998	4.8	4.6	0.7
51628 at			AI377910	4.8	9.0	0.4
21020 at			AA009692	4.8	2.8	
85530 at			R64696	4.8	3.2	
63817 at	OKEZDA3AB303 protoip		AI732798	4.8	0.5	1.4
58026 r at			AA099904	4.8	2.6	6.3
73656 1 24	riypouleucal protein		AI979070	4.8	1.1	3.3
64152 at			AI719644	4.8	1.2	6.1
50608 at			AA703523	4.8	0	0.4
75080 at			H11817	4.8	0.1	9.2
18635 r at			A1333655	4.8	0	0.3
10000 at			T95654	4.8	2.1	2.6
อรบบา สเ		•	1031501	0 /	,	

Figure 11BBBB

50134_at		,	R66534	8.4	1.5	5.8
73439_at	hypothetical protein MGC3156		AA349855	4.8	2	2.8
63373_at			AA194033	4.8	4.8	2.2
73574_at			AI290214	4.8	3.7	8.1
64577_at			H60064	4.8	2.1	2.9
44066_s_at	G protein coupled receptor kinase interactor 1	GIT1	AI887641	4.8	2.8	5.5
53546_at			AI168683	4.8	3.7	6.7
62165_at	x 006 protein		W72231	4.8	3.2	5.9
45580_s_at			A1983200	4.8	3.6	1.8
53680_at			AI130786	4.8	0	1.3
51813_at			AI797095	4.8	7.1	1.8
46237_at			AW001342	4.8	2.5	6.7
58682_at	DEAD/H (Asp.Glu-Ala-Asp/His) box binding protein 1	Idaxaa	AI348378	4.8	6.2	Ō
52347_at	CGI-60 protein		AI985204	8.4	0.3	1.4
54989_at			H43374	4.8	4.9	1.2
51697_r_at			AA649308	4.8	m	4
55601_at			AI742770	4.8	2.9	0
47608_at			AI697401	4.8	1.1	1.2
47330 at			W81697	4.8	1.5	9.3
70054_i_at			T99829	4.8	1.7	3.5
73569 r_at			AI708856	4.8	6.0	2.7
75232_at			N31820	4.8	1.1	1.3
80059_at			H79244	4.8	1.1	3.4
84212_i_at			AI203819	4.8	0	2.6
38716_at		CAMKK2	AB018330	4.8	0	2.4
41603_at	transducin (beta)-like 3	TBL3	002609	4.8	3.8	5
39866_at	ubiquitin specific protease 22	USP22	AB028986	4.8	2.6	5.9
40113_at	GS3955 protein		D87119	4.8	3.1	4.1
40824_at	RAN binding protein 16	RANBP16	AB018288	8.4	2.5	5.3
38943_at	holocytochrome c synthase (cytochrome c heme-lyase)	SOOH	U36787	4.8	2.9	4.4
38733_at	X-ray repair complementing defective repair in Chinese hamster cells 5	XRCC5	M30938	4.8	1	4.3
	(double-strand-break rejoining; Ku autoantigen, 80kD)					
33198_at	binder of Arl Two		AA206524	4.8	2.3	6.8
56520_at	Inudix (nucleoside diphosphate linked moiety X)-type motif 5	NUDTS	AI188576	4.8	3.3	4.3
45307 at			AI921204	4.8	1.6	5.9

50244_at	nucleotide binding protein 2 (E.coli MinD like)	NUBP2	AA552351	4.8	7.0	V 3
45878_at			1	4 8	0.0	1.0
39971_at	lymphoblastic leukemia derived sequence 1	LYL1	M22637	2 4	0 0	t
38612_at	tetraspan 3		M69023	4.7		1 0
38630_at	_		AI 080192	4.7		0.0
39486 s at	KIAA1237 protein		W28968	47	5 -	0.1
1713_s_at	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	丄	4.7	0	5.6
39410_at	development and differentiation enhancing factor 2	DDEED	02070004	1	C	
40202_at		RTFR		4.7	0.7	9.1
40064_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3	ALS2CR3	⋖	4.7	0.8	1.5
40470_at	oxoglutarate dehydrogenase (lipoamide)	HOBO	D10523	- V	9 0	
32820_at	CCR4-NOT transcription complex, subunit 4	CNOTA		1	3.0	0.0
39310_at		COONIC	\perp	1,1	4	10.4
610_at	adrenergic, beta-2, receptor, surface	ADRR2	M15169	4.7	0.0	4.6
33492_at			L	1 1	50.	7
35285_at	solute carrier family 4, sodium bicarbonate cotransporter, member 4	SLC4A4	1	4.7	0.1	1.8
40310_at	toll-like receptor 2	CA IT	AF051152	1	i.	
35190_at	KIAA0469 gene product	KIAAAAG	┸	† \	3.5	0
37977_at	KiAA1528 protein	Cotovali	┸	4.7	1.3	2
39141_at	ATP-binding cassette, sub-family F (GCN20), member 1	000	A1138834	4.7	2.4	0.4
467_at	osteoclast stimulating factor 1	ABCFI	AFUZ/30Z	4.7	4.1	0
42270 at		11.00	U63/1/	4./	2.5	0
56991_at			W24320	4.7	1.5	6.1
57016_at	hypothetical protein FLJ11264		A1927139	4./		6.5
52287 at	long-chain fatty acid coenzyme A ligase E		A1032513	4./	6.4	10
76152 s at			AA514342	4.7	0.8	0
81262 at			A1634548	4.7	0	0.7
89955 at			AI280818	4.7	9.0	0.2
66849 at			AW020975	4.7	-	0
58452 at	O monitor bateinosse magas		1	4.7	1.4	1.8
75150 at	שמיניון שמינים מוווצפון א	SPAG9	AL079765	4.7	2.4	11.1
7 JI JU al			A1631846	4.7	3.8	1.1
63391_at			A1638800	4.7		α

Figure 11DDDD

t t translocase of inner mitochondrial membrane 10 (yeast) homolog t translocase of inner mitochondrial membrane 10 (yeast) homolog t translocase of inner mitochondrial membrane 10 (yeast) homolog translocase of inner m							
A A A A A A A A A A		hynothetical protein FLJ22995		D20046	4.7	10.6	2.9
A A A A A A A A A A	<u> </u>			41962194	4.7	3.1	4.8
A A A A A A A A A A	٠ ١ ,	sitative brain professivaterd protein		41792919	4.7	1.3	5.5
A A A A A A A A A A	I '	התימווגב הומוו וותכוכתו לימו פריכה הוכנים		4L048402	4.7	3.1	1.6
at	0/039 at		1	4A436007	4.7	4.7	3.1
at at A A A A A A A A A A A A A A A A A	0/903 at			AI874267	4.7	4.2	0
at FLN29 gene product at FLN29 gene product at cytochrome c oxidase subunit Vb t t translocase of inner mitochondrial membrane 10 (yeast) homolog t t translocase of inner mitochondrial membrane 10 (yeast) homolog t CGI-99 protein t hypothetical protein	58160 at			T83663	4.7	1.6	0.5
at FLN29 gene product at FLN29 gene product t t ymphocyte-specific protein 1 t translocase of inner mitochondrial membrane 10 (yeast) homolog t t CGI-99 protein t hypothetical protein t Inymphothetical protein t t inymphocyte-specific protein 1 t translocase of inner mitochondrial membrane 10 (yeast) homolog t t inymphocyte-specific protein 1 t Inymphocyte-spec	8//8/ at		-	T69727	4.7	4.4	8.2
A A A A A A A A A A	8/8/4 at			N66563	4.7	1.5	2.3
A A A A A A A A A A	55911 r at			H68862	4.7	3.1	7.3
at at FLN29 gene product A at at at at at at at below by the strength of th	86833 r at			AA417797	4.7	3.8	6.1
A A A A A A A A A A	44202 at			AI765157	4.7	1.8	0.7
A A A A A A A A A A	12072 dt			AA894564	4.7	5	4.3
A	52204 at			AA630392	4.7	2.3	0
A	_11			AA160048	4.7	0.1	1.9
at file of the product at the file of the product at the file of the product at the file of the product at the process of inner mitochondrial membrane 10 (yeast) homolog at the protein at translocase of inner mitochondrial membrane 10 (yeast) homolog at the protein at the pro	02391 at			AA604268	4.7	3.1	2.4
at FLN29 gene product s at FLN29 gene product s at at FLN29 gene product at at Cytochrome c oxidase subunit Vb at cytochrome c oxidase	44300 at			N42884	4.7	1.2	0.3
A A A A A A A A A A	12314 at			AI762856	4.7	4.8	1.4
r at FLN29 gene product f. at FLN29 gene product at at cytochrome c oxidase subunit Vb at DKFZP56601646 protein at imphocyte-specific protein 1 at translocase of inner mitochondrial membrane 10 (yeast) homolog at cG1.99 protein at thypothetical protein at hypothetical protein	0450/ at			AL043934	4.7	0.8	0
tat FLN29 gene product at at state of the control	40010 at			N36861	4.7	2.1	5.5
at at cytochrome c oxidase subunit Vb at cytochrome c oxidase subunit Vb at cytochrome c oxidase subunit Vb at cytochrome c oxidase subunit Vb at lymphocyte-specific protein at lymphocyte-specific protein at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 at CGI-99 protein at hypothetical protein at hypothetical protein	7/680 r at	El N29 gene product		AW002527	4.7	7	6.3
at at cytochrome c oxidase subunit Vb at cytochrome c oxidase subunit Vb at cytochrome c oxidase subunit Vb at DKFZP56601646 protein at Immorphocyte-specific protein at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 at CGI-99 protein at hypothetical protein at hypothetical protein	75782 c at			N93263	4.7	3.4	0
at cytochrome c oxidase subunit Vb s. at cytochrome c oxidase subunit Vb at DKFZP56601646 protein at lymphocyte-specific protein 1 at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 at CGI-99 protein at hypothetical protein	40402 3 at			AA027059	4.7	2.2	1.7
at cytochrome c oxidase subunit Vb cox5B s. at cytochrome c oxidase subunit Vb at DKFZP56601646 protein at lymphocyte-specific protein at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 at CGI-99 protein at hypothetical protein	52670 at			AA664156	4.7	17.4	9.1
to cytochrome c oxidase subunit Vb at DKFZP56601646 protein at Iymphocyte-specific protein 1 at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 at CGI-99 protein at hypothetical protein	53676 at			AI885781	4.7	11.3	14.6
at Cytochrome c oxidase subunit Vb at DKFZP56601646 protein at Iymphocyte-specific protein 1 at translocase of inner mitochondrial membrane 10 (yeast) homolog at CGI-99 protein at hypothetical protein	32033 at			AA191495	4.7	1.4	0.5
at DKFZP56601646 protein at lymphocyte-specific protein 1 at translocase of inner mitochondrial membrane 10 (yeast) homolog at CGI-99 protein at hypothetical protein	39443 c at	loctochrome c oxidase subunit Vb	COX5B	M19961	4.7	2.3	5.7
at lymphocyte-specific protein 1 at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 at CGI-99 protein at hypothetical protein	41335 at	DKF2P56601646 protein		AL050084	4.7	2.3	3.8
at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 at CGI-99 protein at hypothetical protein	36793 at		LSPI	M33552	4.7	1.1	8.8
at translocase of inner mitochondrial membrane 10 (yeast) homolog TIMM10 at CGI-99 protein at hypothetical protein	56906 at			AA193416	4.7	4.1	4.6
at CGI-99 protein at hypothetical protein	45254 at	mitochondrial	TIMMIO	W02499	4.7	4.6	4.9
at hypothetical protein	48860 at			AI342336	4.7	2.7	6.4
at hypothetical protein	50855 at			AA789332	4.7	2.9	
	44705 at			AA133356	4.7	3.9	6.4
	47907 at			AI094180	4.7	2.2	4.5

44833 s at	44833 s at Theat shock 70kD protein 8	HSPA8	A1986374	4.7	6.0	6.7
42831_at			AI201843	4.7	4.2	4.7
45492 at			AW002385	4.7	5	4.7
44823_s_at			AA521476	4.7	4.4	4.8
43929_at			AA225263	4.7	4.6	4.4
55940_at			AI701480	4.7	2.3	3.4
47875_at			W15284	4.7	1.9	3.6
48769_at	hypothetical protein MGC4368		AL121013	4.7	3	6.1
	glutathione-S-transferase like; glutathione transferase omega		U90313	4.6	6.5	0
at	KIAA0414 protein		AB007874	4.6	2.2	4.6
39906_r_at	ADP-ribosylation factor GTPase activating protein 1	ARFGAP1	AA402332	4.6		2.7
31345_at	airway trypsin-like protease		AB002134	4.6	2.7	15.7
31916_at	killer cell lectin-like receptor subfamily A, member 1	KLRA1	AF047445	4.6	1.3	5.6
40427_at	COX17 (yeast) homolog, cytochrome c oxidase assembly protein	COX17	AA149486	4.6	2	6.0
32738_at	NADH dehydrogenase (ubiquinone) Fe.S protein 2 (49kD) (NADH. coenzyme O reductase)	NDUFS2	AF050640	4.6	1.3	0
38904_at	v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog	SRC	AF077754	4.6	1.9	12.7
33760_at	peroxisomal biogenesis factor 14	PEX14	AB017546	4.6	3.4	0.2
35166_at	Down syndrome critical region gene 3	ENOSO	D87343	4.6	7.1	5.7
40612_at			AB029040	4.6	9.9	3.6
427_f_at	interferon, alpha 10	IFNA10	V00551	4.6	0.5	25.4
35613_at			AL042599	4.6	2.9	27.9
37493_at			H04668	4.6	4.7	3.3
1860_at	tumor protein p53-binding protein, 2	TP53BP2	U58334	4.6	9.9	0.5
36889_at		FCER1G	M33195	4.6	1.2	1.8
36953_at		MADH4	U44378	4.6	3.1	3.4
37711_at	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	S57212	4.6	2.0	8.7
56131_at			A1146837	4.6	1.8	2.4
64966_at			AI668641	4.6	5.2	6.1
65518_at	RNA polymerase I transcription factor RRN3		N22730	4.6	3.9	1.6
75179_at	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	UBE2D3	R81146	4.6	4.3	2.1
90289_at			AI827330	4.6	4	0

Figure 11FFFF

73715 at			A1126206	4.6	1.9	12.3	
66690_at			Н92909	4.6	0.5	0.1	
61224_at			T71614	4.6	0	1.5	
44060 at	selenoprotein W, 1	SEPW1	AA625451	4.6	1.9	17.2	
79626 at			AA962105	4.6	2.3	0	
46457_at	splicing factor (CC1.3)		AI400626	4.6	3	1.3	
62818_at			AI202885	4.6	2	2.2	
83402_at			AA700080	4.6	3.4	3	
84383_at			AI949708	4.6	2.2	6.2	
65480_at			AA166751	4.6	4.5	1.7	
47471_at			AA916868	4.6	0.4	6.0	
44749 at			T66226	4.6	5.6	1.1	
87408_at			AI221305	4.6	0.3	3.5	
43151_at			T87150	4.6	6.0	3.7	
69446_at			AA862900	4.6	4.5	2.7	
77935_at			A1939620	4.6	2.5	3.9	
87284_at			AA044789	4.6	3.8	9.0	
42947_at			AA042952	4.6	1.3	4.3	
51074 g at			N49836	4.6	4.1	0.4	
45336_at	peflin		AL046918	4.6	2	0	
72133_at			W90634	4.6	2.1	0.3	
75525_at	KIAA0336 gene product		R34331	4.6	6.7	2.1	
82032_at			AI823999	4.6	5.2	3.5	
44643_at			AI633734	4.6	0	0	
42630_r_at	hypothetical protein FLJ13220		H88129	4.6	2.8	2.9	
81769_at	heparan sulfate (glucosamine) 3.0 sulfotransferase 3A1	HS3ST3A1	N71828	4.6	3.3	2.2	
46112_r_at			AI700523	4.6	2	0	
55264_at	hypothetical protein SBBI67		W79937	4.6	0.5	0	
62477_at	squamous cell carcinoma antigen recognized by T cell		W81246	4.6	1.3	0	
47359_at			AA887112	4.6	0	6.0	
46211_at	hypothetical protein dJ1141E15.2		AI190033	4.6	2.6	1.6	
80778_at			AA179496	4.6	0	0.1	
55362_at			AI653767	4.6	18.2	19.8	
43295_at			AA033783	4.6	3.3		
45914 at			H46965	4.6	0.5	2.5	

Figure 11GGGG

36444 s at	36444 s. at small inducible cytokine A5 (RANTES)	SCYAS	AF088219	4.6	3.7	4.5
41749 at	ES1 (zebrafish) protein, human homolog of	C210RF33	U53003	4.6	3	4.1
41727 at	KIAA1007 protein		AB023224	4.6	2.9	5.2
41562 at	murine leukemia viral (bmi-1) oncogene homolog	BMII	L13689	4.6	3.5	4.3
32562 at		ENG	X72012	4.6	4.7	9
38041 at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	GALNT1	U41514	4.6	3.3	3.5
l	acetylgalactosaminyltransferase 1 (GalNAc-T1)					
38789 at	transketolase (Wernicke-Korsakoff syndrome)	TKT	L12711	4.6	3.3	4.9
48810 at	hypothetical protein DKFZp761H221		AI547243	4.6	3.7	6.5
43824 at			AI952129	4.6	2.5	5.3
44632 at			AA007697	4.6	2.4	4.7
45758_at			AA034095	4.6	3	5.9
65620 at	hypothetical protein FLJ14005		W52855	4.6	4.4	4.7
50036 at			AI189011	4.6	3.9	4.4
53935 at			W74486	4.6	2.4	4
55571_at			W58459	4.6	1.5	3.1
37119 at	vesicle associated membrane protein 4	VAMP4	AL035296	4.5	2	6.0
34530_at			W73822	4.5	7.6	1.2
33019_at	Parkinson disease (autosomal recessive, juvenile) 2, parkin	PARKZ	AB009973	4.5	2.3	10.5
33283_at	arrestin, beta 2	ARRB2	AF106941	4.5	0.8	0
31524 f at	H2B histone family, member K	H2BFK	280782	4.5	1.4	7.4
33665_s_at	33665_s_at colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-	CSF2RA	M73832	4.5	2.3	0.4
34312 at	Independent coactivator 2	NCOA2	AI040324	4.5	m	7.6
33773_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila)		1_	4.5	0	2.6
l 	homolog); translocated to, 10					
33504_at	neurexophilin 2	NXPH2	AF043467	4.5	1.4	0.8
37828 at	hypothetical protein FLJ11220		AL050064	4.5	1.2	4.4
36703 at	small inducible cytokine subfamily A (Cys-Cys), member 25	SCYA25	L-	4.5	1	2.9
36452_at	synaptopodin		AB028952	4.5	1.6	3.6
35826_at	suppressor of Ty (S.cerevisiae) 5 homolog	SUPT5H	AF040253	4.5	3.1	3.6
36897_at	KIAA0027 protein		D25217	4.5	1	1.3
37941_at	myosin-binding protein C, fast-type	MYBPC2		4.5	1.3	6.7
38355_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome	DBY	AF000984	4.5	2.3	0.7
56367 at			AI630997	4.5	1.8	1.1

Figure 11HHHH

65139 at	hypothetical protein FLJ12150		A1925240	4.5	8.6	0.8
			AA764974	4.5	1.4	0.5
76356 at			AA203497	4.5	1.6	1.6
59043 at			AI243147	4.5	0	0.4
82499 at			AI925051	4.5	1.1	0
56803 at	wingless type MMTV integration site family, member 5A	WNT5A	AI968085	4.5	1.3	0
67164 at			AI367020	4.5	2.1	0.1
65478 at			AI744031	4.5	3.9	1.2
43273 at			AI655806	4.5	0.8	1.4
68245 at			H48278	4.5	2.5	1.7
79480 i at			N49201	4.5	1.7	1.7
J 10	hypothetical protein FLJ12701		AI338045	4.5	2.5	1.4
49469 at			AI871490	4.5	1.4	1.4
73771 at			AI632232	4.5	2.5	3.7
57270 f at	glutaminase	GLS	AI968420	4.5	4.8	0.3
86475 f at			AI337926	4.5	3.1	3.1
63849 at	karyopherin beta 2b, transportin		AI885873	4.5	0	9.0
86015 at			AI652445	4.5	0.6	0.4
87673 at			A1982610	4.5	9.0	0.2
84407 r at			AI032906	4.5	9.0	1
85125 g at			A1074707	4.5	2	3.6
53978 at			AW024692	4.5	1.2	11.3
45918 at			N53560	4.5	1.6	3.9
43356 s at	D-type cyclin-interacting protein 1		A1970622	4.5	1.4	0
62261 s at	LIM domains conta	LIMDI	A1933287	4.5	3.7	1.7
45661 at			N90348	4.5	5.5	6.7
60188 at			AA629050	4.5	8.1	3.1
65892 at	fatty acid binding protein 1, liver	FABP1	AA001405	4.5	2.7	0
53997 at	seven transmembrane domain orphan receptor		AA622413	4.5	1.7	0.7
54521 g at	-		AI084224	4.5	4.3	1.4
46234 at	CGI-148 protein		AA043242	4.5	4	4.9
54067 at			AI982669	4.5		0
48633_at	KIAA1254 protein		AI770067	4.5	3.3	0.7
62971 at	hypothetical protein FLJ12428		AI799804	4.5	2.9	2.3
61005 at			AA009648	4.5	3	4.1

57423 at			AA433928	4.5	0.5	0.8
87232 at			AA487296	4.5	1.2	5.3
33308 at	glucuronidase, beta	GUSB	M15182	4.5	0.8	4.8
32317 s at	sulfotransferase fa	SULT1A2	U34804	4.5	3.1	4.1
39135 at	KIAA0767 protein		AB018310	4.5	3.7	4.3
47714 at			AA018412	4.5	2.4	2.7
33689 s at	D-dopachrome tautomerase	TOO	AF012434	4.5	1.8	4.7
55301 at			AI634118	4.5	2.6	4.3
			AA419263	4.5	3.9	4.1
58468 at			C17704	4.5	4.5	4.3
58647 at	glutathione S-transferase M1	GSTM1	AA203289	4.5	3	3.2
46594 at	hypothetical protein FLJ20186		AW014780	4.5	4.3	4.6
44079 at	general transcription factor IIIA	GTF3A	AA166851	4.5	3.9	4.9
43485 s at			AI633875	4.5	2.9	3.
47104 at			AI760368	4.5	3.4	4
47561 at			AA877614	4.5	3.5	5.7
39385_at) aminopeptidase (aminopeptidase N,	ANPEP	M22324	4.4	3.5	0.1
	ᅴ					
36347_f_at	H2B histone family, member D	H2BFD	AA873858	4.4	1.4	6.4
40407 at	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	KPNA2	U28386	4.4	2	2
31342_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	GALNT2	X85019	4.4	1.3	3.9
	acetylgalactosaminyltransferase 2 (GalNAc-T2)					
32635_at	transcriptional intermediary factor 1 gamma		AB029036	4.4	3.7	6.1
32693_at	KIAA1040 protein		AB028963	4.4	0.7	13.5
33219_at	KIAA1097 protein		AB029020	4.4	3.7	1.7
41770_at	monoamine oxidase A	MAOA	AA420624	4.4	0	0
34655_at	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member	MPP2	AI951832	4.4	0.5	10.4
	2)					
38982_at	TRF2-interacting telomeric RAP1 protein		W28865	4.4	1.6	4.3
35213_at	WW domain binding protein 4 (formin binding protein 21)	WBP4	AF071185	4.4	1.9	2.6
41584_at	nudix (nucleoside diphosphate linked moiety X) type motif 3	NUDT3	AF062529	4.4	0.9	6.4
35007_at			AC004940	4.4	0.5	0.8
37403_at	annexin A1	ANXA1	X05908	4.4	2.6	4.1
37088 at	serine/threonine kinase 13 (aurora/IPL1·like)	STK13	AF059681	4.4	2.6	3.9
56940 g at	т		A1963304	4.4	3.6	4.3

Figure 11JJJJ

48118 at	CGI-97 protein	AA044743		4.4		1.8
56456 at	hypothetical protein dJ1181N3.1	AI63292	56	4.4	2.2	9.0
81567 at		A1190905)5	4.4	1.7	6.0
47459 at		AI290653	53	4.4	2.3	4.1
76717 at		AI375865	55	4.4	0.5	3.3
		AA285069	69	4.4	2.7	9
64991 at		AI762686	36	4.4	0	0
ч _	nuclear factor (erythroid-derived 2)-like 2	NFE2L2 AW023229	29	4.4	2.7	2.9
82372 at		AA907150	50	4.4	6.0	0.9
84765 at		AI446030	30	4.4	7.1	1.9
49312 at	CGI:102 protein	AA747303	03	4.4	3.2	7.4
63398 at	similar to Bos taurus P14 protein	AA130220	20	4.4	6.9	2.1
67890 at		AI613399	66	4.4	3.2	1.3
87942 at		AA936705	05	4.4	2.7	1.6
45280 at	hypothetical protein DKFZp566G1424	AA703316	16	4.4	1.5	1.1
47565_at	myeloid/lymphoid or mixed lineage leukemia (trithorax (Drosophila)	MLL W55861	11	4.4	1.4	2.9
	homolog)					ľ
70379 at		AI744361	61	4.4	1.2	0.0
44328 at	hypothetical protein MGC5487	AA905113	13	4.4	2	6.1
62495 f at		A1433785	85	4.4	17.4	28.1
43367 at	hypothetical protein FLJ20730	A1979164	64	4.4		0.4
43489 at	hairy/enhancer.of-split related with YRPW motif-like	HEYL ALO40197	97	4.4	3.2	5.1
43931 at	hypothetical protein FLJ11269	A1741524	24	4.4	1.9	6.3
56384 i at		R17914	14	4.4	1.3	0.5
48696 at		H48142	12	4.4	0	0
56264 at		AA703335	335	4.4		2.9
89969 at	ribosomal protein S15a	RPS15A AW003898	398	4.4	2.9	0
83888 r_at		AI031837	337	4.4	0	0.8
72475 r at		AA063087	787	4.4	0.2	1.2
72928 at	•	AI638648	548	4.4	1.9	Ĉ
45876 at		AA536137	137	4.4	9.0	2.1
60537_at		AL038866	366	4.4	1.3	0.3
60124_at		H61529	29	4.4	3.1	3.6
74302 at		AA028209	509	4.4	1	2.6
41928_at		AA029647	647	4.4	3.2	1:0

/8/90_1_at	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	ITGAE	AI735664	4,4	2	2.9
42048_at			AA897644	4 4	2.5	37.2
48992_at			AA435933			6.4
77840_f_at			AI720888		8.1	16.6
			AF052185		3.3	4.3
33601_at			AF052145	4.4	2.2	3.1
41213_at	peroxiredoxin 1	PRDX1	X67951	4.4	2	5.1
34764_at	leucyl-tRNA synthetase, mitochondrial		D21851		1.4	38
33916_at	imidazoline receptor candidate		AB023192		8 %	3.6
	KIAA0911 protein		AB020718		2.4	3.6
	histone deacetylase 2	HDAC2	U31814	4.4	2	4.7
	acidic protein rich in leucines		Y07969	4.4	2.9	5 1
37967_at	lymphocyte antigen 117	LY117	AF000424	4.4	1.8	4.4
65144_at			AA625373	4.4	4.7	4.9
43406_s_at	ZAP3 protein		AA890650	4.4	3.1	4.5
44297_at			AA613167	4.4	4	4.3
48094_at			AA531025	4.4	3.8	4.1
44085_at			AL040188	4.4	4	4.6
52479_r_at			AI888055	4.4	0.8	4.9
7	- 1		AA524968	4.4	3.9	4 4
<u>, </u>	ribosomal protein, large, P0	RPLPO	AA588862	4.4	4.1	7.9
1			AL049228	4.3	2.7	7.2
$\overline{}$	mpera	BN51T	M17754	4.3	1.6	5.8
#	A kinase (PRKA) anchor protein 7	AKAP7	AF047715	4.3	0.7	5.2
\exists	zinc tinger protein 173	ZNF173	009825	4.3	2	16.9
	zinc finger protein 267	ZNF267	X78925	4.3	2.9	3.9
1448_at	proteasome (prosome, macropain) subunit, alpha type, 3	PSMA3	D00762	4.3		5.6
_	killer cell lectin-like receptor subfamily B, member 1	KLRB1	U11276	4.3	0.8	4.5
ä	ein FLJ2069		U95822	4.3	5.7	3.1
_	H2B histone family, member S	HZBFS	AJ223352	4.3	1.2	3.5
s at	kinectin 1 (kinesin receptor)	KTN1	D13629	4.3	1.1	0
Т	perforin 1 (pore forming protein)	PRF1	M28393	4.3	1.2	0.8
33900_at		FSTL3	U76702	4.3	0	5.7
4006_s_at	34006_s_at mitogen-activated protein kinase 8	MAPK8	L26318	4.3	0.7	9.0

Figure 11LLLL

35253_at	GRBZ-associated binding protein 2	GAB2	AB011143	4.3	1 2	
463 g at	Inuclear factor I/B	NFIB			7.7	
39975_at	KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing,		Æ	4 4 0 K	0.0	2.9
0000	pro			•	<u> </u>	r.
40332 at	7.60 protein		AF100134	0 4		i
36899_at	special AT-rich sequence binding protein 1 (binds to nuclear	10TAO	103134	0.4	7.4	5.3
	matrix/scaffold-associating DNA's)	מאומו	/87/6M	4.3	4.8	6.6
37188_at	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	DOKA	002000	(
36989_at	dystroglycan 1 (dystrophin-associated plyconrotein 1)	CAS			5.2	0
38796 at	Complement component 1 a subcomponent heta polypeptide	DAGI	-			1.9
56837 at	globotriaosylceramide/CD77 synthase. Gh3/CD77 synthage: 1	A) IO	- 1	4.3	3.9	0
	galactosyltransferase; 4-N-acety/glucosaminyltransferase		AA769110	4 ω	1.4	0.4
56927_at			00000			
91181 at	Iuncharacterized hematonoletic stem/progenitor polity and a supplied to the su		W49628	4.3	4.5	7.8
	MDS031		AW044698	4.3	0	0
57414_at			00,000			
58260 at			AA8/8480	4.3	1.3	3
87639 at	Bulkaryotic translation initiation factor of 1		AA806364	4.3	2	4.5
89954 at	Cysteinyl-tRNA synthetase	EIF2C1	_1	4.3	3.1	0.4
49278 p at	C THE THE PARTY OF	CARS		4.3	2.7	1.8
			AA534436	4.3	6.0	1.9
80554 s at			AI032972	4.3	0	0
85293 at			AW004040	4.3	6.0	0
90699 at			AI468014	4.3	0	0
43708 at			AA434032	4.3	2.5	0.4
68195 at			R10307	4.3	0	4.1
68496 at			AI627334	4.3	6.0	25
86306 r at			AI653006	4.3	1.3	i e
70302 at			AI656897	4.3	1.5	2.2
56319 at	Cofactor required for Coll transmisting		~	4.3	1.6	0.3
1B_C100	coración required for opt transcriptional activation, subunit 6 (77kD)	CRSP6	C05931	4.3	2.7	4.8
49539 at	tryptophanyl tRNA synthetase 2 (mitochondrial)	WARSZ	R40635	4 3	1 7	
44077 at			AA524061	4.3	1 -	
65484_t_at	Iglutaminase	6.5		4 3	5.0	

Figure 11MMMM

Titie: Response of Dendritic Cells to a... Inventors: Nir Hacohen, *et al.*

56299_at			AI004324	4.3	1.5	0
43246_at			N66550	4.3	0	1.3
61207_at			N54899	4.3	3.4	9.7
79246_at			AW008270	4.3	1.2	0
63800_at			AA195158	4.3	2.9	3.3
55443_at			AA631027	4.3	1.7	4.2
65846_at			A1268230	4.3	1.8	0
55431_at	KIAA0986 protein		AI218624	4.3	0.4	1.3
64466_at	RNA binding motif protein 7	RBM7	A1990688	4.3	2.5	3.7
55361_at			AI821565	4.3	6.5	8.3
84659_at			A1658664	4.3	0.8	4.4
912_s_at	phospholipase A2, group IB (pancreas)	PLA2G1B	M21056	4.3	0.2	2.3
38935_at			X72790	4.3	2.3	14.1
87358_i_at			AA226717	4.3	2.9	0.7
89544_r_at			171320	4.3	1.7	1.3
32116_at	expressed in activated T/LAK lymphocytes		AB002405	4.3	1.1	5.3
40848 g at	40848 g at KIAA0750 gene product		AB018293	4.3	4.2	4
35199_at	KIAA0982 protein		AB023199	4.3	2.7	4.4
33920_at	diaphanous (Drosophila, homolog) 1	DIAPHI	AF051782	4.3	3.2	3.8
36185_at	alanyi-tRNA synthetase	AARS	ĺ	4.3	1.3	3.7
38424_at	KIAA0747 protein		⋖	4.3	2.9	4
210_at	phospholipase C, beta 2	PLCB2	M95678	4.3	3.7	3.6
64269_at			AW023766	4.3	9	8.5
59411_at			AA130954	4.3	1.4	2.5
51983 at			C00851	4.3	4.3	3.8
53906_at	differentially expressed in FDCP (mouse homolog) 6	9J3O		4.3	4.3	4.3
59761 r at			AA648933	4.3	4.2	3.9
44127_at			AA604375	4.3	2.8	9.9
46236_at	gap junction protein, beta 2, 26kD (connexin 26)	GJB2	AA442698	4.3	0.7	5.3
46572_at			AI924230	4.3	2.3	4.2
65930_at	30S ribosomal protein S7 homolog		N78337	4.3	2.5	4.4
54158_at			AI453531	4.3	2.8	4.6
45115_at			AA909042	4.3	4.2	4.5
54969_at			AI829724	4.3	3.5	4
42700 i_at			T86284	4.2	6.0	0.5

Figure 11NNNN

35076_at	mitercenular agnesion molecule 4, Landsteiner-Wiener blood group	ICAM4	X93093	4.2	6.0	2.8
1532 g at			1150535	0 1	C	-
39386_at	gene predicted from cDNA with a complete coding sequence		D14811		7.1	9.1
31889_at		MLANA	106452	200	/: 1	10.0
32053_at	cyclin T2	CUL	AF048731	2.4	200	12.0
1638_at	ets variant gene 6 (TEL oncogene)	FTVE	L	4:5	<u>n</u>	9.6
2050_s_at	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP	PAC1		7.4	0 0	1.6
	binding protein Rac1)		0 /06 7 10	4. 7.	<u>ب</u> نر	1.2
40874_at	endothelial differentiation-related factor 1	FDF1	A 1005259	0 4	-	1
35480_at	D.aspartate oxidase	000	L	7.7	0 1	2.7
38571_at	FGFR1 oncogene partner		L	4.6	0.0	5.8
41189_at		TNEDCE12	┙	4.4	5.4	0
	chain association membrane protein)	77 100 111		4 Z:	2.3	0.5
338_at	activating transcription factor 6	ATER	AE005007			
40555 at	phosphatidylinositol glycan, class F	PIGE		4.4	4:1	0.1
40813 at	solute carrier family 5 (inosital transporters) member 3	2 2	ᆚ.		5.4	0.2
35245 at	V (proaccelerin Jahila fact	SLC5A3	1		1.6	0
39684 at		5	- 1	4.2	0	0.4
; ; ;	(3)	MPP3	U37707	4.2	0.5	8.6
36486_at	KIAA0805 protein		0,00,000			
36171 at	activated RNA polymerase II transcription cofactor A		AB018348	4.2	1.4	1.9
1. ^	anshorter similar to C		AI521453	4.2	5.8	2.7
58842 at			AJ005866	4.2	0.5	0.5
54971 at	1		AI084071	4.2	3.1	0.3
	e definer of 184, receptor, transporter, alpha	FCGRT	AW024627	4.2	2	1.4
;	Linear Compliant Compliant		AA422178	4.2	2.8	3.2
+ c	acytrodencymie w oxidase 3, pristanoyi	ACOX3	A1992213	4.2	4.5	0
61067 r 2t	Sympaxii 10		AI290467	4.2	3.4	C
42720 ct			AA470798	4.2	3.7	6.4
42/39 at			190760	4.2	2.3	11
44010 at	M continuous		238762	4.2	1.2	4.7
75764 at	כפו המעלה בלו וותפסב ואו	CPM	- 1	4.2	2.5	1.8
62602 at			AA808948	4.2	2	0.4
62147 at	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		AA418402	4.2	3.5	0
0214/_al	Inypotnetical protein FLJ11155		A1265860	4.2	\ \ \ \	15

89381 r at			TOUCEA	C V	ď	0
85343 at			A107004		7.7	2.1
59089 21	hydroxycteroid (17 beta) dehydrossesses 7		MIO/0039	7:4	0.4	TI
1 401	1. Deta) deligal oggilase	HSDI/B/	AA811920	4.2	1.6	0
21401_at			AA780679	4.2	2.2	2.2
56231_at			AA151678	4.2		0.0
88436_at	hypothetical protein MGC4827		AI655261	4.2	6.0	2.1
73576 at			AI088029	4.2	0.3	C
914/4 at	hypothetical protein FLJ10339		177538	4.2	0.8	C
71341 r at			AI914025	4.2	1 9	17
10	TANK-binding kinase 1	TBK1	N20936	4.2	2.2	
80118 i_at			AI864659	4.2		22
50338 g at	KIAA1594 protein		AA197062	4.2	1.6	1.3
49211_s_at	49211_s_at hypothetical protein FLJ10826		AI817242	4.2	2.8	Ċ
4544 / at			R54026	4.2	4.4	5
63369_at			AI830095	4.2	0.7	0.4
54267_at			AA209471	4.2	3.6	5.6
54214_at			AI936575		26	2.5
75192_at	restin (Reed-Steinberg cell-expressed intermediate filament associated protein)	RSN	AW008377	4.2	4.3	0.2
49598_at			H79016	0 4	c	
46410_at	RAB9-like protein		N21460		2.1	4 L
45030_at			AA532743	7.7	0.0	3.6
53933_at			A1525910	1 4.6	0 0	n
47845 at			A1142061	4.6	5 .	0.3
76832_at	hypothetical protein FLJ10707		AI052775	1 4.2	7.0	7 4
48245_at			AA180163	4.4	0.7	0.1
54604_at	hyaluronan synthase 3	HAS3	A1338972	4.2	2.00	7.5
48315 at			AA286940	4	4 9	, r
55406_at			W25528	4.2	0	0.0
42162_at			T54906	4.2	3.5	7.2
60690_at			AA203328	4.2	4 4	7.2
			T88970	4.2	1.0	4.6
54157 at			3155163	4.2	1 9	7
69571_at			AI075770	4.2	2.2	1 0
78732_f_at			A1094933	4.2	6 9	10.01

Figure 11PPPP

79773_at			AI685649	4.2	1.4	0.7
87057_i_at			R07361	4.2	1.3	1.5
32237_at	KiAA0265 protein		D87454	4.2	2.8	4.8
1675_at	RAS p21 protein activator (GTPase activating protein) 1	RASA1	M23379	4.2	2.1	3.8
38483_at	hypothetical protein		AJ011916	4.2	1.5	6.5
39561_at	dynein, axonemal, light polypeptide 4	DNAL4	AL008583	4.2	1	6.8
56968_at	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)	MEF2D	AL118605	4.2	2.7	3.7
53848_at			A1422099	4.2	3.7	5.4
57066_at	hypothetical protein		AI023043	4.2	2.1	9
51713_at			AI660536	4.2	3.8	4.2
뉽	chromosome 20open reading frame 3	C200RF3	H09341	4.2	2.7	5.8
45285 at	proteasome (prosome, macropain) subunit, alpha type, 7	PSMA7	AA877820	4.2	3.4	5.1
81574_at	caspase recruitment domain protein 9		AI307612	4.2	3.6	4.2
50293_at			AI823782	4.2	4.5	4.9
49071_at			AI541411	4.2	1.4	4.2
51188 at	- 1		AA454038	4.2	3.6	4.2
61366_at	hypothetical protein MGC3731		AA700395	4.2	2	2.4
52908_at	hypothetical protein FLJ21324		AA865619	4.2	3.9	4.1
62552_at			AA287801	4.2	m	3.3
49210_s_at			AW023011	4.2	3.2	4.3
39551_at	KiAA1696 protein		29986N	4.1	2.6	2.2
31909_at	KIAA0754 protein		AB018297	4.1	2.3	2.3
2066_at	BCL2-associated X protein	BAX	L22474	4.1	4.6	8.6
32643_at	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	GBE1	ĺ	4.1	4.8	0.4
40779_at	smg GDS-ASSOCIATED PROTEIN		U59919	4.1	2.4	
41147_at			AF038186	4.1	15.4	3.6
35944_at	ring finger protein 1	RINGI	AL031228	4.1	2.5	0.2
436_at	interleukin 5 (colony-stimulating factor, eosinophil)	115	X04688	4.1	1:1	
33439_at	transcription factor 8 (represses interleukin 2 expression)	TCF8	D15050	4.1	2	8.6
39627_at	tigen 1, 162kD	EEA1	L40157	4.1	0	9.0
40615_at	eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD)	EIF3S1	AA780049	4.1	5.9	9.0
1728_at	murine leukemia viral (bmi-1) oncogene homolog	BMi1	L13689	4.1	0.4	4.4
36833_at	Bruton agammaglobulinemia tyrosine kinase	BTK	U78027	4.1	7.2	1.1

721 g at	heat shock transcription factor 4	HSF4	D87673	4.1	=	6 6
37001_at	calpain 2, (m/II) la	CAPNZ	M23254	4.1	4.8	
37669_s_at	ATPase, Na+/K+ tr	ATP1B1	016799	4.1		1.4
37640_at	hypoxanthine phos	HPRT1	M31642	4.1	5.7	0.1
37980_at	CBF1 interacting corepressor		U03644	4.1	9.1	8
38301_at	adenosine kinase	ADK	U50196	4.1	1.1	7.9
63309_at	CGI-15 protein		AI241474	4.1	0.4	4.9
58414_at	KIAA1350 protein		AI276062	4.1	2	0.9
46472_at			AI765222	4.1	1.6	3.4
43022_at	hypothetical protein FLJ22351		AA196189	4.1	2.1	4.6
50751_at			AA181800	4.1	1.6	1.2
76909_at			AI243872	4.1	m	0
77058_at			AA044778	4.1	7.5	2.8
85607_at			AI681283	4.1	3.7	0
44188_at			AI864170	4.1	2.5	0.4
91895_f_at			AI335251	4.1	6.3	3.2
78947_at			AI033572	4.1	0.8	1.2
76920_at			AA745592	4.1	3.6	4.6
79408_at			A1128226	4.1	2.1	6.0
79900_at			A1803624	4.1	0.3	1.9
80150 r at	copine VII	CPNE7	AI278055	4.1	m	2.8
81568 r at			AI356410	4.1	o	28.4
ال			AA621047	4.1	3.8	4.3
82421_i_at			AI554417	4.1	6.2	8.8
1185_at		IL3RA	D49410	4.1	3.4	0.8
64298 r at	arrestin, beta 2	ARRB2	_	4.1	0.8	0
59054_at			AA489100	4.1	6.6	4.8
8/801 at			AA604144	4.1	2.4	5.4
43566_at			AI674899	4.1	1.3	4.1
79414_at			AI435069	4.1	2.1	9.0
56226_at	_	EIF2C2	A1146465	4.1	2.4	0
32243 g at	-	CRYAB	AL038340	4.1	2.1	5.2
6/455_at	ets variant gene 2	ETV2	AI188430	4.1	1.2	2.8
59605_at			AA528070	4.1	1.2	1

Figure 11RRRR

69628 i_at			AA548333	4.1	1.6	0.3
48655_r_at			AA992185	4.1	2.4	5.5
80391_at	kinesin-like 2	KNSL2	AI953141	4.1	3.8	6.4
52656_s_at	ATP-binding cassette, sub-family A (ABC1), member 1	ABCA1	AW019972	4.1	0.7	0.7
70972_i_at			H79034	4.1	1.9	1.8
72504_at			AA702785	4.1	4	1.9
74148_at	hypothetical protein FLJ11783		AI978929	4.1	2.4	2.7
66139_at			AW051206	4.1	1.1	2.6
50359_at			AI887904	4.1	0	1.7
45730_at	hypothetical protein FLJ10290		A1086362	4.1	1.4	1.5
57599_at			AA767955	4.1	2.5	4.8
48616_at			197723	4.1	2.7	3.3
86588_r_at			AA759052	4.1	1.4	2.8
53225_at			Z41563	4.1	2.1	m
77654_r_at			177065	4.1	0.2	2.6
53332 r_at			AI261813	4.1	2.9	2.8
44652_at	hypothetical protein FLJ22313		AL048867	4.1	5.9	0
74233_i_at			AA758402	4.1	1.6	0.7
65650_at	hook2 protein		AW001108	4.1	2.1	0
62582_at			AI821408	4.1	2	6.9
46400 at			198967	4.1	1.3	1.4
45993_at			N51961	4.1	2.4	4
46122 at	NY-REN-58 antigen		W52480	4.1	0.7	0
57660 r at			R43504	4.1	3.4	5.6
51883_at	hypothetical protein		A1972120	4.1	5.3	0
62940_f_at	retinoic acid receptor responder (tazarotene induced) 1	RARRES1	AI669229	4.1	1.8	9.0
73211_at	solute carrier family 16 (monocarboxylic acid transporters), member 3	SLC16A3	AI659960	4.1	1.4	0.3
46736_at	ring finger protein 3	RNF3	AI301953	4.1		0.2
48317_at			AI703372	4.1	1.1	2.7
44884_at			AA039908	4.1	7.3	6.8
66983_at			AI023807	4.1	3.2	2.3
63885_at			AL038379	4.1	1.7	1.8
50790_at			2840225	4.1	2.8	1.7
89110 at			AA554257	4.1	2.2	0

Figure 11SSSS

70878_at			AI189108	4.1	3.7	1.8
77905_r_at			A1287423	4.1	0.5	0
41103 at	bromodomain and PHD finger containing, 1	BRPF1	M91585	4.1	3.1	3.7
288_s_at	lamin B receptor	LBR	L25931	4.1	1.5	2.5
31896_at	neuroblastoma-amplified protein		AL050281	4.1	1.5	2.7
36443_at	dynein, axonemal, heavy polypeptide 9	DNAH9	X99947	4.1	4.1	3.7
32253_at	arginine-glutamic acid dipeptide (RE) repeats	RERE	AB007927	4.1	1.9	3.4
38956_at	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase		AF052111	4.1	3.1	3.9
41342_at	RAN binding protein 1	RANBP1	D38076	4.1	3.8	4.7
38671_at	KiAA0620 protein		AB014520	4.1	4.3	5.3
41535_at	deleted in oral cancer (mouse, homolog) 1		AF006484	4.1	1.5	4.8
35331_at	catenin (cadherin-associated protein), alpha-like 1	CTNNAL1	790760	4.1	3.3	4.1
37010 at	general transcription factor IIA, 2 (12kD subunit)	GTF2A2	AI203737	4.1	3.7	4.3
37029_at	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	ATP50	X83218	4.1	2.2	4.6
	(oligomycin sensitivity conferring protein)					
48833_at	HSPC040 protein		Ai749098	4.1	3.2	4.1
50282_at	hypothetical protein FLJ10975		AA522810	4.1	2.4	4.2
66623_r_at			AA971467	4.1	3.9	2.6
44078_at			W95017	4.1	5.1	5.5
58200_at			AI818585	4.1	e	3
57045_f_at	ribosomal protein L23	RPL23	AW015905	4.1	2.5	4.3
51223_at	phosphoinositide-3-kinase, catalytic, beta polypeptide	PIK3CB	AI916796	4.1	1.8	3.7
64036_at	hypothetical protein FLJ10716		AI968206	4.1	2.2	3.5
45284_at	butyrate-induced transcript 1		AF169958	4.1	2.9	3.8
48106_at	hypothetical protein FLJ20489		H14241	4.1	3.6	3.9
45335_at	CGI-28 protein		AI037884	4.1	2.7	4.4
46242_at			AA215796	4.1	2.8	4.1
87839_at			AA860301	4.1	4.1	3.6
52841_at			AA731740	4.1	4	4
46247_at	succinate CoA ligase, GDP forming, alpha subunit	SUCLG1	AA826261	4.1	3.3	5.5
54948_at			AI684747	4.1	3.5	3.9
52856_at	potential nuclear protein C50RF5; GAP-like protein		AA430306	4.1	8.0	4.6
48731_at			AI948491	4.1	1.6	4.4
33004 g at	33004 g at NCK adaptor protein 2	NCK2	A1275502	4	0.5	0.3

Figure 11TTTT

41447_at	KIAA0990 protein	KIAA0990	AB023207	4	0.8	0.7
37484_at	integrin, alpha 1	ITGA1	X68742	4	2.3	3.4
1786_at	c-mer proto-oncogene tyrosine kinase	MERTK	U08023	4	1.4	2.6
40719_at	adenosine A2b receptor pseudogene	ADORA2BP	AL022398	4	2.9	2.3
39419 at	sperm associated antigen 9	SPAG9	AB011088	4	1.6	5.1
34933_at		PAX9	AJ238381	4	0	2.1
41860 at			AF070559	7	2.5	1.3
648_at	arginine vasopressin receptor 1B	AVPR1B	L37112	4	2.7	6.0
38201_at	branched chain aminotransferase 1, cytosolic	BCAT1	U21551	4	1.2	1.2
38512_r_at	38512_r_at ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	ELAVL3	D26158	4	1.5	5.1
40616 at	eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD)	EIF3S1	049260	4	0.7	6.3
33267_at			AF035315	4	1.5	3.9
32747_at	aldehyde dehydrogenase 2, mitochondrial	ALDH2	X05409	4	4.5	0.1
37383_f_at	major histocompatibility complex, class I, B	HLA.B	X58536	4	2.7	4.3
32324_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation	үмнав	X57346	4	1.7	6.0
	protein, beta polypeptide					
35965_at	heat shock 70kD protein 6 (HSP70B')	HSPA6	X51757	4	0	4.6
34782_at	jumonji (mouse) homolog	LML	AL021938	4	4.3	1.4
37350_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	PSMD10	AL031177	4	2.7	1.8
34823_at	peptidase	DPP4	X60708	4	0.4	9.0
1274_s_at	cell division cycle 34	CDC34	L22005	4	3.4	1.4
37328_at	pleckstrin	PLEK	X07743	4	2.8	1.9
37373_at	UDP glucose pyrophosphorylase 2	UGP2	U27460	4	1.6	0.2
38341_at	staufen (Drosophila, RNA-binding protein) homolog 2	STAU2	AL079286	4	2.5	6.2
75498_at			AA868356	4	1.2	3.2
91377 g at	hypothetical protein FLJ11132		AA707653	4	3.2	0
56854 f_at			AI742034	4	0.4	0.2
90417_at	ribosomal protein S6 kinase, 90kD, polypeptide 5	RPS6KA5	AI382181	4	0	0
74763_at	cold shock domain protein A	CSDA	AI081577	4	0.5	1
76133_at			AI654230	4	1.6	0.7
76046_at			AA702810	4	2.4	0.1
82368_at	olfactory receptor, family 7, subfamily E, member 12 pseudogene	OR7E12P	AI809176	4	1.4	3.2
53732 at			AA055909	4	1.4	0.7

Figure 11UUUU

	AWC)25683	4	2.1	4.5
	AIF	83999	4	0	0.2
	AI7	99862	4	2.1	2.5
	AI9	23675	4	5.6	2.2
	A!7	61622	4	3.1	7
	AI9	39511	4	2.1	1.2
	AI9	85614	4	2	4.3
	AI1	90864	4	2.2	2.8
	AAC	127103	4	0	2.6
	AAS	70454	4	3.7	4.7
	- RC	2815	4	0.3	2.3
	AWC	123438	4	0.5	0.3
	AI6	55284	4	1	2.3
transmembrane protein vezatin; hypothetical protein DKFZp761C241	A18	.05297	4	2.2	0
KIAA1376 protein	M	56118	4	2	17.8
inc finger protein	AI7	83578	4	1.2	4.6
	AIZ	16606	4	2	0.5
	2	3916	4	1.2	2
	Ï	52268	4	0.2	0.8
	AI7	68785	4	1.6	0
	R	12560	4	1	0
	AIZ	91705	4	3.1	3.4
hypothetical protein FLJ23112	AIS	37612	4	9.5	0
	Z	7,007	4	5.6	1.5
	AI3	193573	4	0	0
hqp0256 protein	AIA	.94647	4	9.0	0
hypothetical protein FLJ20195	AIS	49010	4	3.5	8.7
	AA4	179481	4	1.5	3.8
	AA	907783	4	2.5	6.0
	AI5	963083	4	2	0.1
	AA.	147325	4	0.1	5.3
	AIS	307378	4	1.3	4.8
xylosyltransferase II	AA(043495	4	0	0
	ă.	96525	4	1.6	2.2
	transmembrane protein vezatin; hypothetical protein DkFZp761C241 KiAA1376 protein Kruppel-type zinc finger protein hypothetical protein FLJ23112 hypothetical protein FLJ20195	tein vezatin; hypothetical protein DkFZp761C241 FLJ23112 FLJ20195		AW025683 AW025683 AW025683 AW025683 AW025683 AW025675 AW023675 AW023473 AW027438 AW027438 AW023438 AW023783 AW023033 AW023033 AW02325 AW023225 AW023225 AW023225	AM025683 4

Figure 11VVVV

101/101			AAA53187	_	C	i c
46378_at			AA010567	1		0.0
43818 at	calcineurin-binding profein calcarcin. 1		7561000	4	0.3	0.9
65887 24			٦,	4	2	0.7
41057 at	nalisancei di Endoz, z	TOB2	٩	4	3.4	5
44000 -1			Z39887	4	1.1	4.8
44809 at	hypothetical protein FLJ10803		AW008368	4	9.0	0.3
25025 at			N22687	4	5.9	7.5
22383 at	4		AA454036	4	2.4	2.5
48691 at	nucleoporin p54		AL040287	4	1 7	40
42242 at			AA978128	4	1 4	0.0
75712_at			AW007237	P		2.7
86430_r_at			R09516	4	100	2 6
328/4_at	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3	ļ	4	1.9	2
41430_at	WD repeat domain 7	ZAUM	AB011112	-	-	
33857 at	D47		001113	t	7.7	3.8
20771 24	100		NZ5122	4	4	3.8
39/41_al	hydroxyacyi-coenzyme A denydrogenase/3-ketoacyi-Coenzyme A	HADHB	D16481	4	0	4.9
	tiliolase/elloyi-Coefizyme A nyaratase (trifunctional protein), beta		-	_,_	•	
Ŀ	L					
		ITGB5	M35011	4	3.7	3.5
39/94 at	ubiquitin specific protease 8	NSP8	D29956	4	2.3	3.6
40129 at		PRKDC	U47077	4	3.2	8.8
40//0 t at	heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	AB017019	4		0.00
31873_at	Rho GTPase activating protein 4	ARHGAP4	U52112	4		0.0
35170_at		MAN2C1	AF044414	4		, i
35631_at	polymerase (RNA) II (DNA directed) polypeptide H	POLR2H	U37689	4	17	0 %
343/1_at		PPP4R1	U79267	4	-	0.0
35723_at		NUDTI	D16581	4	3 1 8	
34828_at		POLRZI	AL037557	4	000	97
33569_at			D50532	4		1
36102_at		VDAC3	AF038962			1
36104_at	ubiquinol-cytochrome c reductase hinge protein	HOORH	1	+ <	200	J.C.
37307_at	guanine nucleotide binding protein (G protein), alpha inhihiting activity	CIVINO		1	4.7	4./
l	polypeptide 2	GINAIS	X04828	4	1.6	5.3
				_	_	

1665_at	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	ERCC3	M31899	4	2.4	4.3
37982_at	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	DCI	225821	4	8	3.5
63866_at	cathepsin C	CTSC	AI246687	4	-	0.0
48055_at			N66640	4	1.0	3.9
57532 at	dishevelled 2 (homologous to Drosophila dsh)	DVL2	AW016304	4	5.0	1.0
5/32/_s_at	_s_at_ribonuclease, RNase A family, k6	RNASE6	AW026402	4	2.7	7.4
50926_s_at	50926_s_at_lfatty acid hydroxylase		R54585			
58963_at	hypothetical protein FLJ10535		W74642	4	0	2 6
64410_at	KIAA1150 protein		AAR13014		t u	0.0
49061_at	inorganic pyrophosphatase		AI806119	1 <	2.0	3.0
57201_at	hypothetical protein FLJ10968		10707014	,	0.1	4.5
64486 at	hypothetical protein DKFZp7621166		A:0/0401	4		4.2
57697 at			AI341234	4	2.2	4.5
57035 24	CD74 continue (included and included and inc		AI445628	4	2.2	2.7
מלה היים	complex, class II antigen-associated)	CD74	N22918	4	3.2	3.7
31792_at	1	CAVIAA	000000		,	
31861 at	limmunoglobulin mu binding protein 2		00002181		5	1.1
33082 at		IGHMBP2	L14754	3.9	1.4	4.9
32294 9 34	Interior hormone (choriconal)	IIGA10	AF074015	3.9	1.1	8.5
44	hasis transmitting forth 2 Hill 1	LHCGR	M63108	3.9	3.2	7.5
-1 '	Dasic Hallscription (actor 3, 11Ke)	BTF3L1	M90354	3.9	0.2	
33151 of	neterogeneous nuclear ribonucleoprotein C (C1/C2)	HNRPC	M16342	3.9	2.2	0.7
3877 at	Kan Gilfrage activating protein 1	RANGAP1	X82260	3.9	2.5	0.5
23770	Zinc Higgs plotein 230	ZNF230	U95044	3.9	2	0.7
33740 at	Immor instocompatibility antigen HA-1		9Z698Q	3.9	Ø.C	
32902 at		CTH	S52028	3.9	0	7.0
32954 at	UKFZP434U193 protein		U79263	30	0.0	,:,
34/59 at			1168494	0 0	10	1 000
1070_at	general transcription factor IIB	GTF2R	M76766			23.3
34785_at	KIAA1025 protein		00000000		7.4	2.5
36737_at	crystallin, beta A4	AAGVOO	1150057		2.3	3.2
823 at	Small inducible outoking subfamily D (Ove Y3 Ove) mamber 1	#WO 1 NO	/20,600	3.5	٥	3.6
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	Smail magazine Sycamic subjecting D (Cys.Ast.Cys), Helliber 1 (fractalkine, neurotactin)	SCYDI	U84487	3.9	1:1	13.9
			_		_	

Figure 11XXXX

3/645_at	COOS antigen (pou, early 1-cell activation antigen)	7 10500	722576	0 0	00	
37912_at	TNF receptor-associated factor 4	1	0/0777		000	4.5
37962 r at	syntaxin binding protein 3	T	20200	20.0	0.7	0.5
39150 at		SIABR3 U	D83506	3.9	0.7	2.3
63313_at		+	009339	3.9	3.2	6.1
51174_at	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal	SCA7 ALC	AA418636	20.00	2.2	0.6
			76664	υ V	4.4	3.2
56399_at	PABP interacting protein 2	AIZ	AI792631	3.0		9
80913_at		AIZ	A1791953	0.00	100	0.0
75996_at		a	R18374		700	1
59520_at	MARK	AA	44126520		6.0	2.0
53790_at	actin-related protein 3-beta	AA	AA772242	0.0	1.0	
77680_at		AIA	AI809979	0.0	7.7	0.1
74525_at	enhancer of polycomb 1	71V	A1701E24	0.0	7.	3.1
50563_r_at			21034	3.3	7	3.4
61191 at		AIZ	A1224125	3.9	5.5	2.5
		AIS	A1539443	3.9	14.2	9.4
		Z	N73778	3.9	1	5.2
48956 at	hypothotical protain El 190331	AIZ	AI217733	3.9	2.9	4.1
53358 at		ż	N73934	3.9	2.6	9.9
73014 s at	RAR13 member DAS oncomes family.	┪	AI279946	3.9	0.7	1.1
90173 at		RAB13 AW(AW001549	3.9	1.4	0
83915 at		AAZ	AA203229	3.9	0.1	0.8
81889 r at		AIZ	AI703123	3.9	2.7	1.5
54633 at	hynothetical protein El 112878	AI8	AI819070	3.9	1	1.2
82223 at		AA1	AA195077	3.9	1.9	0
82481 at		A18	AI871160	3.9	2.3	3.4
		AIZ	AI243249		1.3	0
91935 at		AI1	AI148712	3.9	1.3	3.3
62334 c at		AI6	94752	3.9	2	6.0
47724 r at		15	T94015	3.9	4.8	0.8
5/8/2 24		RS	R92163	3.9	2.5	4
63069		AI7	AI758780	3.9	0.7	0
67401 at		AA5	AA521016	3.9	0.1	0
07491-41		AA8	AA872025	3.9	2.7	1.9
63094_at		R1	R10311	3.9	6.0	0.7

Figure 11YYYY

68186_at			AA465263	3.9	2.2	2.7
88152_at			AA706908	3.9	0.3	1.1
70238_at			AA521399	3.9	2.3	8.5
73171_at			AI953346	3.9	1.9	0.7
72375_at			AA316630	3.9	1.2	0
58913_at			AI916598	3.9	0.1	0
48136_at	hypothetical protein FLJ20371		AA032184	3.9	2.3	7.3
33180_at	protein phosphatase 1, regulatory (inhibitor) subunit 2	PPP1R2	U68111	3.9	2	1
58356_at			AA142978	3.9	2.3	3.8
66322_at			N95416	3.9	2.4	2.2
85177_at	H2B histone family, member R	H2BFR	AI336982	3.9	0.4	0.5
48589 s_at			N98652	3.9	0.3	1.6
65815_at	ZYG homolog		AI080334	3.9	2.1	0
84284_at			A1056418	3.9	1.6	0
64015 g at			AA130159	3.9	3.3	1.3
53485_at			A1521545	3.9	1.8	5.2
52540_at			AI467915	3.9	8. 8.	2.6
58577_at			AI392933	3.9	2.2	0
52090_at			AI198126	3.9	က	
46732_at			AA075666	3.9	9.0	0
46090_at			AA806216	3.9	0.8	4.7
55289_at			W86056	3.9	0.3	0.2
			AA630405	3.9	2.5	2.8
47371_at			AA017037	3.9	7	13
47964_at	KIAA1014 protein		A1083506	3.9	1.5	0
37929_at	immunoglobulin superfamily, member 4	IGSF4	AB017563	3.9	0.2	0.5
44058_at			W60953	3.9	2	5.2
65579_at	SH3 and PX domain containing protein SH3PX1		AA455005	3.9	1.2	0
37747_at	annexin A5	ANXA5	005770	3.9	1.5	1.8
37611_at	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	TNFRSF11B	AB008822	3.9	0	0
57717_at	CGG triplet repeat binding protein 1	CGGBP1	AA903358	3.9	1.6	6.0
49762_at			T86307	3.9	2.6	3.4
64851_at			AA399994	3.9		4.3
47614_at			AI021988	3.9	2.9	1.5

Figure 11ZZZZ

1339 s at			X14675	3.9	3.3	2
70261_at			AI808755	3.9	0.7	0
70832_at			AI739235	3.9	-1	2
75686_f_at			AI734065	3.9	5.2	8.8
78611_at			AI378890	3.9	0.8	0.4
37454_at	small inducible cytokine subfamily A (Cys-Cys), member 13	SCYA13	AJ001634	3.9	0.2	3.6
40266_at	KIAA1036 protein		AB028959	3.9	3.7	4.3
33448_at	serine protease inhibitor, Kunitz type 1	SPINT1	AB000095	3.9	2	3.9
40139_at	FK506 binding protein 12-rapamycin associated protein 1	FRAP1	996880	3.9	2.2	3.3
36610_at	KIAA0029 protein		D21852	3.9	3.7	3.7
34314_at	ribonucleotide reductase M1 polypeptide	RRM1	X59543	3.9	2.9	2.8
41504_s_at	v·maf musculoaponeurotic fibrosarcoma (avian) oncogene homolog	MAF	AF055376	3.9	3.2	4.1
35261_at	glia maturation factor, gamma	GMFG	W07033	3.9	2.6	4.3
36194_at	low density lipoprotein-related protein-associated protein 1 (alpha-2.	LRPAPI	M63959	3.9	0.5	4.5
	macroglobulin receptor associated protein 1)					
37298_at	GABA(A) receptor-associated protein	GABARAP	AF044671	3.9	1.6	7
37609_at	nucleotide binding protein 1 (E.coli MinD like)	NUBP1	U01833	3.9	0.8	3
52238_s_at		TACC3	A1990642	3.9	3.4	3.5
56821_at	-1		A1963454	3.9	4.1	4.8
43422_at	CD27-binding (Siva) protein		AW025365	3.9	3.3	4.7
65813_at	≃:	ZFP36	N32721	3.9	2.8	4.8
55718_at	hypothetical protein FLJ10890		AI494412	3.9	2.3	2.3
54662_at	ribosomal protein S9	RPS9	AA194261	3.9	3.4	3.9
54869_at			AA287799	3.9	3.7	4.4
63544_at			N33295	3.9	2.7	4.5
65761_at			AA525969	3.9	2.8	3.6
43495_at			192245	3.9	2.1	4.7
60863_s_at	hypothetical protein from EUROIMAGE 2021883		AA526910	3.9	2.8	4.3
50252 at			AA149410	3.9	2.9	3.9
88182_at			AI084454	3.9	2.6	5.8
51105_at	Rho guanine nucleotide exchange factor (GEF) 3	ARHGEF3	N57933	3.9		3.2
44343_s_at			AI074877	3.9	3.1	3.8
47634_at			AW052044	3.9	3.6	2.8
56267_at	adaptor-related protein complex 1, sigma 2 subunit	AP1S2	AP1S2 AA151802	3.9	3.2	3.7

Figure 11AAAAA

12121 dt	neat snock protein hsp/U related protein		AA742240	3.9	2.8	4
5309/_at	clone FLB5214		AA532452		26	f
5/210_at			AI862775	30	3.3	
43384_at			AWOODGO		0.00	
55564_at	spleen tyrosine kinase	SYK	1	0 0	0.7	Ö
57222_at			1		0.0	0.0
52313 at	hydroxyacyl-Coenzyme A dehydrogenese/3 ketosoyl Coenzyme &		4	3.3	5.6	3.5
	thiologise/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	НАСНА	Al972144	9.6 6.	2.4	4.6
47640_at	Nedd-4-like ubiquitin-protein ligase		0020000			
41411 at	CGI-65 protein		MI000/00	3.9	4.1	5.
	actin binding protein; macrophin (missofilament and missofilament)		A15668//	3.8	1.3	2.4
3-1	cross-linker protein)		AB007934	3.8	3.6	4.7
39809_at	HMG-box containing protein 1		AF019214	8 %	V C	C
724_at	adrenergic, beta, receptor kinase 2	ADREKO	1_	0 0	4.0	7
40094_r_at				0.0	0.0	0.5
40462 at	DKFZP727M231 protein	2	020000	3.0		
41753 at	٦.		٦,	3.8	3.3	
40932 at		ACIN4			1.5	
35408 : 21	TO VOVI A diotora variation		- 1	3.8	10.4	1
2200E c 24		ZNF44		3.8	1.5	16.8
32500 s at		TPS1	8E00EW	3.8	2.3	3.6
32809 at	thiopurine 5-methyltransterase	TPMT	AL118582	3.8	0 6	1.6
34/89_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	SERPINB6	S69272		2.1	
33541_s_at	leukocyte-associated Ig-like receptor 2	COIVI	20000100	C		
37694_at	KIAA0244 protein	71117	- 1	x) c	0 0	0
38412_at	protein phosphatase 1, regulatory (inhibitor) subunit 11	1101000	152500	0 0	3.5	
58106 at		7 7 1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	000000	3.8	1.4	1.6
66357 at			AA496024	3.8	0.3	0.5
74270 r at			AA778876	3.8	1.8	1.5
78490 34			AI733391	3.8	2.4	
61324 at	,		AA206363	3.8	2.2	1.3
01324-41	cargo serection protein (mannose o phosphate receptor binding protein)		AI636693	3.8	ĸ	3.5
82566_at			AA285320	80	c	
75243_s_at	75243_s_at basic transcription element binding protein 1	BTEB1		0 00) -	2 6

Figure 11BBBBB

91452_at			41792922	86		C
82064_at			AA552150		1.0	
91683_at			A1968374	0 0		2.4
67375_at			AI829707	2000	2.3	
49751_at			AA169778	α κ		1.6
51674_at			N28262	0 00 0 00	3.2	
78986_at	ubiquitin specific protease 25	USP25	AI092963	3.8	17	
63108 at			AI741779	3.8	3.3	
49925_at	hypothetical protein FLJ10120		AI971227	3.8	1.5	
43188_at			AI732568	3.8	1.9	
50761_at	BANP homolog, S		AI738764	3.8	6.5	111
63543_r_at	suppressor of S. cerevisiae gcr2		AI954776	3.8	3.4	00
63669 at			AI546970	3.8	2.2	
58350_at	hypothetical protein FLJ20651		AW014619	3.8	5.5	
44347_at			N53347	3.8	1.3	4
59613_r_at			H78589	88	12	i le
68675 at	ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen)	FCN3	AI652910	3.8	4.7	
43006 at			AI871342	3.8	2.1	
/3095 at			AI335277	3.8	6.0	
46196 at			AI580948	3.8	1.1	00
43049_at	hypothetical protein FLJ13433		H06431	3.8	2.9	
48150 at			R02297	3.8	1.6	3.2
65255 r at	\neg		AA393998	3.8	3.4	2.5
90207_at	HDCMA18P prote		AI968653	3.8		0.2
49/69 at	hypothetical protein FLJ13611		R61558	3.8	3.7	1.3
20316 at			A1497833	3.8	1.5	3.1
2/040 at			A1198956	3.8	2.3	
20242 at	KIAAU493 protein		AA863228	3.8	4.8	2.5
46931 at	MAA1085 protein	KIAA1085	AI692989	3.8	1.5	
65645 at	IGF-II MKNA-binding protein 2		AI675886	3.8	0	
68410 r at			T96375	3.8	3.8	4.9
80380 at			AI278983	3.8	0	
60349 at			AA921855	3.8	1.1	9.0
53056_at			N91168	3.8	2.2	
45932_at			D59841	3.8	0.8	1

Figure 11CCCCC

45191_at	protein phosphatase 1, regulatory subunit 6	PPP1R6	AI680750	3.8	80	C
51053_at			AI122787		4 8	7 7
54379 at			N56947		2 0	200
35281_at	laminin, gamma 2 (nicein (100kD), kalinin (105kD), BM600 (100kD), Herlitz iunctional enidermolysis hullosa)	LAMC2	<u> </u>			1.8
54215 at	1 0		0.0000	0		
54049_at			AA/42993	89.0	2.2	2.5
57207_at			ALOAECAI	200	5.6	Ō,
36880 at	NAD(P)H menadione oxidoreductase 2. dioxin.inducible	COCANIA	AL043041	8.0	1.2	0
62557_at	in FLJ12820	ZHOWIN	007/36	X C	0.2	2
47052_at			A1120540	20.00	4.6	0.8
74664 s_at	UBX domain-containing 1	100001	A4420248	3.8	3.1	2.2
46283 at		ODVOCT	AA430224	3.8	2.7	0.6
48318 at			AL0441/1	3.8	2.4	0
48710 at			AA872062	3.8	1.9	3.4
55660 at			AA480092	3.8	4.2	0.1
33009 at			A1266650	3.8	1.2	2.1
2007			A1992368	3.8	4.2	r.
48/b/ at	ALEXI protein		AI693923	3.8	200	16.6
65982_at	hypothetical protein		AA740774	3.8	000	17.0
52888 r at			AI923987	3.8	1 7	
7546/ at			AI917245	3.8	2.2	000
78852 at			AI076830	3.8	1.7	4.4
20526 at			AA889052	3.8	2.2	200
70550 - at			AA019714	3.8	1.5	1
41201 of	00000		AA456976	3.8	0.4	3.6
20017 c 24	_		AB002306	3.8	1.6	3.4
3301/ 3 at	pulative Caylycres		AF040105	3.8	2.3	27
170 at	incital cytochrome c reductase core protein	UQCRC1	L16842	3.8	1.7	4 1
450 c ct	incolor polypriospriate phosphatase, 145kD	INPP5D	U57650	3.8	m	m
439_s_dt	oringing integrator 1	BIN1	U68485	3.8	29	30
3 2 624_at	ceroid-lipotuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)	CLN2	AF039704			4.3
33348_at	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	TCF12	M80627	3.8	1.5	3.6
40818_at	H-2K binding factor-2		D14041	3.8	2.4	3.3

Figure 11DDDDDD

36188_at	general transcription factor IIIA	GTF3A	D32257	3.8	1 6	3.6
	ATPase, Class VI, type 11B	ATP11B	AB023173		1 2	0.0
1768_s_at	c-src tyrosine kinase	CSK	ı	38	00	1.0
36799_at	frizzled (Drosophila) homolog 2	FZD2		3.8		7.6
55755_at	growth suppressor 1		<	3.8		3.6
48066_at			AI768720	3.8		
76484_at			AA789296	38	8	
61126 at			N22262	3.8	2	0.0
6/162_r_at			AI366683	3.8	i m	m
44/12_at			AI139894	3.8		2
60046 at			AI796241	3.8		8
4409/ at	UKFZP586C1324 protein		AI928466	3.8	2	
56323_at			AI890133	3.8		3.6
63997_s_at	vacuolar protein sorting 11 (yeast homolog)	VPS11	AW007365	3.8	1.	5.1
49110 s at			T48132	3.8	2	4 3
3848/_at	KIAA0246 protein		D87433	3.8	8	
44569 at			AA961420	3.8	3.6	
54/65 at	xeroderma pigmentosum, complementation group C	XPC	,	3.8	28	4.2
46132_at			AA210738			2.5
46569_at			AA552976		200	0.0
49197_at	solute carrier family 16 (monocarboxylic acid transporters), member 1	SLC16A1	Al129459	3.8		2.7
56980_at	hypothetical protein FLJ23309		AI762891	88	-	3.6
48952_at	hypothetical protein FLJ21634		AI985274		3.1	0.0
38697_at	DKFZP566C243 protein		AL050274		0.8	100
40/00 at			036500	3.7	13.3	10
37468_at	Janus kinase 2 (a protein tyrosine kinase)	JAK2	AF058925	3.7		3.1
3904/ at			AB020880	3.7	3.4	
39856 at	ribosomal protein L36a	RPL36A	Ai708983	3.7		
41853 at	rophosphate synthe	PRPSAP2	1	3.7	1.7	10
31/86 at	Samb8-like phosphotyrosine protein, T.STAR			3.7	2.4	5.2
4/1 t at	tubulin, beta, 4		U47634	3.7		2
40434_at	podocalyxin-like	PODXL	U97519	3.7		149
40589_at	Syntrophin, beta 2 (dystrophin-associated protein A1, 59kD, basic	SNTB2	U40572	3.7	2.2	1.8
	component 2)					

Figure 11EEEEE

32731_at	FE65-LIKE 2		AB018247	3.7	1.7	2.2
41226_at	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1 related)	DUSP3	L05147	3.7	1.9	2.2
35927_r_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	LILRBI	AF004230	3.7	1.5	2.2
39267 at	N-acety/glucosamine-phosphate mutase		AF102265	3.7	3.5	7.8
	microtubule associated protein 4	MAP4	M64571	3.7	3.5	0.4
31671_at	RNA binding motif, single stranded interacting protein 1, pseudogene	RBMS1P	D82351	3.7	4.6	3.9
36968_s_at	Opa-interacting protein 2		AL050353	3.7	1.8	1
35214_at	UDP-glucose dehydrogenase	HGDN	AF061016	3.7	2	5.6
1565_s_at	growth factor receptor bound protein 2	GRB2	M96995	3.7	3.6	1.1
39657_at	keratin 4	KRT4	X07695	3.7	0.3	3.4
34370_at	archain 1	ARCN1	X81198	3.7	2.7	3.1
36001_at	methyltransferase-like 1	METTL1	Y18643	3.7	2.5	0
35265_at	fragile X mental retardation, autosomal homolog 2	FXR2	U31501	3.7	e	0.4
41823_at	staufen (Drosophila, RNA-binding protein)	STAU	AJ132258	3.7	2.8	1
32628_at	zinc finger protein 161	ZNF161	D28118	3.7	3.5	7.2
35847_at	ubiquitin specific protease 24	USP24	AB028980	3.7	m	4.7
40390_at	serine dehydratase	SDS	J05037	3.7	5.2	16.9
37375 at	KIAA0638 protein		AB014538	3.7	1.3	2.1
38012_at	fibrillin 2 (congenital contractural arachnodactyly)	FBN2	U03272	3.7	2.4	2
37572 at	cholecystokinin	SCK	AW043690	3.7	0.7	7.1
38082_at	KIAA0650 protein		AB014550	3.7	m	12.1
840_at	zinc finger protein 220	ZNF220	U47742	3.7	2.5	2.6
37890_at	CD47 antigen (Rh-related antigen, integrin-associated signal	CD47	X69398	3.7	5.4	
56042 at	phospholipase C. heta 3. neighbor pseudogene	PI CR3NP	A1023365	7.6	2.0	000
58005 at	u		A1480253	3.7	6.7	ς,
80967 at			AA703048	3.7		ά
66231_at			AA573860	3.7	2.4	5.7
66316_at			N24645	3.7	0	3.3
52939_at			N36115	3.7	1.7	3.1
66473_at			AI677843	3.7	9.0	1.5
76576 at			AA813745	3.7	1.4	2.4

Figure 11FFFFF

58893_at			AI697856	3.7	33	2.5
78005_at			AI459248	3.7	0.8	2.7
74867_at			AI038997	3.7	4.3	c
90852_at			AI147384	3.7	6.0	2.8
90884_r_at			AA699634	3.7	2.5	2.6
82382_at			AA921947	3.7	2.5	1.7
75265_at			AI821772	3.7	0.2	0.3
51366_at			AI188748	3.7	2.5	2.5
56575_at	CGI-108 protein		AW025521	3.7	1.1	0
52074_at			AI218119	3.7	1.8	2.5
80265_at			AI420422	3.7	1.2	3.9
53351_at	epidermal growth factor receptor substrate EPS15R		AA083211	3.7	1.6	0.7
83640_at			AI948598	3.7	1	9.0
51578_at			T91195	3.7	1.1	3.6
83566_at	- 1		AI366705	3.7	2.3	1.4
54763_at	hypothetical protein FLJ20303		AL043081	3.7	2.1	0.2
64149_at			N51587	3.7	1.6	0
59084_at			AA126814	3.7	1.7	0
43173_at			AA661990	3.7	0.5	1.1
68376_at			AA927862	3.7	2.8	1.5
68146_at			AA661520	3.7	2.3	2
88280 <u>r_</u> at			AA703174	3.7	6.0	5.4
88282_at			AA765234	3.7	2	3.5
88805_at			AI761186	3.7	0.3	9.0
63554_at			N64735	3.7	1.1	1.9
70664_at			AI823511	3.7	0.9	0
72134_at			A1686860	3.7	1.6	O
89772_r_at			A1567466	3.7	9.0	1.8
49740 at	CGI-69 protein		AI279567	3.7	3.1	8.6
65839_at	PC3.96 protein		AW022836	3.7	4.4	6,3
43990_at	uncharacterized bone marrow protein BM040		AI676178	3.7	3	0.8
66026_at			H44949	3.7	3.7	0.3
42804 at			W86160	3.7	5.1	5.4
51933_at			AW023193	3.7	2	4.4
78757_at	selenoprotein X, 1	SEPX1	W92110	3.7	9	0.4

Figure 11GGGGG

1		7188/7	3.7	4.1	2
nypothetical prot	FLJ23591	R91222	3.7	2.3	00
myeloid/lymphoid	MLL3	AI640514	3.7		
	HSPCA	AA199881	3.7	, 0	0.0
at		AA205787	3.7	1 6	, ,
43492_at hypothetical protein FLJ10439		AI818133	3.7	3.9	
7		AI417988	3.7	2.4	000
ا'ہ		AI694702	3.7		2.0
53171_at		N51557	7 %	7.0	4,0
		W31963	37	1.0	2.5
		AA121481	3.7	3.1	2.2
at		AA058944	37	0.0	0.0
at PRO1073 protein		AL037363	3.7	21-	; i
56582_at cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	COX7A2	AI611424	3.7	2.6	
ч.		AI734899	3.7	5.1	16
		AW022635	3.7	1.1	0.5
0,0,0,0,0 at		AA148929	3.7	5.7	4.9
100		N98235	3.7	4	5.4
43301.5 at sylucted 1	SDC1	AI972735	3.7	5.1	0
to 1.0102		AI123757	3.7	2.4	14.7
57305 g at		AI824210	3.7	9.0	2.4
33186 jat		AI768674	3.7	1.4	2
		AL046961	3.7	0.1	3.2
41758 at Chromosome 22 once reading fearer		Ai499298	3.7	0.7	4.1
Cyclin, dependent	C220RF5	AL096879	3.7	2	3
bladder cancer as	_1	AF041248	3.7	2.3	9.0
DKFZP4340156 n	BLCAP	AL049288	3.7	1.8	3.2
auinoid dihydront		AA447263	3.7	1.1	4
at seven transmemb	ODPR	M16447	3.7	1.9	2.2
T		Y18007	3.7	1.5	3.9
54986 at Ihvoothetical protein MGC3103		AA582193	3.7	3.2	3.7
t high-mobility ago.		AI992073	3.7	1.3	3.4
;]	HWGIA	AW005489	3.7	0.7	4
80889_at		00600300	100		

Figure 11HHHHH

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Inventors:

60009_at			A1673085	3.7	3.5	26
54698_at			W56253	3.7	2.9	3.5
68924_at			AA969377	3.7	3.1	3.6
44646_r_at	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	EIF2S3	N38902	3.7	3.4	6.6
49591_at	hypothetical protein FLJ10504		AI888436	3.7	2.2	3.2
45607_at			AI810669	3.7		3.6
43801_f_at	mannosyl (alpha-1,3.)-glycoprotein beta-1,4.N. acetylglucosaminyltransferase, isoenzyme B	MGAT4B	1~	3.7	2.7	5.7
57195_at			A1935271	3.7	22	3.6
47390_at			AA928060	3.7	3.7	3.7
65923_at			Al344311	3.7	3.2	4.2
55653_at			AA524700	3.7	2.1	3.5
34469_at	ABO blood group (transferase A, alpha 1-3·N·	ABO	X84746	3.6	0.3	9.1
	acetyigalactosaminyltransferase; transferase B, alpha 1-3- galactosyltransferase)					
39338_at	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light nolyneptide (n.11))	S100A10	AI201310	3.6	1.2	3.2
853_at	nuclear factor (erythroid-derived 2)-like 2	NFF212	S74017	3.6	0	
31410 at	Itransmembrane activator and CAMI interactor		AE000514	5 0	6.0	7
40811 at			Ar023514			3.7
	muscle RAS opcodes homolog	O V CO	AB011148	3.6	1.7	0.4
411EE of		MKAS	Ar 043938	3.6	1.7	0.1
41155 at	caterin (cadnerin-associated protein), alpha 1 (102kD)	CTNNA1	003100	3.6	1.7	0
41/35 at	KIAAU8/U protein		AI808958	3.6	1.2	0
40930_at	\Box	SULT4A1	W25958	3.6	1.1	11.3
38900_at	paired box gene 3 (Waardenburg syndrome 1)	PAX3	002309	3.6	1.1	3.1
33//4_at	caspase 8, apoptos	CASP8	X98172	3.6	2.9	1.7
39243 s at	_	PSIP2	U94319	3.6	2.8	4.5
3439/_at			AF069250	3.6	6.0	0
641_at		PSEN1	L76517	3.6	2.1	2.2
36042_at		NTRK2	X75958	3.6	0.4	e
34846_at	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	CAMK2B	⋖	3.6	2	3.6
36711_at	V maf musculoaponeurotic fibrosarcoma (avian) oncogene family. protein F	MAFF	AL021977	3.6	2.6	Ö
895_at	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	MIF	119686	3.6	1.3	1.6
				-		

Figure 11IIIII

36906_at	cannabinoid receptor 1 (brain)	CNR1	U73304	3.6	0.4	4.6
1271_g_at	v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65))	RELA	L19067	3.6	2.9	4.5
37368_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	NFATC4	NFATC4 AA292277	3.6		6.7
37399_at	aldo keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	AKR1C3	D17793	3.6	3.5	0.1
38732_at	chloride channel, nucleotide sensitive, 1A	CLNS1A	X91788	3.6	4	0
56186_at			AA745496	3.6	2.3	2.2
42300_at			AW006996	3.6		3.6
58119_at			AA481066	3.6	1.9	3.4
50666_at			AI911873	3.6	9.0	10.7
42449_at			AA609232	3.6	2.3	1.7
76140_at			A1688663	3.6	3.3	2.9
81453_at			A1243808	3.6	9.0	1.2
61896_at			AL038511	3.6	4.4	8.7
74374_at			AA923305	3.6	1.3	1.8
74681_at			AI018220	3.6	1.4	14.5
65239_at			AI141949	3.6	4.2	0
51425_i_at			AA971774	3.6	1.5	3.1
57028_at	RAB, member of RAS oncogene family-like 2B	RABL2B	AI760941	3.6	2.8	0
59252_at			AJ230805	3.6	2.4	2.3
91502_at			AA490519	3.6	2.1	1.9
85189_at			Al 186064	3.6	2.1	1.6
48526_at	hypothetical protein FLJ10582		AI190311	3.6	4.6	1.1
63408_i_at			AA226131	3.6	2	1.3
43105_at			198171	3.6	3.7	9.5
85442_at			AI791175	3.6	1.7	1.3
87217_at			AA468768	3.6	0.7	3.8
59119_at			AL038787	3.6	0	0
68570_at			AA496390	3.6	0.3	0.2
70187_at			AL037446	3.6	2.9	1.3
71549_r_at			AA699538	3.6	2.2	5.4
44936_at			T93893	3.6	10.2	59

01270 7 01		AI887362	3.6	2.8	-
013/U [at		AA578920	3.6		
72732_s_at		07000014	0 0).	5
50237 at Ihypothetical protein FL J11109		A1990602	3.6	2.1	1.
s at BAB10 member			3.6	1.7	1.6
בסיים בייום בייום בייום בייום	RAB10	`	3.6	7.9	00
74330 at secretory carrier memorane protein 2	SCAMP2		3.6	1.3	1
05.055_at		H06408	3.6	1.3	4 4
77450 2+		AA948400	3.6	1.1	
/12/28 at		AI807366	3.6	2.1	2
85505 f at		AA565834	3.6	2.9	7.4
aiotora relociona		AA844551	3.6	6.0	1 9
T	domain) NOL3	\supseteq	3.6	1.7	0
64756 at NAG22 protein		AI890286	3.6	2.1	
		AI826107	3.6	1.2	5.4
47048 at		AI085580	3.6	E	
40305 at		AI971235	3.6	1.9	
ARREA r at fibronoctin 1		AI633514	3.6	1.9	C
7	FNI	AW021977	3.6	1.4	3.5
43383 s. at hypothetical protein El 190707		AI351368	3.6	3.6	2.2
manal managed for		AW000901	3.6	1.1	0.5
72742 at		R98495	3.6	2.4	4.2
47874 at		AA250992	3.6	3.3	3.7
53354 at		AA281757	3.6	2.5	
Alport condrama		AI668938	3.6	0	
	viasia and AMMECR1	AI032981	3.6	2.1	4.6
		H72583	3.6	7.0	
60568_at		N49962	0.00	200	1.0
		AA634254	0 0	6.0	2.3
61314_at KIAA0203 gene product		AI 043152	0.00	2.3	3.8
5181/_at		A1991014	0.00	0.0	
62456 at		AA207074	2 4	1.0	0.0
_		AA573272	3.6	7.0	2.5
7	PELO				3.9
hyl X3 at IK AA1 705 protein			2.5		?

Figure 11KKKKK

57280 f at	57280 f at Tmajor histocompatibility complex, class I, B	HLA:B	A1985880	3.6	2	7.7
91767 s at	nentidyl prolyl isomerase H (cyclophilin H)	HIdd	AA741049	3.6	6.0	3.2
63124 at			AA631399	3.6	1.7	7.8
52310 at			2969463	3.6	0.4	1.1
74606 r at			AA122219	3.6	2.4	1
75969 f at			AI985333	3.6	1	6.3
٦ [-	F.box only protein 9	FBX09	AL031178	3.6	1.6	4.5
41733 at			AC003007	3.6	2	3.9
38161 at	Not56 (D. melanogaster) like protein		Y09022	3.6	3.2	2.1
36372 at		HK3	U51333	3.6	0.7	3.6
40782 at	short-chain dehydrogenase/reductase 1		AF061741	3.6	2.3	3.2
32234 at	dystonia 1. torsion (autosomal dominant; torsin A)	DYT1	AF007871	3.6	1.6	2.1
32832 at		MAEA	AF084928	3.6	1.9	5.7
34332 at		GNPI	D31766	3.6	6.0	3.3
34826 at	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	SDHA	L21936	3.6	0.8	4.4
36482 s at	tous	ATP2A3	Y15724	3.6	2	3.5
33956 at			AB018549	3.6	0.2	3.6
36571 at	fondisomerase (DNA) II beta (180kD)	TOP2B	09089X	3.6	2.7	5.1
32578 at	MAX.like bHLHZIP protein		AW005997	3.6	0.3	3.5
38270 at	poly (ADP-ribose) glycohydrolase	PARG	AF005043	3.6	1.3	3.4
48052 at			A1936906	3.6	2.6	2.1
58206 at			W63702	3.6	3.7	2.5
47431 at			AI742206	3.6	1.5	e
57545 at			AA706499	3.6	1.7	4.9
90257 at	hypothetical protein DKFZp547D065		AI089323	3.6	2.6	3.7
58240 at	bridging integrator 2	BINZ	AI760011	3.6	1.7	2.5
62850 at			AA703170	3.6	3.3	2.7
53966 at	second mitochondria-derived activator of caspase		AF039235	3.6	0	m
59595 at			AA045175	3.6	3.2	3.2
45249 at			AA775778	3.6	2.2	3.8
51056 at	hypothetical protein DKFZp434D0412		AW025176	3.6	3.3	5.6
53879 at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	B3GALT3	AA167825	3.6	1.1	3.5
43992 at			R61748	3.6	3.3	3.1
51163 at	hynothetical protein FLJ22405		AA115361	3.6	2.9	4.5
65465 at			AI953614	3.6	2.8	3.5

Figure 11LLLLL

h., Intors: Nir Hacohen, et al.

57757_r_at			AA425516	3.6	3.2	
50845 at	putative seienocysteine lyase		AA775419	3.6	1.5	
64314 s at			AI653557	3.6	3.4	2 8
62189 at			AI440192			2.0
63971_s_at	sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 2	SIRTZ	A1984394	3.6		5.8
55678_at			W72885	3.6	3.0	2
80251_r_at	ATPase, Ca++ transporting, ubiquitous	ATP2A3	AI380736			3.6
4621 / at			AI439688	3.6	9 0	
54062_at	LCAT-like lysoph		AA972732	3.6	23	c
8//54 g at		SDCCAG3	W02630	3.6	3.3	3.6
37729 at	carbonyl reductase		AI382182	3.6	2	2
38639_at	Suppressor of clear, C. elegans, homolog of		. `.	3.5	3.3	4.8
30070 at	KINANGS2 STATES PROTEIN 313	ZNF313		3.5	3.2	5.6
33030_dl	NAMOSZ protein; prosopnila multiple asters" (Mast)-like homolog 1		AB014522	3.5	2.2	3.3
39436_at	BCL2/adenovirus E1B 19kD interacting protein 3-like	BNIP3L	AF079221	3.5	191	
38129 at		A.D.	L13943		2	
31845 at	E/4-like factor 4 (ets domain transcription factor)	ELF4	U32645		3.1	
30156 at	extra spindle poles, 5. cerevisiae, homolog of		D79987	3.5	1.1	
70000 at		C3AR1	U62027	3.5	2	7
31510 c at	Historia family 3D (U3 3D)	PRKCBP2	U48250	3.5	1.1	"
41233 at	Day I (Hendr) homolog cubbanity B marks	H3F3B	- 1	3.5	1.3	7.7
1925 at	Overlin F	DNAJB6	AB014888	3.5	0.5	
33814 at	Drotein kinase related to S. cerevisiae STEON affector for Canadia	CCNF	236714			2.5
32964 at	exf-like module containing mucin-like hormone recentor like	1011	AF005046	3.5	2.3	15.
1	sequence 1	באואים	A814/9	3.5	1.6	2.2
36239_at	POU domain, class 2, associating factor 1	POU2AF1	749194	4	1	
38138_at	S100 calcium binding protein A11 (calgizzarin)	S100A11	D38583		7.7	0.8
35185_at	fatty acid binding protein 7, brain	FABP7	12		2.3	† †
40300 g at	G-protein coupled receptor				T ≪	4 0
2450Z at	solute carrier family 2 (facilitated glucose transporter), member 5	SLC2A5	M55531	3.5	2.6	4
34804 at			AL049246			
30834_at	JUKFZP564G2UZ protein		AL080058	3.5	C	/ 7

Figure 11MMMMM

37023 at	Numphocyte cytosolic protein 171 plactic)					
37.35E at	Day (Hand) homelas a the sile of	LCP1	J02923	3.5	2.6	1.1
37.000 at		DNAJB2	X63368		2.3	0.5
3/688 T at	I'c tragment of IgG, low affinity IIa, receptor for (CD32)	FCGR2A	M31932	3.5	0	С
3/558 at	IGF-II mRNA-binding protein 3		U97188	3.5	110	12.0
38020_at	KIAA0652 gene product		AB014552		3.2	18.5
37948 at	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD	ATP6C	J05682	3.5	2 5	0 1
56410_at	40S ribosomal protein S27 isoform		AA156232	3.5	26	0 1
48497_at	membrane-associated nucleic acid binding protein		AI380524	3.5	2	38
812/6 at			N63894	3.5	5.5	7.2
50825 at			W23499	3.5	2.8	12.4
70472 r at			AA910786	3.5	1.7	18
74200 at			AI732852	3.5	0.4	4.1
78401 v ot			AI740774	3.5	0.5	9.0
76750 r at			AW025517	3.5	6.0	3.8
53860 24			AI224653	3.5	1.1	1
5.0000 at	70.00 to 10.00	H49544	3.5	2	0.7	
24035 at	nypotnetical protein FLJ12526		Al186169	3.5	0.7	m
18 7/7C0			AA492507	3.5	1.2	2.4
03000 at			AI703109	3.5	1.7	2.9
02043 at			AI939451	3.5	1.8	9.0
4/3/0 at			AA126059	3.5	1.3	2.6
43201 at			AA481181	3.5	5.5	7.1
50371 a st	100000000000000000000000000000000000000		AI500650	3.5	1.5	0.6
5000F at	hippulletical protein		AW003291	3.5	1	0
87285 at	hypothetical protein FLJZZBU9		AA700816	3.5	4.2	1.5
60337 at			AA679812	3.5	1.1	5.9
56722 at	hynothetical protein MCC 4174		AI925894	3.5	9.0	O
59619 at			AI291406	3.5	9.0	1.1
19600 at			AW007238	3.5	0.1	0.5
49000 at	DD domain contains 4		AI936984	3.5	3.9	7
72443 at	TO COLITAIN THE REAL PROPERTY OF THE REAL PROPERTY	PRDM4	W22625	3.5	1.7	7
76006 at			R95898	3.5	e	2.3
53650 r at	UKE7D434D193 protoin		AI953059	3.5	2.4	1.4
23471 at	11 4740123 protein		AA453704		5.1	1
/34/1_at			AW009414	3.5	0.8	4.2

Figure 11NNNNN

49158_at	Imyosin IXA	MY09A	AI435029	3.5	3.6	5.2
52846_at	hypothetical protein from BCRA2 region		AI809961	3.5	1.7	2
78473_at			AW051926	3.5	0.7	9.0
90038_at	sin3 associated polypeptide, 18kD	SAP18	AW006624	3.5	5.8	5.5
42699_at			AA490077	3.5	2.1	2.1
54195_at			AA604910	3.5	2.1	2.9
87678_at			AI270326	3.5	6.0	0
84420_r_at			A1580853	3.5	9.0	1.2
75923_at			AI356228	3.5	1	0
68633_s_at	hypothetical protein		AI650829	3.5	6.0	0.3
49640_s_at	CGI-81 protein		N21189	3.5	2.3	1.8
50284_at	LIM and cysteine-rich domains 1	LMCD1	AA156689	3.5	2.2	2.3
45711_at	hypothetical protein FLJ20396		N37049	3.5	2.6	2.8
45347_at			AA533633	3.5	1.8	3.6
63361_at	spondin 2, extracellular matrix protein	SPON2	AA570505	3.5	3.2	3.2
61871_r_at	WW Domain-Containing Gene		AI963349	3.5	4.3	1.5
64543_at			AI668557	3.5	2.4	7.9
87221_at			AA829405	3.5	5.4	3.1
72183_f_at			AI587180	3.5	2.3	1.9
45206_at	zinc finger protein 277	ZNF277	AA102582	3.5	4	2.5
58622_at			AA463374	3.5	5.3	9
62167_at			AI866590	3.5	1.1	1.2
46608_r_at			AI885018	3.5	3.1	0
55933_r_at			AI732404	3.5	0.7	1.8
89908_f_at	GDP dissociation inhibitor 1	GDI1	AW004027	3.5	5.2	1
87890_at	folylpolyglutamate synthase	FPGS	AI745045	3.5	2.1	0
78749 g at		HNRPA2B1	AI963008	3.5	1.8	0
49709_at	hypothetical protein FLJ10116		AA127924	3.5	5.1	0.4
42093_at			AA398660	3.5	4.6	4.5
57452_at			AA451798	3.5	2.8	4.7
58958_f_at			H05039	3.5	2.3	4.5
70323_f_at			AI743616	3.5	4.4	3.4
31432 g at	Fc fragment of IgG, receptor, transporter, alpha	FCGRT	U12255	3.5	2.3	3.5
31820 at	hematopoietic cell-specific Lyn substrate 1	HCLS1	X16663	3.5	2.3	4.3

	glucosyltransferase		AJ224875	3.5	1.8	3.6
40504_at	paraoxonase 2	PONO	AE001601	2 5		
40872_at	cytochrome c oxidase subunit VIb	COXER	1		3.2	2.5
41139_at	melanoma antigen, family D. 1	1000	1		7.0	5.8
41224 at	KIAA0788 protein	IVIAGEUT	W25533	3.5	1.8	1.9
33399 at	ribosomal protein S6			3.5	1.1	4.2
3907 24		RPS6	ı	3.5	1.8	2.9
36647 at		EIF4G3	AF012072	3.5	2.4	3.2
7700	ilypotifical protein regions		AA526812	3.5	17	2
34400 at	low molecular mass ubiguinone binding protein (9.5kD)		AI540957	3.5	2.7	0.0
35343_at	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	GOT1	M37400	3.5	3.4	2.9
32510_at	aldo keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	AKR7A2	AF026947	3.5	2.1	4.1
36136_at	p53-induced protein		1			
1427 g at	Src-like-adanter		۲	3.5	1.7	2.4
37346 at	ADP-rihosylation factor E	SLA	- 1	3.5	3.7	5.1
37900 at	actor J	ARF5		3.5	1.6	3.8
38780 at	116	PEX11B	AF093670	3.5	2.2	29
39160 at	Dyrinyate debydrogeness (linearing) 1, inemper A1 (aldehyde reductase)	AKR1A1	J04794	3.5	0.8	3.8
39172 at	District deligate (apparline) beta	PDHB	D90086	3.5	2	3.3
65033 at			AL049319	3.5	2	3.3
59410 at	hynothetical protein El 110688		AI052571	3.5	2.7	3.6
56238 at	PD7.1 IM profess mystics a		AA192438	3.5	3.8	1.4
56248 at			AI589776	3.5	3.4	3.5
63673 at			AI885374	3.5	2	6.0
45518 at	chromosome 22 onen reading frame 4		AI635057	3.5	1.3	4
47982 at	Soli seadili Britania	C220RF4	AW026098	3.5	1.8	3.1
43798 s at		AQP3	AA630981	3.5	3.4	3.1
49165 at	hypothetical protein PRO2013		AI347938		2.1	4.3
60062 s at	hypothetical protein		AW024795	3.5	0.7	3.4
	3		AI027140	3.5	2.9	3.7
57132_at	RNB6		012/11/02			
43857 s at			A1341402	3.5	3	3.3
			AA5/00/0	3.5	2.3	3.7
			αννακονν	Ti C	C	4

Figure 11PPPPP

l.

49326_at	matrix Gla protein	OW	00000			
57461_at		5	-		3,	3.7
82156 at			MI4/2111		.,	3.4
52072	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		AW044081	3.5	3.5	2.1
52975 at	nypotnetical protein FLJ10330		AA683501	3.5	2.	3.1
20162_at			AAGIOR38	3.5		100
43795_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV)	NDUFA8	1 -	3.5	2.	4.1
45531_at			1010101			
62462 at	hypothetical protein dJ473B4		A1970101		3.2	2.5
54547 at	hypothetical protein DKFZp434G0522		A4133432		m	3.3
52842 at			MA14/040	3.5		3.5
47057 at			AL110412	3.5	3.6	2.9
55446 at			D20714	3.5	3.4	4
00440 at			A1199032	3.5	3.3	3.4
337.32 at			AW004042	3.5	2.2	33
48354_at			A1929033	3.4		9 4
34470_at	transcription factor EC	TFEC		3.4	i c	2.0
1313_at	proteasome (prosome, macropain) subunit, beta type, 7	PSMR7	1	700		
37824_at	KIAA1074 protein		700000	1 0	0.4	0.5
1903 at	RAP1B, member of RAS oncogene family	0.00	AB020997		1.2	1.4
40148 24	1/	KAPIB	X08004	3.4	1	1.6
40140_at	anijyou beta (A4) precursor protein binding, family B, member 2 (Fe65-like)	APBB2	U62325	3.4	0.1	7.2
40598_at			W20139	700		1
35488_at	Small nuclear RNA activating complex, polypentide 1, 43kh	CNIADO	144754	0.4	2.4	0.5
41185_f_at	r of mif two 3, veast) homolog 2	CMTSUS	A1071724	3.4	0.8	13.9
32259 at	enhancer of zeste (Drosonhila) homolog 1	ZUCTIAIS	H13/1/24	3.4	2.7	5.2
32786 at		LZH1	۲۱	3.4	3.4	3.5
33779 at	mombrane	JUNB	1	3.4	1.2	2.4
30868 24	-1.	VAMP1	AF060538	3.4	0.1	5.4
37107 at	leandcyte tyrosille Kinase	LTK	X52213	3.4	1.2	2.9
20110			AI147237	3.4	60	6.7
39344 at			U53209			200
31690_at	Glutamate dehydrogenase-2		108997		11.0	5 6
33835_at	KIAA0721 protein		AR018264		1.7	7.7
678_at	alkaline phosphatase, placental (Regan isozyme)	41 PD	1		0 -	
37242 at	hypothetical protein MGC5149	MGC5140		3.4	7 0	6.9
33510 s at	Plutamate recent	INGCOL43	0/3/00	3.4	2.	5
.5.0100	Black lack	ZYS	131216	7 %	<u> </u>	0

Figure 11QQQQQ

icillity pignicil	Sa z (Millikeu recessive)	RP2	AJ007590	3.4	2	
carboxypeptidase		CPD	06290	3.4	1 7	
Ţ	ein DKFZp586F1122 similar to axotrophin		1		/ 1	
\neg	N ethylmaleimide sensitive factor attachment protein, gamma	NAPG	1		† r	
at	letase	GARS	1	3.4	2.1	0
	t-complex-associated-testis-expressed 1-like	TCTF11			0.7	
201_s_at beta-2-microglobulin		MCB			6.3	
heterogeneous nu	clear ribonucleoprotein M	NO ON O	⊥		7.7	3.5
DKFZP564M1416	protein	NAT TO THE PARTY OF THE PARTY O	4		1.2	
aldehyde dehydro	penasa 8		AL0499	3.4	2	
sperm associated	otings O	ALDH8	_	3.4	0	2.
מלה מלה מים מים מים מים מים מים מים מים מים מים	annigen /	SPAG7	≤	3.4	4.6	
ă ;				3.4	2.8	14.8
T	conditions translation illitiation factor Z-alpha Kinase 3	EIF2AK3	1	3.4	2.6	5
54885 at hypothotical protein			AA010757	3.4	9.0	0
inyportierical profe			AI458882	3.4	1.4	
542313 at UCBC163 ====================================			AA470110	3.4		
į ;			AA044747	3.4	1.6	
42400_dl			A1004422	3.4	4.1	9
7 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -			A1033495	3.4	2.8	1.5
speriff associated	antigen 4	SPAG4	AI168233	3.4	1.9	0.4
76905 at			AI971242	3.4	3.1	
90500 at			AI674760	3.4	0.7	7
66819 at			AA491286	3.4	0.4	1.2
59883 r at			AA984073	3.4	1.6	6.5
42599 at			Al150628	3.4	2.4	4.6
78618 at			T82459	3.4	2	1.2
78742 at			AI889955	3.4	0.3	0.5
58530 r at			A1939581	3.4	1.2	6.4
82592 at			T66185	3.4	2.5	5.3
83060 at			AI916523	3.4	3.4	1.1
5393 <u>4</u> at			AI335004	3.4	1.2	1.4
54720 at			AI291699	3.4	1.5	4.4
7inc finger protein	1/3 (clope pH7 1)		_1	3.4	10.4	2
himpethotical protei	17.71.16 DI 17.17)	ZNF143	AA932870	3.4	1.7	0.7
	TI MUSUKO		A1341661	,		

Figure 11RRRRR

83898_at	NADPH oxidase, EF hand calcium binding domain 5	NOX5	A1091544	3.4	c.	0
82051_at	hypothetical protein FLJ20321		AA535115		000	0.5
91689_at					7 -	-
82470 at			AI858051	3.6	2.5	2.4
47688_at			H78083	3.4		
85291_at			A1467796	3.4		27.0
			AA142984	3.4	2.6	4 4
84709 at			AI700770	3.4		C
84761_at			AI476355	3.4	0.5	
46309_at	_	TUBB	AL039239	3.4		E C
43850_s_at	PP1201 protein		AA668732	3.4	5.4	5
59047_at			AI825998	3.4	9.0	3.5
87096_at			AA335058	3.4	1.5	2.2
87135_at			AI239715	3.4	8.6	1.2
74635_at		CDK2	AI989454	3.4	0	
65764_at	RAB18, member RAS oncogene family	RAB18	D12273	3.4	6.3	0.3
/1001_at			AI863286	3.4	2.7	26
71272_at			AI928726	3.4	80	1 5
43439_at	hypothetical protein FLJ11252		AA741298	3.4	6.0	
43407_at	DKFZP586F1524 protein		AW014654	3.4	1.6	2.7
56662_at			AI627666	3.4	0.2	0
592/8_at			Н98683	3.4	2.1	0.4
	LISI-interacting protein NUDE1, rat homolog		AI863849	3.4	1.6	2.1
			AA029446	3.4	8.0	2.5
8/894 at			H65062	3.4	1.9	1.6
57575 at			AI033153	3.4	0.5	9.0
/1616_r_at			R27430	3.4	-	1.3
42/09 at	Wolf-Hirschhorn syndrome candidate 1-like 1	WHSC1L1	241537	3.4	0	7.2
49776 at			AA648525	3.4	1.6	2.4
62321 at			AA482950	3.4	2.6	3.4
63620_f_at	_	RPL39	AA280641	3.4	8.0	1.2
60011_at			H62663	3.4	3.7	0.3
65660_at		NFX1	AA744238	3.4	1.6	1.9
55086 at	hypothetical protein MGC3262		278349	3.4	1.2	1.2
65662_at			AA019910	3.4	1.6	0.2

Figure 11SSSSS

1407.794			N78066	3.4	3.2	3.5
T			AI458735	3.4	2.4	
1	SUMU-1 activating enzyme subunit 2		AA974493		F C	1
at	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isoenzyme B	MGAT4B	1	3.4	1.2	3.8
at			104010	,		
87481_at	hypothetical protein FLJ10698		0/948/	3.4	1.1	3.4
äţ	KIAA1096 protein		AI951927	3.4	0	0.5
at	Droteasome (prosome macropain) activator gubunit 1 (pagos -1-1-1)		AA976741	3.4	1.5	2
	3	PSME1	AA662670	3.4	4.3	0.8
is is		CYBS	39945	3.0	9	
at	transmembrane protein 4	TMEM4		F (c)	0.0	0.0
T			AA279956	7 7	4.4	2.5
	alpha thalassemia/mental retardation syndrome X-linked (RAD54 (S. cerevisiae) homolog)	ATRX	1	3.4	1.8	1.4
<u></u>			. 00000			
Г	CCAAT/enhancer binding protein (C/ERP), bets	1	A1698684	3.4	4.7	5.3
Τ		CEBPB	AW025406	3.4	2.4	
49837 at			AI830502	3.4	2.3	6.0
45751 g at			AI209180	3.4	2	7.3
7			AA528592	3.4	0.8	C
72954 at			W03586	3.4	2.7	2.6
Γ	GCN5 (general control of amino acid everthosis 2004 E		AA883059	3.4	0.7	0.8
	The same control of anning acid synthesis, yeast, nomology. IIke 2	GCN5L2	AF029777	3.4	2.5	0.2
寸	cysteine and glycine rich protein 1	CSRP1	M33146	3.4	0	
39729 at	peroxiredoxin 2	PRDX2	L19185	3.4	3.5	4.4
١,	nomolog of mouse quaking QKI (KH domain RNA binding protein)		AL031781	3.4	1.0	0.0
Į.	ilypoureucal protein FLJ11585		A1743654	3.4	2 6	1 0
ğ	NIMIUMU protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2		AB029003	3.4	2.3	2.1
T		HADH2	AF035555	3.4	1,6	2
, a	Citrate synthese	RECQL	AI685944	3.4	2.4	2 -
; ;	chromosome condescration 1 11/2	SO	AF047042	3.4	2.1	4.2
Τ	makorin ring finger profess 1	CHC1L	AF060219	3.4	2.9	22
		12022	1.0.1			

Figure 11TTTTT

35289_at	rab6 GTPase activating protein (GAP and centrosome associated)		AJ011679	3.4	2.4	3.2
35159_at	tubulin-specific chaperone e	TBCE	U61232	3.4	1.9	3.1
34381_at	cytochrome c oxidase subunit VIIc	COX7C	AI708889	3.4	1.6	5.4
1924_at	cyclin H	CCNH	U11791	3.4	2.3	3.2
36945_at	endoplasmic reticulum lumenal protein		X94910	3.4	6.0	3
37672_at	ubiquitin specific protease 7 (herpes virus associated)	USP7	272499	3.4	9.0	3.9
37264_at	zinc finger protein 131 (clone pHZ·10)	ZNF131	009410	3.4	2.5	e
32610_at	LIM domain protein		X93510	3.4	2.4	3.4
33121 g at	regulator of G-protein signalling 10	RGS10	AF045229	3.4	1.5	4
138_at	mitogen activated protein kinase kinase kinase 1	MAP4KI	U66464	3.4	3.7	2.8
40745_at		AP1B1	L13939	3.4	2.7	3.2
41038_at	neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2)	NCF2	M32011	3.4	1.4	3.1
58498_at	KIAA1378 protein		AI082236	3.4	2.5	3.4
80436_at			AI935644	3.4		7
44713 at	HSPC009 protein		018006	3.4	1.9	7
45577_s_at			AI471038	3.4	4.9	5
45276 g at	protein x 0001		W30943	3.4	m	4.9
43382_s_at	C-terminal binding protein 1	CTBP1	AI991853	3.4	2.5	3.8
65724_at	KIAA1423 protein		AI684729	3.4	3.5	3.6
57156_at	HSPC023 protein		W92964	3.4	3.2	4.9
51173_at		P2RX4	AI872092	3.4	2.9	3.4
46261_at	hypothetical protein FLJ10283		AL045512	3.4	1.7	2.3
45543 <u>r</u> at			Al359916	3.4	3.4	2.8
44842_at	COP9 complex subunit 7a		AI971871	3.4	2.9	4.8
46871_r_at			W32096	3.4	3.1	2.9
47101 g at			AI972460	3.4	2.6	3.4
64436_at	arginyl aminopeptidase (aminopeptidase B) like 1	RNPEPL1	AI926755	3.4	2	
54483 <u>a</u> t			AA760777	3.4	3.4	3.4
62559 at	hypothetical protein FLJ11230		W31010	3.4	1.6	3.3
44828_s_at	ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATP1A1	AI610470	3.4	2.6	3.7
47082_at	NAG-5 protein		AW003127	3.4	2.7	3.6
54507_at			AA912049	3.4	1.9	2.8
32464_at	defensin, beta 2	DEFB2	AF071216	3.3	6:0	1.4
35074 at	jerky (mouse) homolog-like	JRKL	AF004715	3.3	0	3.6

Figure 11UUUUUU

11438 at	KIAA1451 protein		10011	2.2	0	G
Τ	thyroid hormone receptor associated protein, 240 kDa subunit	4	AB011165	3.3		
T	thy fold marketing	1	AF007130	3.3	0	
1	hypothetical protein		D87437	3.3	1.6	7.0
٦	KIAA0250 gene product	IINS	AF051850	3.3	0	-
٦		1	D30655	3.3	2.4	4.8
	ōΓ	TANNE	123805	3.3	1.4	0.2
	catenin (cadherin associated protein), alpha 1 (102KU)	POKNIA	103106	3.3	1.6	1.5
	cyclin-dependent kinase inhibitor 1A (pZ1, Cip1)	上	44868382	3.3	1.2	1.3
ĺ	major histocompatibility complex, class II, DQ alpha 1	1	A) 021366	3.3	2.8	3.3
	PHD finger protein 1	4	ALUZ1300	2.5	2.6	1.3
34221 at	KIAA0194 protein		003770	200	82	3.4
34678 at	fer 1 (C.elegans) like 3 (myoferlin)	rekil3	AL090/13	5.6	1 2	1.5
10000	lentin recentor gene-related protein		Y126/U			V C
34755_at	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 2	ADPRTL2	AJ236876	3.3	7.7	4.7
			U67322	3.3	2	2.8
	HBV associated factor		W26762	3.3	6.9	0
33285_i_at	١,	RAB32	U59878	3.3	0.2	0
41523_at	As oncogene rarnity	MADSKA	AF002715	3.3	1.9	0.2
35651_at	mitogen-activated protein Kinase Kinase Kinase 4		AR007870	3.3	1.9	0
40018 at	KIAA0410 gene product	1000	2001004		1.5	1.1
35296 at	phosphate synthase 1	GGF31	AB019030	5	, c	
2000	A binding protei	GABPB1	01331/	3.3		
35943 s. at 38037_at	diphtheria toxin receptor (heparin-binding epidermal	DTR	M60278	<u>ო</u> ო	4.	1.3
	growth factor)	MAL	X76220	3.3	8.0	5.4
38051_at		CFRPB	X52560	3.3	3	0.4
38354_at	CCAAT/enhancer binding protein (c/ Epr.), Deta		N66625	3.3	2.3	4.2
55376_at	MIL1 protein		AA504346	3.3	2.2	4.9
61487_at		H1FX	AW015141	3.3	1.1	2.3
60070 f at	H1 histone family, member X		44418074	3.3	1.3	4.5
50757_at			AID51390	3.3	0	0
80698_at			W87283	333	ō	2.3
76039_at			VI276023		1.5	0
47427_at	hypothetical protein FLJ20539		AA820524		m	4.4
66523 at			A1732902	3 8	0	0
81813 at			AI 36 306 1	222		

aceptor 2 (interferon gamma transducer 1)
-
-

69376_at			AI655430	3.3	1.5	3.8
47902_at			W74622	3.3	1.6	1
62466_at	lymphoid blast crisis oncogene	LBC	AI797853	3.3	2.7	0.8
53334_at			H12612	3.3	1.1	6.9
49581 <u>g</u> at			AA779208	3.3	2.1	2.4
44421_s_at			D59337	3.3	8.0	1.4
51254_at			A1090139	3.3	3.6	4.9
60138_at			AI823497	3.3	1.1	5
52575_at			H66727	3.3	E	3.6
63980_at	hypothetical protein FLJ10618		H46637	3.3	2.9	
52083_at			AL040341	3.3	2.8	
46126_at			A1498592	3.3	0	0.8
63457_f_at			AA022988	3.3	2.2	4
64909_at	hypothetical protein DKFZp762B226		AI341683	3.3	3.6	1
58630_at			AA187854	3.3		
54900_at	f-box and leucine-rich repeat protein 3A	FBXL3A	AI983021	3.3	1.5	2.
64266_at	stromal antigen 2	STAG2	AA476504	3.3	1.2	1.6
72376 r at	cathepsin K (pycnodysostosis)	CTSK	AI282317	3.3	6.0	0.8
46052_at			AA250767	3.3	4.2	6.5
47155_at			AI300571	3.3	2.2	0.5
48896 <u>a</u> t	carboxypeptidase A3		AI082244	3.3	3.6	14.2
56710_at			AI762244	3.3	1.4	2.3
74710 s at	epithelial membrane protein 3	EMP3	AW005790	3.3	2.4	3.0
34477_at	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	UTY	AF000994	3.3	1.9	2.8
40414_at	valyl-tRNA synthetase 2	VARSZ	X59303	3.3	2.8	8
40764_at	glutamic.oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	G072	M22632	3.3	2.4	3.9
250_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	NFATC3	141067	3.3	3.2	3.3
1287 <u>a</u> t	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	ADPRT	J03473	3.3	2.1	
32455_s_at			U88153	3.3	2.6	3
33340_at	KIAA0438 gene product		AB007898	3.3	1.3	4
36417_s_at	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-	ACAA1	AF035295	3.3	0.8	3.9
	Coenzylle A unolasty		_	_	_	

36093 at KIA 34842 at sm 35323 at euk 36637 at and 32588 s at but 479 at dis	KIAAA614 aratein		AB014514	 	3.1	5.0
s at						
at s at	mail auclear ribonic leonrotein polynentide N	SNRPN	U41303	3.3	2	3.1
at s at	Small flucteral fluctuation factor 3 subjust 9 (eta 116kD)	EIF3S9	U78525	3.3	1.9	3.4
s at	(aryotic translation illitiation lactor 3, subutite 3 (ctd. 120)	ANXA11	L19605	3.3	1.7	4.2
s at	annexin A11	BRF2	X78992	3.3	2.4	3.1
	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)	DAB2	U53446	3.3	e	3.4
-	() () () () () () () () () ()	AMPD2	M91029	3.3	3	2.9
at	adenosine morbinospilate dearminase 2 (13010111 2)	RPA1	M63488	3.3	2.3	(*)
a.	incation protein of (2000)	CENPB	X05299	3.3	3.3	(1)
aĭ	Centrolline Protein B (50hB)		T84485	3.3	2.7	3.5
at	nypothetical protein i collinea		AI078187	3.3	2	2.6
T	diotect of desired	Z Z	AI654857	3.3	2.5	4.3
-	-14		AA593768	3.3	3	3.1
Sal	Hypothetical protein i caso acc		A1992128	3.3	2	2.5
48/81_s at			A1090386	3.3	2.4	1.8
56265_at 66112_at tra	translocase of inner mitochondrial membrane 17 (yeast) homolog A		AA234191	3.3	1.4	4
1	7000		AI760042	3.3	3.1	
ar •	nasa in insensition i		AA150502	3.3	1.5	3.1
je i	asthatical protein El 120160		AA133311	3.3	3.3	3.
, g	וואסטווופווימו או סיפון ו בסבסבסבס		AA913312	3.3	2	3.2
ă	The state of the state of the HODACE		R69311	3.3	1.9	2.5
ă	CHILD 1 activation engine cubinit 1		H98166	3.3	2.6	4
52932_at ka	kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))	KAI1	W51778	3.3	2.9	2.6
10077			AA479016	3.3	3.1	3.
3007/at			H15571	3.3	1.3	3.1
43984 at			A1141764	3.3	ĸ	1.
85/01 at			AA740928	3.3	2.1	Υ
44004 at	Col 39 protein: cell death regulatory protein GRIM19		AA181145	3.3	3.7	4.
T	-1>	PREB	3 AI924136	3.3	1.3	3.
_	.1 🗆		AL046381	3.3		3.3
010+0 k at	אַסטוורווסמן אַזיסטוויי במבדיי		R55295	3.3	3.3	2.6

	section welface casted channel lek-related family member 3	KCNE3	A1148745	3.3	2.9	2.9
44550 at	porassium voitage garea enamen, con enamen.		A1672040	3.3	2.1	3.2
45/95 at			AL042592	3.3	3.1	4.4
30071 at			A1953658	3.3	3.1	3.4
23340 at	hymothetical protein El 120859		AW006969	3.3	1.5	3.7
045002 s at	naporiformal short.		A1131178	3.3	3	3.7
40220 at	ubiquitin like 4	UBL4	AW043826	3.3	2.3	Э
00942 at		CSNK1E	A1831641	3.3	2.8	2.9
51116 g at	UDP-N-acetyl-alph		AW021000	3.3	2.5	2.5
46307 at	endomembrane protein emp70 precursor isolog		N24239	3.3	2.4	χ.
	Libiquitin-conjugating enzyme E2L 3	UBE2L3	S81003	3.2	1.6	1.1
30007 at	hypothetical protein FL 122512		AI432190	3.2	0.2	0
	linovitransferase		AB017566	3.2	0.1	m
	far unstream element (FUSE) binding protein 1	FUBP1	U05040	3.2	3.4	0
31826 at			AB014574	3.2	2.4	2.4
31389 at	oxidative stress induced like	TISO	U46752	3.2	2.2	-
40790 at	hasic helix loop-helix domain containing, class B, 2	ВНГНВ2	AB004066	3.2	1.5	0.3
1367 f at	ubiquitin C	OBC	M26880	3.2	2.2	9
35868 at	advanced plycosylation end product specific receptor	AGER	M91211	3.2	1	16.7
2082 s at		CDH1	F08299	3.2	2.9	5.3
32859 at	ō	STAT1	M97935	3.2	18	
39227 at		PTPRT	AB006621	3.2	1.8	2.9
31673 s at		CMAR	X65784	3.2	2.7	Ö
33935 at	calcyclin binding		AL035305	3.2	1.7	2.3
32249 at		HFL1	M65292	3.2	6.0	6.0
34396 at	KIAA0978 protein		AB023195	3.2	2	m
36706 at	serine/threonine kinase 9	STK9	Y15057	3.2	1.3	3.6
35262 at		ITGB4BP	AF022229	3.2	1.2	0.3
41789 r at	KIAA0669 gene p		AB014569		3.6	2.8
32665_at	T	PPM1B	AJ005801	3.2	0.4	1.3
	isoform			0		
40034_r_at			D86864	3.2	<u>x</u> .	<u> </u>
	endothelial cells		1003001	000	0	2.1
35747_at	stromal cell derived factor receptor 1		AFU3528/	3.4	1.3	4:17

		7767	· ·	0.0	\ . T
Ī	small inducible cytokine sublatifily A (cys-cys), inclined 17	L	3.2	9.0	1.2
T	Tragile histidine triad gene	 	3.2	1.9	1.1
je.	FIDOSAJIACION I Jactor V alpha	4	3.2	1.8	1.4
Ţ	- 8		3.2	7.7	6.7
T	odycostosis)	L	3.2	0	6.2
T	camepsin A (pycilodysosiosis)	٩	3.2	1	3.2
T	Serine/Integralia Ailase 17a (apoptosis inducins)		3.2	0.2	4.1
Т	nuclear receptor coactivator	A1934556	3.2	0.4	3.4
T	on in a constitution response.68 protein	AA524064	3.2	3.1	1.7
	Ipopoliysaccialide specific response of process	AI346493	3.2	2	3.2
T	סטנוופווכמן קוסופוון ו בסבסקקס	AI150441	3.2	5.1	3.4
1	binothotical protein Et 120417	N99181	3.2	1.2	1.3
_	טסנוופווכמו טוסנפוון ובסבסידי	A1525683	3.2	2	1.4
5/784 S at		AA699653	3.2	1.8	5.6
54955 at		AI301060	3.2	1.1	1.4
56495 at		AI001809	3.2	0.5	2.3
/5/21 at		H54203	3.2	2.9	5
1	V. E for basis knimael like factor	AI799087	3.2	2.4	0.5
	TIBALL TOT DASIC ATUPPED THE TACKS	AI733141	3.2	4.4	1.6
/669/ at		AA862450	3.2	2.2	4.2
66685 at		AL079769	3.2	3.6	0
/6513_at		AA806526	3.2	2.3	8.2
///5/ t at		AA886300	3.2	0.3	3.9
51//1 at		AA434579	3.2	0.7	1.6
//U45 at		AA421929	3.2	1.2	2.6
52/93 L at		AI209116	3.2	0.8	5.8
02004 at		AI700571	3.2	3.9	2.3
54624 at		A1305286	3.2	3.4	5.8
i j	Athatical protein HDCMC04P	AI352449	3.2	0	1.6
Sat	hypothetical protein ribomocal	AI917726	3.2		0.5
81197 at		Al351861	E.	2.5	1.9
03100 at		A1633758	3.2	1	0.0
03/09 at		AA602573	3	3.5	4.8
04320 01		R97050	3.2	1.5	2.4

					1 6	C
		AA63	AA634479	3.2		
35091_at		26H	H92507	3.2	2.6	3.4
47667_at		A139	A1394150	3.2	4.5	8.9
85174_r_at		A192	A1927605	3.2	2.2	0
84825_at		A195	A1952956	3.2	8.0	0.1
84187_s_at	KIAA0729 protein	AA50	71504	3.2	0.1	1
63106_at		AIGE	A1652996	3.2	1.3	2.6
79344_at		AAS	00290	3.2	2.9	2.3
68707_at		7NF265 ALO	AL047537	3.2	2.4	1.6
63884_at	zinc finger protein 265		32101	3.2	1.6	0
59594 <u>r</u> at		AIG	AI684748	3.2	1.7	0.7
69821_at		AIA	17549	3.2	1.8	1.2
44153_at	hypothetical protein LOC56/55	PA9	10175	3.2	1.1	0
71519_at	.il and transport & respect type II.	TGFBR1 AF0	54598		1.8	0.3
1957_s_at	transforming growth factor, beta receptor I (activiti A receptor type in					
	like Kinase, מסאט	AIO	41279	3.2	2	C:/
72313 at		AAO	AA010008	3.2	1.3	0.4
72703 at		CIA	88733	3.2	1.6	1.3
47011 at	G-substrate	800	06001	3.2	0.1	1.5
89838_at		AAT	AA151917	3.2	2.2	4.4
49168 at		SIA CACVIAA	A1829903	3.2	0	0
61697 at	ankyrin repeat, family A (RFXANK-like), 2	_L	20202	000	0.4	0.1
57337_s_at	hypothetical prot		AA640/93	3.5		
		AA	AA195009	3.2	3.8	0
65562_at	twisted gastrulation	AA	AA232718	3.2	2.4	1.2
60473_at		AIT	AI765698	3.2	4.6	3.4
50081_at		AA	AA324765	3.2	2.8	0.3
85965_at	two-pore channel 1, homolog	Z	N54910	3.2	2.1	5.6
56228 r at		AA	AA180358	3.2	2.7	1.8
42675_at		AA	AA938414	3.2	1.1	0.8
79804 at		A	AI740499	3.2	0.3	1.8
86993 at		A	AI417686	3.2	2.1	1.9
64628_at		A	A1144421	3.2	0.7	2.8
54439_at	hypothetical protein FLJ12387 Similar to Milesin ilginoriani		H25689	3.2	2.3	3.1
44586_at			H29258	3.2	2.1	4.2
43004 at						

Figure 11BBBBBB

Ti. Response of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

		AI400203	3.2	1.9	o
			3.2	2.7	
Zinc finger protein 155 (pHZ-96)	ZNF155	4	3.2	1	1
		N54407	3.2	1.2	·Ω
		H51694	3.2	1.4	2
peramily 1, BMP	CKTSF1B1	AA912445	3.2	0	9.0
		D80679	3.2	1.1	4.8
attinization of the management of the section of		ŀ	3.2	0	2.8
suppliession of turnorigenicity to (melanoma differentiation)	ST16	- 1	3.2	2.6	4.
inc finger protein 201		W88422	3.2	1.2	1.6
לוויט ווויוצבו הוסיבווו לסד	ZNF281	AI796083	3.2	1.8	Э.
MFK partner 1		AA074601	3.2	2.2	0
ווורוג לימו זוופן ז		AA056667	3.2	1.9	1
UCBC142		AI640524	3.2	9.0	0
		AA186623	3.2	1.7	0.5
		AA524036	3.2	1	0.8
		AI859233	3.2	0.4	
bromodomain-containing 2	BRD2	AI343297	3.2	2.8	
historial protein FLJZUDUS			3.2	0.7	9.0
Diotillidase	BTD		3.2		C
		AI769154	3.2	0.3	0.8
Figure 1 (Describite)		AI804917	3.2	1.2	6.0
Ingriness I (Drosophila) nomolog	FLII	A1696805	3.2	1.7	
		AA282531	3.2	0.4	3.
		AI817130	3.2	3.7	
		3096417	3.2	2.1	4
		3144365	3.2	1.6	2.2
		AI016237	3.2	5.4	2.6
hypothatical protein El 1901 Ed		H53956	3.2	9.0	
apididymal secretary arotain 7.10 E.D.		AF070644	3.2	1.4	3.
KIAA1028 protein		AI525834	3.2	1.5	4.7
land (hacterial lantihiotic syntheters compound to the 1		AB028951	3.2	1.3	2.6
oxidate (ortochrome c) accombly 1 like	LANCL1	Y11395	3.2	2.9	2.8
	OXA1L	X80695	3.2	3.1	5.4
	OR2F1	U56421	3.2	2.8	0.3
72281 at 58980 at 58980 at 53402 at 44453 at 53156 at 53156 at 53156 at 53157 at 46221 at 46583 at 46522 at 46522 at 46522 at 46522 at 46523 at 46523 at 46523 at 46523 at 46523 at 46523 at 55819 at 55819 at 55819 at 55819 at 33273 at 4652 at 33273 at 3327	72281_at 58980_at zinc finger protein 155 (pHZ-96) 53402_at 24453_at 2455_at 2455_at 25195_at	zinc finger protein 155 (pHZ-96) zinc finger protein 155 (pHZ-96) Suppression of tumorigenicity 16 (melanoma differentiation) zinc finger protein 281 REK partner 1 HSPC142 protein biothinidase biothinidase biothinidase biothinidase cGI-44 protein; suffide dehydrogenase like (yeast) flightless I (Drosophila) homolog CGI-44 protein; suffide dehydrogenase like (yeast) flightless I (Drosophila) homolog KIAA1028 protein Lanc (bacterial lantibiotic synthetase component C)-like 1 CATS CATS ANA 1028 protein Lanc (bacterial lantibiotic synthetase component C)-like 1 CATS CATS ANA 1028 protein Lanc (bacterial lantibiotic synthetase component C)-like 1 Oxidase (cytochrome c) assembly 1-like Olfactory receptor, family 2, subfamily F, member 1	zinc finger protein 155 (pHZ-96) zinc finger protein 155 (pHZ-96) suppression of tumorigenicity 16 (melanoma differentiation) zinc finger protein 281 MEK partner 1 HSPC142 protein HSPC143 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC142 protein HSPC143 protein HSPC144 protein HSPC142 protein HSPC142 protein HSPC143 protein HSPC144 protein HSPC145	Advaged	Alignostic

Figure 11CCCCCC

709 at	tubulin, beta polypeptide	TUBB	100314	3.2	1.2	3.7
40478 at	hypothetical protein		AL021396	3.2	2.8	2.6
40568_at	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2	ATP6B2	L35249	3.2	1.8	4.3
294 s at	cell division cycle 2-like 1 (PITSLRE proteins)	CDC2L1	U04815	3.2	2	1.4
35869 at	ociated		AB020499	3.2	2.3	2.9
34291 at	phenylalanine tRNA synthetase-like	FARSL	U07424	3.2	1.6	3
33819_at	lactate dehydrogenase B	ПРНВ	X13794	3.2	2.4	4
41309 g at		CTBP1	U37408	3.2	2	3.6
39637_at		SLC26A2	U14528	3.2	3.2	3.2
39672_at	protein tyrosine phosphatase, non receptor type 7	PTPN7	M64322	3.2	4.4	4.6
40296_at	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane bound	XPNPEP2	AL023653	3.2	2.7	3.2
36846 s at	U6 snRNA-associ		AA121509	3.2	2.8	3.3
36957_at		PRKCBP1	W22296	3.2	2.5	3
36974 at	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	PSMF1	D88378	3.2	1.4	2.7
37385 at	CIk associating RS-cyclophilin		U40763	3.2	1.2	2.2
37700 at	bleomycin hydrolase	BLMH	X92106	3.2	1.4	2.7
38811_at	5-aminoimidazole-4-carboxamide ribonucleotide	ATIC	D82348	3.2	1.9	3.1
	formyltransferase/IMP cyclohydrolase					
56483_at			AA309047	3.2	2.1	4
75801_at			AI620827	3.2	2.4	3.2
58579_s_at	p47		W07096	3.2	2.3	3
63374_at	mucolipin 1	MCOLN1	AI816064	3.2	1.5	3.8
47463_at	eukaryotic translation initiation factor 2C, 1	EIF2C1	AA453723	3.2	3.1	2.9
54865_at	coronin, actin-binding protein, 1C	COROIC	N27805	3.2	2.9	3.2
60471_at	hypothetical protein FLJ22439		AA625133	3.2	2.9	3.1
65736_at	hypothetical protein FLJ20671		AA165689	3.2	0.5	4
72108_at	FSHD region gene 1	FRG1	AA856746	3.2	1.5	3.2
72643 i_at			AI758570	3.2	2.8	3.2
50235_at			AA207254	3.2	2.6	2.2
49242_at			N51263	3.2	2.6	3.2
43408 g at	DKFZP586F1524 protein		AW014654	3.2	1.6	3.3
43926_at			N36085	3.2	2.7	3.2
43967_at	ATP-dependant interferon response protein 1		AI826411	3.2	0	2.5
45331_at	hypothetical protein FLJ10355		AA102468	3.2	m	2.7

52691 at			AW014700	3.2	3.2	3.2
56441_at			W05842	3.2	1.7	3 M
65900_at	KIAA1436 protein		A1694579		m	3.7
56638_g_at			AI436183	3.2	1.8	3.2
53956_at			AA449296	3.2	2.6	2.8
46232_at	COP9 complex subunit 4		AI745197	3.2	1.6	3.5
54093_at	hypothetical protein		AI307252	3.2	2.7	2.4
74764_g_at	testis enhanced gene transcript (BAX inhibitor 1)	TEGT	AW013869	3.2	2	5.4
55664_at	annexin A11	ANXA11	AI923271	3.2	1.9	3.9
61119_at	CCAAT/enhancer binding protein (C/EBP), alpha	CEBPA	AI971171		2.7	3.1
52340_f_at	MYC-associated z	MAZ	AA025883	3.2	2.4	2.6
	factor)					
54978_at	solute carrier family 25 (mitochondrial carrier; ornithine transporter)	SLC25A15	AI885329	3.2	E	1.4
-1						
64517_at	KIAA0747 protein		A1972594	3.2	2.4	8
68682 f at			AI636095	3.2	2.8	2.8
55565_at	hypothetical protein FLJ20424		AI745491	3.2	2.5	3.2
47156_at			AI032786	3.2	2.5	2.9
46714_at	kiaa iso protein		AA524098	3.2	2.2	4.1
38688_at	KIAA0461 protein		AB007930	3.1	3.3	7.4
37472_at	mannosidase, beta A, lysosomal	MANBA	U60337	3.1	5.6	3.5
31851_at	ret finger protein 2	RFP2	AJ224819	3.1	0.4	1.9
31853_at	embryonic ectoderm development	EED	AF080227	3.1	4.3	0
34997_r_at	frizzled (Drosophila) homolog 5	FZD5	U43318	3.1	1.7	4.1
31884_at	hypothetical protein		L40399	3.1	0.8	0
40049_at	death associated protein kinase 1	DAPK1	X76104	3.1	0.7	0
40282 s_at	D component of c	DF	M84526	3.1	2.4	0
452_at	SWI/SNF related,	SMARCC1	U66615	3.1	6.0	0
	chromatin, subfamily c, member 1				•	
32804_at	RNA binding motif protein 5	RBM5	AF091263	3.1	1.3	1.2
33887_at	hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	D84064	3.1	1.6	0
39099 at	Sec23 (S. cerevisiae) homolog A	SEC23A	X97064	3.1	2.2	0
39620_at	POU domain, class 6, transcription factor 1	POU6F1	221966	3.1	1.8	2.2
35335_at	Rho associated, coiled coil containing protein kinase 2	ROCKZ	AB014519	3.1	2.7	9.9
35703_at	platelet-derived growth factor alpha polypeptide	PDGFA		3.1	1.2	0.8

Figure 11EEEEEE

40013_at	chloride intracellular channel 2	CHCS	Y12696	3.1	1.41	0.0
1660_at	ubiquitin conjugating enzyme E2N (homologous to yeast UBC13)	UBE2N	D83004	33.1	1 6 1	7.0
37172 at	carboxypeptidase B2 (plasma)	CPB2	M75106	3.1		12
31481_s_at	_	TMSB10	M92383	3.1	2	2.9
362_at	protein kinase C, zeta	PRKCZ		3.1	0	0.2
37278_at	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial	TAZ	1	3.1	0.1	3.1
	fibroelastosis 2; Barth syndrome)				-	
37564_at	DKFZP434F162 protein		AL080201	3.1	0	2.7
38046_at	IK cytokine, down-regulator of HLA II	三	AJ005579	3.1	2.6	O
38065 at	high-mobility group (nonhistone chromosomal) protein 2	HMG2	X62534	3.1	2.1	1.4
36423_at	p8 protein (candidate of metastasis 1)		W47047	3.1		15.6
36442_g_at	potassium large conductance calcium-activated channel, subfamily M,	KCNMA1	U02632	3.1	1.5	2.3
559 s at	homeo box 11 (T-cell lymphoma 3-associated breakhoint)	100	030777	2 .		,
38842 at		1100	24/000	3.1	7 -	2.0
			A1360291	3.1	3.1	4.9
63919 f at	ectodermal-neural cortex (with BTB-like domain)	FNC1	M85329	2 7	10	2.4
43421 g at	kinesin protein 9 ge		AA625821	3.1	1 8	1.4
57786_at			W02232	3.1	3.1	100
50975 s at	\neg	SCML1	AW022735	3.1	1.4	1.5
43835_at	KIAA1449 protein	KIAA1449	N91136	3.1	2.9	2
83661_r_at	hypothetical protein FLJ22215		AI972942	3.1	1.2	0.5
50801_at			AI276956	3.1	1.7	2.4
66258 at			AA648468	3.1	1.8	3.3
60263_at			AA126730	3.1	4.0	3.2
57524 at			AI821146	3.1	2.2	2.5
81672_at			W38444	3.1	6.0	0
46523_at			AA703310	3.1	1.2	1.8
76786_at			AI733079	3.1	0	3.3
74425_at			AI742694	3.1	1.2	0.7
74487_at			AI733562	3.1	3.4	2.3
78234_at			AI733569	3.1	0.3	2.5
75049 g at	hypothetical protein FLJ13984		AA041295	3.1	2.4	0.7
82436_at			AI242023	3.1		0.5
42613_at			N64684	3.1	1.2	23

Figure 11FFFFFF

80048_at		AA406555	3.1	9.0	
33304g at		A1247411	3.1	2.3	1.7
s at		AI640222	3.1	3	2.4
63310_at hypothetical protein PRU09/1		AI807379	3.1	1.1	1.2
636/1_at		R52673	3.1	0.4	1.9
04194_at		T52159	3.1	1.3	5
4/346 at		H04453	3.1	3.5	2
31010 at		AI740822	3.1	1.7	4.9
02390_1_at		R44193	3.1	6.0	
03148_at	1	AA749167	3.1	6.0	0.8
83060_at		A1569653	3.1	2.3	
60507_at		AI457453	3.1	1.6	C
49363 at Cul-149 protein	1	AA167070	3.1	3.2	0.7
100134 at	/	4A291194	3.1	4.8	10
40223 al	1	4A243661	3.1	2.2	2.4
063/2_at 70355_4	1	AA993965	3.1	0.2	0.1
/ 9350_at	<i>t</i>	AA287513	3.1	1.2	0.3
75/23 at	,	AI793256	3.1	1.5	0.0
8632/J_at		T85261	3.1	4.2	2.6
80300 c.t		AI679563	3.1	0.3	2.2
68/90_rat	/	AI680842	3.1	2.3	
69735 at	,]	AI183829	3.1	1.3	m
09494_at	/	AI703451	3.1	9.0	1.5
64345_s at KIAA1102 protein	A	AW003533	3.1	3.5	23
29/39 Tat		AI743273	3.1	0.8	0.3
70054 at 70142 at	,	AI 798146	3.1	1.8	6.0
10142_d1		AI800042	3.1	1.3	2.8
77876	`	AI422384	3.1	0.4	0.7
100		AI970209	3.1	0.3	0.7
62134_di NELI-SHERICINB Transcription factor	REST /	AI872294	3.1	1.1	1.6
82072 3+	∢	AW024260	3.1	4.1	2.4
75332 at		W15168	3.1	1.1	1.4
61400 : 24	4	AL045360	3.1	2	1.9
01400 at	/	AI952593	3.1	1.8	0
8205/_at	4	AA181363	3.1	2.5	

Figure 11GGGGGG

ln

	A1991451	3.1	1.5	
1 1 2 2 2 2 2 2	AI378363	3.1	2.7	27
hypothetical protein, clone Telethon(Italy_841)_Strait02270_FL142	AI628609	3.1	0	
		3.1	2.6	C.
ribosomai protein 518	RPS18 AI990458	3.1	2.6	
	AI253134	3.1	m	4 1
	A!472026	3.1	0.7	0.2
	AA777488	3.1	1.6	4
	AI792647	3.1	2.3	0 7
	AI521246	3.1	1.7	6.0
	AA626793	3.1	3.6	17
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AI554439	3.1	0.2	00
ilypotrietical protein FLJZ0036	AW006276	3.1	0.4	2.5
	N22751	3.1	7.2	0 1
	A1972964	3.1	1.7	20.0
	AA165313	3.1	2.3	21-
	AI446414	3.1	3.8	12.7
Ovelic AMP phoenhometrie 10 1.5	AI761595	3.1	1.5	1.8
	- 1	3.1	1.8	0.7
		3.1	6.0	0.2
operation in Symmetry (congenital erythropoletic porphyria)	UROS AW016762	3.1	1	2.4
RE1 (TRE1), interacting purplacy factor of	- 1	3.1	П	0.3
KIAA1450 protein	TINF2 W25667	3.1	3.9	1
transmembrane prostate androces indicate only	\rightarrow	3.1	2.5	0.7
mondiane, prostate androgen monced KIVA	TMEPAI AA535819	3.1	1.9	0
	AA968576	3.1	1.9	0.5
KIAA1191 nrotein	AI765321	3.1	4.3	5.6
	N23782	3.1	2.4	0.7
	AI768697	3.1	1.6	8.6
hypothetical protein MCC10264	AA151719	3.1	6.7	3.4
	AA602884	3.1	1.8	1.8
	AI150454	3.1	2.2	5
	N30122	3.1	1.8	1.6
	2825184	3.1	2.9	1.2
	** ***			

Figure 11HHHHHH

Ti.

86451 at			AI683426	3.1	2.8	
38613_at	putative cyclin G1 interacting protein		U61837	3.1	2.1	2.4
1933 g at	ATP binding cassette, sub-family C (CFTR/MRP), member 5	ABCC5	U83661	3.1	2.5	3
38976_at	coronin, actin-binding protein, 1A	CORO1A	D44497	3.1	3.1	m
943_at	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1	RUNX1	D43968	3.1	1.8	m
37835 at	CD1C antigen, c polypeptide	CDIC	M28827	3.1	2.7	2.9
37845_at	hematopoietic protein 1	HEM1	M58285	3.1	1.6	3.3
39783_at	KIAA0100 gene product		D43947	3.1	2.4	3.1
40077_at	aconitase 1, soluble	ACO1	Z11559	3.1	1.9	2.8
40127_at	paired mesoderm homeo box 1	PMX1	M95929	3.1	1.5	3.3
40537_at	KIAA0741 gene product		AB018284	3.1	1.7	2.9
38242_at	B cell linker protein		AF068180	3.1	2.7	3.1
40801_at	DKFZP434C212 protein		AA643063	3.1	1.3	2.8
40879_at	KIAA0699 protein		AB014599	3.1	2.2	3.3
34660_at	ribonuclease, RNase A family, k6	RNASE6	AI142565	3.1	2.7	2.9
35165_at			AF070582	3.1	0.2	e
174_s_at	intersectin 2	ITSNS	U61167	3.1	1.7	2.7
514_at	Cas-Br-M (murine) ectropic retroviral transforming sequence b	CBLB	U26710	3.1	1.3	3.2
41600_at	proliferation-associated 2G4, 38kD	PA2G4	U59435	3.1	2.9	3
880_at	[FK506-binding protein 1A (12kD)	FKBP1A	M34539	3.1	1.2	4.1
36592_at	prohibitin	РНВ	S85655	3.1	2.9	2.1
37031_at	C9orf10 protein		D80005	3.1	1.2	3.4
37268_at	vascular endothelial growth factor B	VEGFB	U43368	3.1	6.0	2.2
32589_at	chromatin assembly factor 1, subunit A (p150)	CHAF1A	U20979	3.1	2.1	1.9
38078_at	filamin B, beta (actin binding protein 278)	FLNB	AF042166	3.1	1.7	2.1
38000_at	pyruvate carboxylase	PC	S72370	3.1	2.6	m
38338_at	related RAS viral (r·ras) oncogene homolog	RRAS	AI201108	3.1	2.4	2.2
48123_s_at			AI022930	3.1	2.1	3.3
	similar to rat nuclear ubiquitous casein kinase 2		A1380204	3.1	2.2	3.8
62311 g_at			W96015	3.1	1.9	2.7
57030_at			W26295	3.1	3.1	3.1
53860_at			AA453352	3.1	1.7	1.8
47909 at	zinc finger protein 106		N26630	3.1	2.6	2.6
62889_at	KIAA0675 gene product		D29070	3.1	3.1	3.1

Figure 11IIIII

52811_at	aryl hydrocarbon receptor nuclear translocator	ARN	AI768497	3.1	2.1	4 1
747.33 at			AA256195	3.1	1.7	2.2
65745 s at			AI479056	3.1	2	3.1
65750 + 2+	1001400014		AI685714	3.1	0.7	3.6
63600 4 24	Hypothetical protein		N75645	3.1	0.1	29
-1 °			AW021173	3.1	2.9	3.2
1031E at			AA677588	3.1	2.5	2.6
65774 at			AI770110	3.1	9.0	2.2
62210 at	TOE3 (FOA) fusion norther (in abiliate and		AI556963	3.1	1	3.8
64272 at	I C. S. L. C. J. Institute (III C. III dried C. Leukernia)	TFPT	AI309849	3.1	2.4	3
10128 24			AW024964	3.1	3.4	3.6
57171 24	in the property of the second order order orde		`	3.1	2.8	2.4
55500 24	hungthatical scatain process of	CHST6		3.1	2.4	m
51203 at	וואסטוופווים איים איים איים איים איים איים איים		AI936523	3.1	1.7	29
00501 at			AA775177	3.1	2.5	000
64594 at	unit-interacting protein		A1660343	3.1	3.5	3.0
04304 at			H87175	3.1	er.	100
32000 at			AI860012	3.1	2 1	200
52179 at			AI302185	3.1	2.2	3.1
021/0 at	UV IOO		AA613328	3.1	-	2 5
45009 at			AA725071	3.1	2.4	6.3
57.337 at	Diatelet/Eridotnellal cell adhesion molecule (CD31 antigen)	PECAM1	L34657	3.1	2.1	23
			W63805	3.1	3.1	i c
48720 at	NATIA, ITIETIDE OF KAS Oncogene family	RAP1A	_1	3.1	2.5	2.7
50238 at			AA627644	3.1	2.9	2.9
37883 i at	hynothetical protein		AI801902	3.1	2.2	2.4
39727 at	dual energiativ photophataca 11 / DNIA / DNIA		AI375033	8	1.6	9.9
39744 at	DEAD/H (Asp. Ch. Als Asp./His) how not most at a	DUSP11	- 1	3	2	0.3
40200	heat shock transmisting facts 1	EXQQ	`	œ	1.5	8.5
40787 at	יופמן אוטכע נומוואכרוטנוטוז זמכנסר ב	HSF1	M64673	8	3.6	0 6
40638 at	in in the factory and in the fac			e	1.5	2.7
1000	spircing factor profile/glutamine fich (polypyrimidine tract-binding protein-associated)	SFPQ	X70944	m	2	0.1
40928_at	DKFZP564A122 protein		2012011	(
1388 g at	7		W20450	n	1.8	2.4
		VDR		m	13	C

Figure 11JJJJJJ

32833_at	CDC-like kinase1	CLK1	M59287	E	2.2	3.0
33470_at			AF052177	m	0	000
31697 s at	ferritin, heavy polypeptide pseudogene 1	FTHP1	J04755	m	1.2	
35218 at	programmed cell death 10	PDCD10	AF022385	m	6.0	C
40290_f_at	sialyltransferase 4A (beta-galactosidase alpha-2,3-sialytransferase)	SIAT4A	L13972	m		2.2
38741_at	pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin-2)	PSCD2	U70728	8	2.7	C
34575_f_at	melanoma antigen, family A, 5	MAGEAS	010689	m	0.4	43
34827_at	unc 51 (C. elegans) like kinase 1	ULK1	AF045458	m	0.3	0.5
34867_at	fatty acid binding protein 3, muscle and heart (mammary derived growth inhibitor)	FABP3	AI041520	m	2	2.1
35317_at	meningioma expressed antigen 5 (hyaluronidase)	MGEAS	AB014579	m	3.3	4 4
36118_at	nuclear receptor coactivator 1	NCOA1	AJ000882	3	4.5	4 4
1102_s_at	nuclear receptor subfamily 3, group C, member 1	NR3C1	M10901	m	1 1	6.4
36963_at	phosphogluconate dehydrogenase	PGD	U30255	e	1.3	0.1
37317_at	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD)	PAFAH1B1	L25107	m	1.4	3.5
37376_at	ORF		M68864	m	1.6	С
38372_at			U66042	3	7.5	C
37943_at	KIAA0321 protein		AB002319	m	1.5	0
37968_at	lymphocyte antigen 117	LY117	AF031137	m	0.7	2.5
33167_r_at	adenylosuccinate synthase	ADSS	X66503	3	0.1	0.2
54686_at	thyroid hormone receptor associated protein, 240 kDa subunit		AA122265	m	2.5	4.5
52207_at	protein phosphatase 4 regulatory subunit 2		W87465	m	0.8	
76949_at			A1187760	e	0.1	2.4
888/9_at			AI378857	8	0	0.8
59096_at			A1082856	m	0.5	1.5
90037_at	Ewing sarcoma breakpoint region 1	EWSR1	AW001288	m	2.8	0.5
66880_at			AI733050	e	m	5.7
/6/04_s_at			AI817195	e	1.7	0.5
78992_at			AI791323	m	0.5	1.3
/9240_at			AI435163	e	0	3.9
802/5_at			R25709	3	1.2	1.9
62048 at			AI192486	3	6.0	3.2
80313_at			AI215686	æ	1.9	3.8

47221_at		H58608	r.	3.9	0.0
55135_at		AI300834	m	1.5	90
67251_at		AI379741	m	0.2	0.0
47240_at		R02354	m	111	0.0
85242_at		AI472855	m	2.1	
85667_at		AI932342	m	17	
		AA651889	E C	8	1
67091_at		AI081782	m	60	1
91495_r_at	major histocompatibility complex, class I, A	HLA.A R99989	3		8.0
88013_at		AI332638	m	1.2	2.9
88052_at		AI018179	m	0.7	2.9
79512_at		AI248270	m	2.5	8.5
88760_at	- 1	AI766117	e	1.9	2.4
5//92 at	zinc finger protein, subfamily 2A (FYVE domain containing), 1	ZNFN2A1 AA399630	က	2.7	3.6
7/814 t at		AI884831	e	1	3.2
70582_at		M79158	e	2	9.0
/0/98_at		A1400344	3	0	0.4
64293_at		A1971000	e	0.8	25.6
/1543_at		AI935074	m	2	1.7
89718_at		AI051304	m	0.8	2.6
85190_at		AA737437	3	0.7	i
73424 r at		A1962748	3		C
66099_at		A1983166	3	2.4	0.0
74354_at		AI982590	m	2.4	12.
	hairy/enhancer-of-split related with YRPW motif 1	HEY1 R61374	m	1.5	
/8114_t_at		AW016419	m	1.8	
8/219 s at		AI018560	8	1.4	
8004/ at		AA689588	c	0.3	6.0
76802 at	core promoter element binding protein	COPEB A1355637	e	0.3	10.1
46229 at		H23103	m	0.8	0
6/6/6 at		AI040114	m	2.3	1.5
88959 at		AA528441	m	2.5	0
52016 at		AI672414	e	2.6	3.1
9016/ at		AI684439	m	2.3	10.3
49172_at	Inudix (nucleoside diphosphate linked moiety X)-type motif 5	NUDT5 AI694646	m	2.5	-

Figure 11LLLLLL

ntors:

56366_at		20000544			
71526 f at		AA700900		4	1.5
46661 at	hypothetical protein El 110474	Al686949		Č	1.4
58597 5 24	_	AA142988	3	2.9	2.4
7000 at		N53553	3	1.2	0.7
40000 at		N81145	3	1 9	200
04443 at	EH-domain containing 4	EHD4 AI971203		30 %	3.5
62489_at	hypothetical protein FLJ13078	AA897088			
54487_at		AA044626	2 6	0 -	4.0
48573_at	zinc finger protein 161	7NF161 AA452188		3.1	3.1
45556_at	KIAA1235 protein	+		0.0	9.0
54902_at		20100410		2.2	2
59066 at		700001		0	1.1
56065 at		AL036615		2	1.7
52892 at		AA524267	e	2.4	1.4
5707E of		AI761092	က	0.5	m.
51100 at		AA810923		1.8	C
01100 at		AA831618		- C	0
63110_at		W91938	7	0 0	-
86346 at	- 1	AA528523			J. 0
39830_at	ribosomal protein L27	PPI 27 AAAAA33		0.0	20.0
39041 at	dihydrolipoamide Stacetyltransferase (F2 component of accounts)	4.		2.7	5.8
1	dehydrogenase complex)	DLA1 Y00978	m	1.6	1.6
37769_at	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor. 4	EDG4 AF011466	3	6.0	1.8
39751 at	DHHC1 protein				
10	isocitrate dehydrogenase 3 (NAD±) heta	۲	3	0.9	3.1
33396 at	glitathione Ctransferson si		3	1.8	m
1468 at	heat shock protein 75	GSTP1 U12472	ĸ	1.3	3.9
41778 at	7.3 (2.2.1) and a second of the second of t		3	1.6	2.7
41000 34	chackpoint currently (iteutial armino acid transporter), member 5	SLC1A5 U53347	e	1.3	00
22207 at	Cleckpoint suppressor 1	CHES1 U68723	ĸ	1.4	200
33337_at	CDF-Clacy/glycerol-:filositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	CDIPT AL050383	Е	1.8	3.2
35167_at	KIAA0433 protein	AB007893	~	2 1	c
39593_at	- 1	FGL2 AI432401	0 0	2 1	2.3
33485 at	Iribosomai protein L4	ı) m	0 0	7.0
35329_at	cytochrome b5 reductase 1 (B5R.1)	١٦	5 6		j (
		דטטענטט וה ן	3	2.8	2.8

Figure 11MMMMMM

35221 at			X91648	m	6	1 6
34369 at	KIAA0214 gene product		D86987	C.	1.4	23
36011_at	syntaxin 10	STX10	AF035531	m	1.6	1
34837_at	KIAA0376 protein		AB002374	m	1.9	2.9
40024_at	src homology three (SH3) and cysteine rich domain	STAC	D86640	m	3.1	3.3
35773_i_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18)	NDUFB7	AA527880	m	2.7	2.6
35796_at	protein tyrosine kinase 9-like (A6-related protein)	PTK9L	۲۱7169	m	1.4	2.9
37306_at	KIAA0068 protein		D38549	m	1.8	4.2
37345_at	calumenin	CALU	AF013759	3	1.1	3.4
36792_at	tropomyosin 1 (alpha)	TPM1	224727	m	ĸ	2.9
37680_at	A kinase (PRKA) anchor protein (gravin) 12	AKAP12	U81607	e	1.1	2.9
37647 at	acyloxyacyl hydrolase (neutrophil)	AOAH	M62840	e	2.2	2.7
38336_at	KIAA1013 protein		AB023230	m	2.5	2.9
43459_at	KIAA0680 gene product		AI472209	m	6.0	3.2
38680_at	small nuclear ribonucleoprotein polypeptide E	SNRPE	M21259	m	2.1	2.9
56426_at	hypothetical protein FLJ22351		AA177127	е	5.6	2.6
65125_at	dolichyl-phosphate mannosyltransferase polypeptide 3	DPM3	AI817330	m	2.7	က
48498_at			AA868896	m	2.7	3.4
53730_at			M60775	8	2.9	m
83320_at	translocase of inner mitochondrial membrane 44 (yeast) homolog		A1494453	က	2.4	2.3
56544 g at	56544 g_at elF4E-transporter		R50754	3	1	1.4
90724_at			AA885833	8	3.3	3.3
80095_at			AI271326	m	1.5	2.5
54648_at			AA810864	c	С	1.8
58321_at			AL048542	3	2.3	2.4
82998_at			AI380429	3	2.6	2.8
54810 i at	KIAA1143 protein		AI745170	3	2.8	2.2
48595_at	hypothetical protein FLJ10210		AA707400	3	2.8	2.8
54867_at			R41296	က	1.8	3.3
63323_at	hypothetical protein MGC3234		C05777	m	2.4	3.1
59616_at			AI621286	3	1.1	1.9
32800_at	retinoid X receptor, alpha	RXRA	066306	3	2.9	2.6
50219_at	ImRNA for FLJ00023 protein		W27853	3	1.3	2.8
43827_s_at			103298	n	2.4	3.7

64061 at	hypothetical protein El 10010E		AW006145	3	3	
64934 at	in FLUZZI 93		AL121007	m	000	6
46315 24	Caralyout, translation Initiation factor 2B, subunit 3 (gamma, 58kD)	EIF2B3	AI660531	o cr	0.0	o c
130EA			AA233808	0 0	0.7	3.4
13634 at			0000000	0	3.5	4.8
51267_at			AW004/30	m	2.8	2.9
864_at	homeo box HB9		_1	3	2.2	2.6
51997_at		HLXB9		3	2.6	
45205_at			AA704789	3	2.7	0
46403 at			N21193	m	2	0
52094 at	Similar to plucosamine. 6. sulfatases		AI984021	E	2.6	200
52120 at			AI688582	m	2.8	
52124 at			AA628439	m	0	2 5
64368_s_at	hypothetical protein FI 110470		AI805463	m	2	
3031_s_at	apoptosis-related r		AW001184	3	2	3.4
46097 at			AA521316	æ	2.9	e e
53626 at			AI831258	m	2.7	5
46677_at			AI417834	m	2.6	10
47046_at			AI762760	3	1.6	27
49549 at	CD36 antigen (collagen type I recentor thrombs		H98090	က	1.3	6
43499_at	tropomyosin 1 (alpha)	CD36	R20784	က	m	00
55611_at	hypothetical protein FI 120011	TPM1	N76371	m	2.6	26
48910_at			AA242757	က	3.4	3.4
39427_at	ubiquinol-cytochrome c reductase hinding protein		AI742347	3	3.1	3.2
.158_s_at	calmodulin 3 (phosphorylase kinase delta)	UQCRB	T79616	2.9	2.2	3.6
40220_at	HMBA·inducible	CALM3	J04046	2.9	1.5	
40546_s_at	NADH dehydrogena		AB021179	2.9	2.5	200
		NDUFA2	AF047185	2.9	1.8	3.3
40435_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	SLC25A6	103592	2.9	1.8	3.7
32774_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI)	NDUFB8	AI541050	2.9	(F)	4.2
41243 at			AR007916			
34/43_at	Inuman homolog of Drosophila Scribble		0.000	6.3	7	2.9
			XTX	2	•	

Figure 11000000

33020_41	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, cultiamily a mamber t	SMARCE1	SMARCE1 AF035262	2.9	1.5	4.2
39588 at	tumor necrosis factor (ligand) superfamily, member 12	TNFSF12	AF055872	60	2.5	60
39516_at	hypothetical protein		AI827793			2
32696_at	pre-B-cell leukemia transcription factor 3	PBX3	X59841	2.9	6.0	
33432_at			AI547308	2.9	1.6	1.6
33641_g_at	allograft inflammatory factor 1	AIFI	Y14768	2.9	2.3	2.8
36030_at	DKFZP58612223 protein		AL080214	2.9	1.5	
36076 g at	putative GTP-binding protein similar to RAY/RAB1C		AL037167	2.9	2.3	2.9
35342_at			AF052159	2.9	2.5	2.6
41824_at	CGI-48 protein		A1140114	2.9	1.6	2.7
35779_at	vacuolar protein sorting 45B (yeast homolog)	VPS45B	AJ133421	2.9	2	2.1
36135_at	nucleolar protein p40; homolog of yeast EBNA1 binding protein		U86602	2.9	2.7	2.9
36624 at	IMP (inosine monophosphate) dehydrogenase 2	IMPDH2	L33842	2.9	2.2	4.2
36644_at	CD151 antigen	CD151	D29963	2.9	1.8	2.8
32971_at	Friedreich ataxia region gene X123		L27479	2.9	2.6	2.6
33660_at	ribosomal protein L5	RPL5	U14966	2.9	2.4	4
37736_at		PCMT1	D13892	2.9	0.7	
38107_at	unc119 (C.elegans) homolog	UNC119	040998	2.9	3.2	2.2
40695_at	IMP (inosine monophosphate) dehydrogenase 1	IMPDH1	J05272	2.9	2.7	κi
37966_at	beta-parvin		AA187563	2.9	9.0	4
38770 <u>a</u> t	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	ADAM12	AF023476	2.9	2.9	2.
37978_at		QPRT	D78177	2.9	2.8	2.7
	pyrophosphorylase (carboxylating))					
	putative glialblastoma cell differentiation related		AF068195	2.9	2	2.6
38282_at	a disintegrin and metalloproteinase domain 15 (metargidin)	ADAM15	U41767	2.9	2.9	1.
38290_at	regulator of G-protein signalling 14	RGS14	AF037195	2.9	2.6	2
	Homer, neuronal immediate early gene, 2		AF093264	2.9	0.5	3.4
48010_at			W02538	2.9	3.3	4.4
48079_at			AI824079	2.9	2.4	2.5
56881 <u>a</u> t			AI807211	2.9	1.6	w.
			AI822003	2.9	2.4	2.5
48271_at			AI683752	2.9	2.8	2.9
78442 at	hypothetical protein MGC4692		AI819340	2.9	2.9	2.9
57818 at	hypothetical protein d 1460009 0		2100001	C	0	٥

Figure 11PPPPPP

51034_at 47994_at 65694_at	in position protein Mac2010		AI077662	7	20	
			AI761602			
	KIAAU/88 protein		A1183987		1.3	6.3
T	eukaryotic translation initiation factor 2C, 2	EIF2C2			1.0	7) (
			上	000	0.00	2.0
74047 r at	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	WAS	1		2.3	3.6
-u,			AW023188		3.4	2.5
44041 at			AA570398	2.9	2.9	16
T	3280 V 81		H03287	2.9	1.5	
T	NIAAUS/ b protein		AA524529	2.9	2.7	5.5
T	apolipoprotein C.1		W75954	2.9	2.1	2.8
Τ	apolipopi oceni oci	APOC1	AW005911	2.9	1.1	2.7
Τ	hypothetical protein El 110041		AW003067	2.9	É	3.3
,	FH domain hinding mitotic phornhological		AI768100	2.9	1.5	2.5
66136 s at			_	2.9	2.1	3.3
60079 s at	hypothetical protein El 190920	TM9SF2		2.9	2.1	4.8
50979 s at			AA999701	2.9	2.4	2.7
	hynothetical protein El 110666		AI968170	2.9	2.1	2.9
			AI684281	2.9	2	2.3
Т	WD reneat domain 3			2.9	1.9	2.8
Γ	:1	WDR3	A1880771	2.9	2.1	3
Γ	heta-site APP-cleaving engyme			2.9	3.6	1.4
÷	cord crowning crityline	BACE	. 1	2.9	2.9	2.9
1 10	hynothetical protein El 110660		AA604243	2.9	2.4	3
Γ	Diobany hydrolasa lika (sarina hydrolasa, hydrolasa)		4	2.9	2.6	3
	associated antigen)	BPHL	AA526961	2.9	1.8	2.7
1			W02300	000	C	
4626/ at 1	hypothetical protein FLJ14153		AI949941	2.9	1 6	3.5
T			AA127629	2.9		8 0
T	enducytic receptor (macrophage mannose receptor family)		AW007248	2.9	1 00	2.6
te 0	jagged 1 (Alacille cyndromo)		AI125581	2.9	2.1	26
; t		JAGI		2.9	6.0	2.9
1 6	יודי ווד מסווימיוווון או חובווו		N90883	2.9	2.7	2.8
25000 at			AI052530	2.9	2.7	26

Figure 11QQQQQQ

Inventors: Response of Dendritic Cells to a...

Inventors: Nir Hacohen, et al.

17001			W61056	2.9	1 6	000
1/304 al			H93046		0.40	2.5
38/U2_at	histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit		AF070640	2.8	2.2	3.1
41462_at	sorting nexin 2	CAINO				
40720_at	adenosine A2b receptor pseudogene	ZYNC	_1	2.8	0.6	2.5
39700 at	Rho GTPase activating protein 1	ADORAZBP	AL022398	2.8	0.5	3.6
40196 at	HYA22 protein	ARHGAP1	Al961929	2.8	1.8	4.3
39772 at	hynothetical protein MGC2683		D88153	2.8	2.1	22
674 0 24	mothylonototraki direktak		AF007157	2.8	г. П.	200
10 10	methenyltetrahydrofolate denydrogenase (NADP+ dependent),	MTHFD1	J04031	2.8	1.9	2.6
	synthetase					
41209_at	lipoprotein lipase					
254_at	H3 histone, family 3A	141	M15856	2.8	2.6	2.3
1676_s_at	ion elongation factor 1	H3F3A	- [2.8	1.3	4.6
33466 at	Paris Againia	EEF1G		2.8	2.6	4.6
37034 at	Dutative human HI A class II associated exetain		AF038182	2.8	2.1	2.4
34330 at	Cytochrome c oxidase subjust VIII2 polyanatida 2 111		U73477	2.8	2	23
33632 g at		COX7A2L	AB007618	2.8	1.7	4
35338 at	paired basic amino		AF023612	2.8	1.4	3.5
	receptor protein)	PACE	X17094	2.8	3.1	3.5
1375 s_at	tissue inhibitor of metalloproteinase 2	TIMADO	10000			
35761_at	aminoadipate-semialdehyde dehydrogenase-phosphopagatathoing	ZHALL	M32304	2.8	0.1	3.7
	transferase	AASOHPPT	AL050073	2.8	1.3	2.5
36856_at			0.000			
37333 at	DNA (cytosine-5-) methyltransferase 1	1111111	W28/43	2.8	1.7	3.3
1138_at	solute carrier family 20 (phosphate transporter) member 1	DININ I	X63692	2.8	1.7	2.2
32585_at	erythrocyte membrane protein band 4 1 like 2	SLCZUAI	L20859	2.8	1.8	3
36798 g at	sialophorin (gpl. 115. leukosiali	EPB41[2	AF027299	2.8	8:0	8
31638 at	guanidinoacetate N-methyltrans	SPN	J04168	2.8	1.2	2.2
1815 g at	transforming prowth factor heta recentor il 70 001.5	GAMT	AC005329	2.8	1.2	23
39113 at	profein distriffide isomerase related profein (70-80KD)	TGFBR2	D50683	2.8	1.4	25
ļ	intestinal-related)		AI262789	2.8	1.6	2.6
39165_at	nitrogen fixation cluster-like		107701	C		
89930_s_at			04/101	2.2	1.1	2.8
			KCC31(/K/V			

Figure 11RRRRRR

56431_at	hematological and neurological expressed 1	HN1	N90863	c.1 80	1.6	2,6
48119 at	nuclear body protein Sp140		AI796726	2.8	1.4	3.2
58872_at			A1983986	2.8	1.5	1.6
53749_at	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	NDUFC2	AL050278	c4 00	2.3	5.6
	Tax interaction protein 1		AW007343	2.8	2	m
31804_f_at	sulfotransferase family, cytosolic, 1A, phenol preferring, member 1	SULT1A1	X78283	2.8	2	1.7
84903_f_at			AI264299	2.8	2.6	2.6
49292 s at	ras responsive element binding protein 1	RREB1	AI097330	2.8	1.6	2.6
65507_at	eukaryotic translation initiation factor 4 gamma, 2	EIF4G2	AI749642	2.8	1.6	2.4
48599_at			AA824370	2.8	1.4	2.5
57086_at	protein kinase C and casein kinase substrate in neurons 2	PACSINZ	AA814516	2.8	2.7	3.9
59113_at			AA513002	2.8	0.8	2.1
75059_at	bridging integrator 1	BINI	AW009683	2.8	2.1	2.8
69646_i_at			AA758581	2.8	2.5	2.8
82472_at	hypothetical protein FLJ10392		AI873281	2.8	6.0	2.7
71094_at			AA027791	2.8	2.2	2.8
57026_s_at	secretory carrier membrane protein 2	SCAMP2	AA825494	2.8	2.1	3.1
45515 s at	45515_s_at methionine sulfoxide reductase A	MSRA	R55759	2.8	3.1	3.3
44071_at	anaphase-promoting complex subunit 4		AA604393	2.8	1.1	3.4
45739_at	hypothetical protein FLJ11210		AA056538	2.8	1.5	2.3
59452_at			AI719167	2.8	2.8	2.9
76856_at			AW025602	2.8	1.8	2.6
65830_at	FXYD domain containing ion transport regulator 5	FXYD5	AA044211	2.8	2.4	2.9
60871_at	AD023 protein		AI924180	2.8	2.5	2.8
61712_at	hypothetical protein PR00823		AI990512	2.8	2.1	3.7
45114_at			AI815763	2.8	2.5	2.7
60289_at	KIAA1323 protein		A1160081	2.8	2	3.8
51960_at	COPZ2 for nonclathrin coat protein zeta COP		AI984000	2.8	3	2.6
75258_f_at	ets variant gene 5 (ets-related molecule)	ETV5	AA224344	2.8	2	2.8
57918_at	DKFZP586G1517 protein		AA779617	2.8	2.6	2.8
46887_at			AI887726	2.8	6.0	3.4
46225 at	MO25 protein		AA524350	2.8	3.3	3.4
51139 at	vacuolar protein sorting 29 (yeast homolog)	VPS29	1_	2.8	2.1	3.6
64005_at	integral inner nuclear membrane protein		AA218866	2.8	2.4	2.4

Figure 11SSSSSS

C C C C C C C C C C C C C C C C C C C	at andon semio rotionitum aline		AI / 39473	2.8	2.6	20
47056 at	endoplasinic reticularn glycoprotein		A1986375	2.8		ilıc
18511 at	TDIADS costois		AA496318	2.8	1.0	0
65798 at	היא ליים היא ליים היא ליים היא ליים היא ליים היא ליים היא ליים היא ליים היא ליים היא ליים היא ליים היא ליים היא		H08320	2.8	1 4	4
55658 at			AI684486		1 4	500
52000 at	- 15		R76178	2.8	2.5	ilc
1000E of	related RAS Viral (r-ras) oncogene homolog	RRAS		2.8	000	2.5
40003 at			AI862553	800	0 0	
39612 at	mitochondrial ribosomal protein L12	MRPL12	X79865	2.7	0.7	2 6
38985 at	leptin receptor overlapping transcript-like 1		AF063605	7.0	22	7.7
39043_at		ARPCIB		27	0.5	
6//_s_at	acid phosphatase 5, tartrate resistant	ACP5	ᆚ	7.70	0.0	4.3
34946_at	_	I SEE	′]⊲	2.7) ! ,	2.2
34960 g at	Fc fragment of IgE, low affinity II, receptor for (CD23A)	0000	1	120	1/	2.7
31852_at	hypothetical protein DKFZp5640	LOENZ	Ľ	2.7	1.8	2.8
31583_at	ribosomal protein S8	0000	1	2.7	1.2	2.6
32120 at	Imitotic spindle coiled coil related protein	RPSX		2.7	2.2	3.8
39184 at	transcription elongation factor B (CIII) material 2 21012		AF063308	2.7	2.4	2.1
	B)	ICEBZ	AI857469	2.7	1.9	2.9
32212_at	programmed cell death 8 (apoptosis inducing factor)	PDCD8	AI 049703	7.0		ľ
33815_at	uridine monophosphate synthetase (orotate phosphorihosyl	JAND.	1	7.7	7	2.
	transferase and orotidine-5' decarboxylase)) 	J03626	2.7	2.2	2.9
412/1_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	SLC7A8	Y18483	2.7	2	2.6
41642 at	SMA5		04.07.			
810_at	Rho guanine nucleotide exchange factor (GFE) 1	100	V/3940	2.7	2.4	2.5
33925_at	neurogranin (protein kinase C substrate RC3)	AKHGEFI	064105	2.7	1.5	2.9
33244_at	chimerin (chimaerin) 2	NAGN	3006X	2.7	2.7	2.7
34866 at		CHNZ	U07223	2.7	2.5	2.5
35306 at	DEAD/H (Asp. Gir. Ala. Asp./His) box polymonatide 15		AF055029	2.7	1.2	2.7
36758 at	CT application you (sitting the last)	DDX15	AB001636	2.7	2.1	3.3
37310 at	plasminogen activator urokinase		AF070578	2.7	2.2	27
37652 at	Calcinetrin hinding protein 1	PLAU	X02419	2.7	8.1	26
37272 at			AB002328	2.7	2.1	28
37690 at	terial acet	ITPKB	X57206	2.7	0	2.5
1000	The Concession acceptate SVIIII asest Ke					

Figure 11TTTTT

38098 at	(subunit 9), isoform 1	ATP5G1	20669X	2.7	2.4	2.4
28115 24	lipin 1	1410	0.000			
30113_at	lung cancer candidate	LPINT	080010	2.7	1.4	1.8
37895 at	Solute carrier family 35 (CMP-cialic acid transporter)		AF055479	2.7	1.4	2
1795 g at		SLC35A1	D87969	2.7	2	-
38727 at		CCND3	M92287	2.7	2.6	. K
33170 at	KIAAAGES protein		M23161	2.7	12	000
39126 at	- 1 7		AB023179	2.7	27	
56336 24	Polyanime:modulated lactor 1	PMF1	AL080101	27	10	0.0
56492 at	antholial protein last in		H45858	2.7	1	٦١٥
56458 at	charterial protein rost in deppresent beta		AI147040	2.7	1	0 4
50809 24	heraran sulfate (alimental) 2.0 %		Z99408	2.7	1 4	50
56531 at	Chromosome 11 open reading from 15	HS3ST2	AI831517	2.7	2.3	٥
47921 at		C110RF15	Al188389	2.7	0 -	30
			AA744496	2.7	2.4	2.5
80157 at			AI582206	2.7	2.5	10
57823 at			AI 130690	2.7	2.1	2.6
79089 at			H18472	2.7	3.1	-
51614 at			AI797610	2.7	1.4	6
64335 at	Orotein kinase interferen indireit.		N98756	2.7	27	000
,	Inhibitor, repressor of (P58 repressor)	PRKRIR	A1990010	2.7	1.9	2.7
60493_at			00044014			
63791_at	NADH dehydrogenase (ubiquinone) 1 alpha suhcomplex 3 (9kh Box		A1344328	2.7	2.5	2.6
	(Ed. Jan.) Jan.	EATOUN EATOUN	95412	2.7	1.6	3.4
60239 at			AI086592	27	70	
1451 6 pt	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		A1695399	27		6.0
04401_1_41	INAUTH derlydrogenase (ubiquinone) Fe-S protein 7 (20kD) (NADH. coenzyme Q reductase)	NDUFS7	F23536	2.7	1.6	2.7
89816_r_at						
44776 at	MUM2 protein		AA743454	2.7	2.5	2.2
56344 at	Vacuolar protein sorting 35 (veast homolog)		AW020777	2.7	2.2	3.2
48218 at	(Sololian con)	VPS35	AI961227	2.7	2.9	5.1
57187 at	Peneral transcription factor IIIC polypoptide 6 (63)-px		T86283	2.7	8.0	2.3
51192 at	hypothetical profein FI 120515	GTF3C5	AI688411	2.7	2	2.2
			AA134926	2.7	2.4	

Figure 11UUUUUU

85325_at						
44583 at			W89075	2.7	2	2.6
56690 at			AA603344	2.7	2	00
44562 at			AW001815	2.7	2	2.1
45541 c at			AA478664	2.7	2.4	2.6
64297 s at	hypothetical protein		AW015697	2.7	2.7	1 9
53131 at	To le la la la la la la la la la la la la la		AW026502	2.7	0.4	4
			N25670	2.7	6.0	3.9
74729 f at	anchor attachment protein 1 (Gaal n. wasch) homelon		_	2.7	2.8	1.9
45659 at	Sold House of the state of the	GPAA1		2.7	1.7	3.2
45690 at	CGi.133 protein		AA582196	2.7	1.8	2.8
46890 at			AA887118	2.7	1.9	3.6
53015 at	hypothetical protein El 120729		AA203361	2.7	2.7	2.3
80415 at	methionine adenosyltransferase II stoka		AI823408	2.7	2.2	2.7
49914 at	in d 1511F16 2	MAT2A	AI969678	2.7	2.1	3.3
37497 at	hematonoietically expressed homochous		۷	2.7	2.3	4.3
32059 at	XONOBILIOII DOSCOLIAZIO CONTROLIAZIONE	HHEX		2.6	2.5	1 6
31952 at	ribosomal protoin E		U79282	2.6	22	2 5
32107 24	Columbia protein Lo	RPL6	X69391	2.6	23	7.7
J212/_at	solute carrier family 25 (mitochondrial carrier, oxoglutarate carrier), member 11	SLC25A11	AF070548	2.6		3.2
1307_at	xeroderma pigmentosum, complementation group A		-1			
40961 at	SWI/SNF related matrix accordated poting description	XPA	ļ	2.6	2.4	2.5
	chromatin, subfamily a, member 2	SMARCA2	X72889	2.6	2.1	2.7
32788_at		COGINTO	20000	C		
32826_at	ectonucleoside triphosphate diphosphohydrolase 1	2 JOHN	042003	7.0	1.8	2
35229_at	carnitine palmitoyltransferase I, liver	COLL	AJ133133	2.6	2	2.5
36013_at	chromosome 4 open reading frame 1	O 101	L39211	5.6	1.4	2
35223 at	alpha integrin binding protein 63	C40RF1	AF006621	2.6	1.4	3.7
31901 at	Dotassium voltage gated channel chalcon		- 1	2.6	1.6	27
	member 2	KCNAB2	AF044253	2.6	1.6	2.5
35252_at	KIAA0528 gene product					
34882_at	Inucleolar protein (KKE/D reneat)		AB011100	2.6	2.3	2.1
36519 at	excision repair cross-complementing rodent repair deficie		Y12065	2.6	2.2	2.5
ı	complementation group 1 (includes overlapping antisense sequence)	ERCC1	M13194	2.6	1.8	2.2

Figure 11VVVVVV

	LANT	75175	2.0	1./	2.3
heat shock 60kD protein 1 (chaperonin)	HSPD1	M22382	2.6	1.6	3.4
Ras association (RaIGDS/AF-6) domain family 2	RASSF2	D79990	2.6	1.3	2.5
HRIHFB2206 protein		L10379	2.6	2.3	2.3
NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH. coenzyme Q reductase)	NDUFS8	AF038406		1.7	2.7
YY1 transcription factor	YY1	M77698	2.6	0.8	29
ribosomal protein L22	RPL22	AI526079	2.6	2.1	2.7
androgen induced protein		AI468699	2.6	2.3	2.5
		AI924940	2.6	2.4	2
major histocompatibility complex, class II, DN alpha	HLA-DNA	AI692538	2.6	2	2.6
isocitrate dehydrogenase 1 (NADP+), soluble	1DH1	AI971036	2.6	1.1	2.7
		AI937449	2.6	2.2	3.5
		AI765712	2.6	1.6	2
		AW016356	2.6	2.2	2.5
- 1		AA932206	2.6	5.6	2.5
hypothetical protein FLJ20668		T66305	2.6	2.4	2.7
		W72919	2.6	2.6	2.7
		AI632438	2.6	1.6	2.5
		AI674163	2.6	2.6	2.5
hypothetical protein FLJ11151		AA570555	2.6	2.1	2.4
HSPC141 protein		U83510	2.6	2.6	3.1
tumor protein p53-binding protein, 1	TP53BP1	AW008856	2.6	1.6	3.2
		AI701895	2.6	2.1	3.8
		AA601045	2.6	2.6	2.6
		AW004635	2.6	1.7	3
		N36764	2.6	2.6	2.4
		AA209239	2.6	0.4	2.1
BCM-like membrane protein precursor		AI697841	2.6	1.9	2.2
		AI652721	2.6	2.2	2.4
density-regulated protein	DENR	AA149864	2.6		3.5
		AI760531	2.6	1.9	2.6
		N37023	2.6	1.8	2.2
		N90917	2.6	2.4	2.2
		CO. C. C. C.	,	,	(

Figure 11WWWWWW

in cors:

44740_at	ein		W73280	000		
50429 at	hypothetical protein FLJ20640		7100000	0.0	1.8	2.8
43977_at	hypothetical protein FLJ20422		1276701	7.0	1.8	2.5
55526_at			AI660497	2.6	2.5	2.7
45714 at	hypothetical profein FI 120568		AA923355	2.6	1.7	42
58595 f at	CD24 antigen (small fell ling carcinoma cluster A		- 1	2.6	8.1	1
	hypothetical protein of 1551 no 5	CD24	4 AA551303	2.6	8	43
51099 s at	coactivator inden		AI627538	2.6	2.2	2.5
53802 at			AA526554	2.6	2.6	i m
60521 at			AA151838	2.6	1.8	2.6
64087 i at	hypothetical protein El 110171		AL043931	2.6	2.4	o e
53361 at			AI022065	2.6		2.6
	kelch-like protein C3IP1		H40238	2.6	2.4	2.4
54186 at			N69560	2.6		26
44143 at	McKusick:Kaufman syndroma			2.6	1.6	2.4.0
64263 s at		MKKS		2.6	3.1	3.5
46226 at	HSPC142 protein		AA725421	2.6	1.7	4 1
54026 at			AA610145	2.6	2.3	7
75187 f at	alpha-2-macroglobutin		W20090	2.6	2	
47405 f at	probibitio	A2M		2.6	0.51	100
50341 s at	riboniclease & oregingon	PHB	AA512948	2.6	2 -	2.3
55091 at	phosphoinositol 3 phosphoto Finding		AI986481	2.6	2.0	0.7
75352 s at	Cytosolic acyl coenzyme A thiocetic Land		AI341312	2.6	2.5	6.2
74541 at	low density linocrotain rolated and 11 year of 2		AW025033	2.6		2.0
	receptor)	LRP1	AI969879	2.6	1.7	2.5
47611_at	(a)	PDF4A	AA523395	2 6	,	
41406 24	phosphodiesterase E2)	!		0.7	7.7	2.9
41400 at	hypothetical protein FLJ21919		41 080172			
39000_at	N-myristoyltransferase 1	LTMM	AE043334	2.5	2.1	2.5
/63_at	glia maturation factor, beta			5.5	1.4	1.7
652 g at	replication protein A3 (14kD)	S C C C C C C C C C C C C C C C C C C C	٦.	2.5	1.1	3.6
40843 at	Integrin cytoplasmic domain-associated protein 1	RFA3	- 1		2.1	2.3
37200_at	Fc fragment of IgG, low affinity IIIb, recentor for (CD16)	1	AF012023	2.5	2.3	2.1
41205 at	Ubiquitin profein ligase F3A (human papilloma vigin E6	FCGR3B	1	2.5	0.5	2.3
		UBE3A	U84404	2.5	0	2.2
					_	_

Figure 11XXXXXX

41214_at	ribosomal protein S4, Y-linked	RPS4Y	M58459	2.5	~	2.7
41732_at			1	2.5		2.4
41746_at	non-histone chromosome protein 2 (S. cerevisiae) like 1	NHP2L1	Z83840	2.5	2.4	
954_s_at	protein phosphatase 1, catalytic subunit, alpha isoform	PPP1CA	X70848	2.5	2.6	3.3
33333_at	KIAA0403 protein		AB007863	2.5	1.9	2.3
34191_at			AB002445	2.5	1.2	2.9
33915_at	melanoma adhesion molecule	MCAM	W22655	2.5	1.4	2.5
34256_at	sialytransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3. sialytransferase; GM3 synthase)	SIAT9	AB018356	2.5	0	2.5
39248_at	aquaporin 3	AQP3	N74607	2.5	2.5	2.4
41236_at	hypothetical protein		U79252	2.5	2.1	2.5
34748_at	KIAA0846 protein		AB020653	2.5	0.8	2.3
35172_at	tyrosylprotein sulfotransferase 2	TPST2	AF049891	2.5	2.2	2.6
39076_s_at	DR1-associated protein 1 (negative cofactor 2 alpha)	DRAP1	A1991040	2.5	0.1	2.9
34402 at	unr-interacting protein		AB024327	2.5	1.6	4.4
35309_at	Suppression of tumorigenicity 14 (colon carcinoma, matriptase, epithin)	ST14	U20428	2.5	5	1.3
36561_at	propionyl Coenzyme A carboxylase, beta polypeptide	PCCB	X73424	2.5	1.9	2.5
36169_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE)	NDUFA1	N47307	2.5	1.3	4.2
36938_at	N-acylsphingosine amidohydrolase (acid ceramidase)	ASAH	U70063	2.5	0	2.8
32553_at	MYC-associated zinc finger protein (purine-binding transcription factor)	MAZ	M94046	2.5	6:1	2.5
32569_at	platelet activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD)	PAFAH1B1	L13385	2.5	1.5	2.7
37408_at	endocytic receptor (macrophage mannose receptor family)		AB014609	2.5	2.2	2.3
37740_r_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	SLC25A5	J02683	2.5	1.8	2.5
38090_at	phosphatidylserine decarboxylase	PISD	AL050371	2.5	2.5	2.5
38443_at	son of sevenless (Drosophila) homolog 1	S0S1	U79291	2.5	1.4	2.1
40756_at	nucleophosmin/nucleoplasmin 3	NPM3	AF081280	2.5	2.2	2.2
40758_at	immature colon carcinoma transcript 1	ICT1	X81788	2.5	1.3	2.5
2028_s_at		E2F1	M96577	2.5	2.5	2.8
39155_at	proteasome (prosome, macropain) 26S subunit, non ATPase, 3	PSMD3	D67025	2.5	1.6	3.7
41084_at			AI659108	2.5	1.7	

57346_at	Mad4 homolog		AA831438	2.5	m	3.6
56197 at			AI783924	2.5	2.3	2.6
48852_at			AI346327	2.5	18	2.8
51684_at	hypothetical protein DKFZp434F0272		W76160	2.5	1.8	2.3
66269_at			AA669114	2.5	2	2.1
88767_at			AW008519	2.5	2.5	2.5
55586_at	period (Drosophila) homolog 3	PER3	AA541537	2.5	1.6	3.9
50890_at	L2DTL protein		AI800576	2.5	2.5	2
57809_at	presentlins associated rhomboid like protein		W63675	2.5	2.8	3
61541_at			AI160808	2.5	2	2.7
62273_at			AI766808	2.5	2.5	2.3
91825_at			AI375222	2.5	2.5	2.5
54787_at			AA046849		1.6	1.4
59809_f_at	poly(A) binding protein, cytoplasmic 1	PABPC1	AW020548	2.5	2.2	4.1
43403_at	methylenetetrahydrofolate dehydrogenase (NADP+ dependent),	MTHFD1	AA618429	2.5	1.1	2.3
	methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase					
59681_at	Jaminin receptor 1 (67kD, ribosomal protein SA)	LAMRI	AA468402	2.5	2.1	3.1
48597_at			AI871648	2.5	1.3	0.5
45268_at			AA205531	2.5	1.5	2
59091_at			AI799698	2.5	2.4	2.8
45475_f_at	hypothetical protein		AW006786	2.5	1.3	2.8
48417_r_at	hypothetical protein PR02849		AA636101	2.5	2.1	2.4
56287_at			AI801756	2.5	1.8	2.2
60821_at	KIAA1226 protein		AW006938	2.5	2.3	2.1
50198_at			AI208272	2.5	2.5	2.5
44036_at			N28741	2.5	1	1.8
50251_at			AA524283	2.5	2	2.6
45354_at			AA658561	2.5	2.1	2.5
43947_at	hypothetical protein FLJ11323		AA669327	2.5	2.5	2.7
89584_at	protease, serine, 15	PRSS15	AI817597	2.5	6.0	2.9
54962_f_at			AI830110	2.5	2.1	2.3
48051_at	cell death-inducing DFFA-like effector b	CIDEB	AA148543	2.5	1.8	2.7
51186_at			A1743603	2.5	2.3	1.5
44519_at			A1140754	2.5	2.2	3.1

Figure 11ZZZZZZ

Al818631 2.5 0.5 PDGFC AA631149 2.5 2.1 N30858 2.5 2.5 N30858 2.5 2.5 N30858 2.5 2.5 N30858 2.5 2.5 Al837945 2.5 1.9 N21390 2.5 1.9 N21390 2.5 1.9 N21390 2.5 2.5 A481256 2.5 2.5 A481256 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 2.5 A445492 2.5 A445482 2.	45149_at	suppressor of variegation 3.9 (Drosophila) homolog 1	SUV39H1	SUV39H1 AA604816	25	00	30
PDGFC AA631149 2.5 1.4	54651_at			A1818631	0 10	2.7	2.3
PDGFC AA631149 2.5 1.4 PDGFC AA631149 2.5 2.1 N30858 2.5 2.5 1.3 NDUFA4 AA890044 2.5 1.3 UBA52 AI857945 2.5 2.5 NZ1390 2.5 1.9 NZ1390 2.5 1.9 NZ1390 2.5 2.3 DOK2 AA864400 2.5 2.5 AA639795 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA454992 2.5 2.1 AA445492 2.5 2.1 AA445440 2.5 2.5 AA4454540 2.5 AA4454556 2.5 AA4454556	4703 fat		COLULT.		6.3	0.0	0.1
PDGFC AA631149 2.5 2.1 N30858 2.5 2.5 A1636250 2.5 1.3 NDUFA4 AA890044 2.5 1.3 UBA52 A1857945 2.5 2.5 AL042817 2.5 1.9 PIP5K2B A1982873 2.5 2.3 DOK2 AA864400 2.5 2.3 AA481256 2.5 2.1 AA4639795 2.5 2.1 AA454992 2.5 2.1			Alroga		2.5	1.4	3.1
NDUFA4 AA890044 2.5 2.5 1.3 1.	5217_at	platelet derived growth factor C	PUCEC	44631149	3 0	·	
NDUFA4 AA890044 2.5 1.7 NDUFA4 AA890044 2.5 1.3 UBA52 AI857945 2.5 2.5 NZ1390 2.5 1.9 NZ1390 2.5 2.3 DOK2 AA864400 2.5 2.5 AA481256 2.5 2.1 AA48492 2.5 2.1 AA48492 2.5 2.1 AA48492 2.5 2.1 AA48492 2.5 2.1 AA48492 2.5 2.1 AA48492 2.5 2.1 AA48492 2.5 2.1 AA484992 2.5 2.1 AA484992 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.1 AA484840 2.5 2.5 AA484	5599 at		5	CHITCOUCIN	2.3	7.7	2.4
NDUFA4 AA890044	3215 at			0000001	2.3	2.5	2.5
UBA52 AI857945 2.5 1.3 UBA52 AI857945 2.5 2.5 AL042817 2.5 1.9 PIP5K2B AI982873 2.5 2.3 DOK2 AA864400 2.5 2.5 AA481256 2.5 2.1 AA481256 2.5 2.1 AA4839795 2.5 2.1 AA4539795 2.5 2.1	1 700			A1636250	2.5	1.7	1.7
Le ribosomal protein fusion product 1 UBA52 AI857945 2.5 2.5 4-phosphate 5-kinase, type II, beta PIP5K2B AI982873 2.5 1.5 6kD DOK2 AA864400 2.5 2.5 Arthetase beta-subunit AA481256 2.5 2.1 ubfamily IIS, polypeptide 1 AI445492 2.5 2.1	1/93_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLRQ)	NDUFA4	AA890044	2.5	1.3	3.5
4-phosphate 5-kinase, type II, beta DOK2 AR864400 2.5 2.3 6.8 2.5 2.3 6.8 2.5 2.3 6.9 2.5 2.3 6.9 2.5 2.5 2.3 6.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	7828_at	ubiquitin A-52 residue ribosomal protein fusion product 1	IRASO	1	2 0	0.0	
4-phosphate 5-kinase, type II, beta PIP5K2B AI892873 2.5 1.5 6kD DOK2 AA864400 2.5 2.3 vnthetase beta-subunit AA8639795 2.5 2.5 ubfamily IIS, polypeptide 1 AA843492 2.5 2.1	6130 at		7000		6.2	C.2	4.2
4-phosphate 5-kinase, type II, beta PIP5K2B AI982873 2.5 2.3 6kD DOK2 AA864400 2.5 2.5 vrithetase beta-subunit AA481256 2.5 2.1 ubfamily IIS, polypeptide 1 AI445492 2.5 2.1	1167 24			ALU4281/	2.5	1.9	1.7
4-phosphate 5-kinase, type II, beta PIP5K2B AI982873 2.5 2.3 6kD DOK2 AA864400 2.5 2.5 vnthetase beta-subunit AA639795 2.5 2.1 ubfamily IIS, polypeptide 1 AI445492 2.5 2.1	10/01			N21390	2.5	1.5	2.5
6kD DOK2 AA864400 2.5 2.5 vnthetase beta-subunit AA639795 2.5 2.1 ubfamily IIS, polypeptide 1 AA639795 2.5 2.1	8/4/_at	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	PIP5K2B	A1982873	25	0.0	ic
Phenylalanyl-tRNA synthetase beta-subunit AA639795 2.5 2.1 Cytochrome P540, subfamily IIS, polypeptide 1 A145492 2.5 2.1	3259_s_at	docking protein 2, 56kD	DOKO	44864400	200	2.7	2.0
phenylalanyl-tRNA synthetase beta-subunit A4481236 2.1 2.1 cytochrome P540, subfamily IIS, polypeptide 1 A1445492 2.5 2.1	7139 at			00000	6.5	C.2	2.4
Cytochrome P540, subfamily IIS, polypeptide 1 A1445492 2.5 2.1	** 0099	Chambelland 4DNA and the standard and		AA481256	2.5	2.1	2.8
Cytochrome P540, subfamily IIS, polypeptide 1	0000 at	pricily alariyith Syrithetase Deta-Subunit		AA639795	2.5	2.1	27
	/62/_at	cytochrome P540, subfamily IIS, polypeptide 1		A1445492	25	0.5	2 0

Figure 11AAAAAAA

affyiD	Gene Name	2000				
1520 s at	endothelin 1	dene symbol	4BA	Score_Ecoli	Score_Can	Score_Influenza
10 C C C C C C C C C C C C C C C C C C C	1	EDN1	105008	4444	283.5	113.7
000_a1	Interleukin 12B (natural Killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	IL12B	M65290	2449.1	761.6	1.2
1369_s_at	interleukin 8	18	M28130	2300 5	308	1 99 1
35822_at	B-factor, properdin	BF	L15702	1635 7	287.1	1727
38299_at	interleukin 6 (interferon, beta 2)	116	X04430	1566 4	101 3	7 700
40385_at	small inducible cytokine subfamily A (Cys.Cys), member 20	SCYA20	1164197	9434		7
91636_at			AI652725	886.7	77	23.8
1404 r at	small inducible cytokine A5 (RANTES)	SCYA5	M21121	834.8		750 1
1491_at	pentaxin related gene, rapidly induced by IL-1 beta	PTX3	M31166	8273		
37187_at		GROZ	M36820	785		1 30
1372_at	tumor necrosis factor, alpha induced protein 6	TNFAIP6	M31165	573 9	7	75.1
2002 s_at	BCL2-related protein A1	BCL2A1	U27467	547.8		7.0.7
1069_at	prostaglandin endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	PTGS2	U04636	495.3	26.7	53.1
77706_at			AA641972	703	Ca	r
408_at	GRO1 oncogene (melanoma growth stimulating activity, alpha)	GR01	X54489	486.7	11.5	7.1
32818_at	hexabrachion (tenascin C. cytotactin)	<u> </u>	77056	0 7 1 7	10	
39402_at	interleukin 1, beta	1 2 2	A15330	4/4 1		
36067 at	Small inducible cytokine subfamily A (Ove Ove) member 10	ירום	USC 1 IVI	468.5	30.5	1
926 at	metallothionein 16	SCYA19	AB000887	394.2	25.2	2.8
53570 34		5 N	J03910	370.2	0.5	1.5
3007 9_at		ALDH9	AI127172	326.5	3.6	2.1
	S100 calcium binding protein A9 (calgranulin B)	S100A9	W72424	313.3	0.5	α C
Z۱.	hypothetical protein		AA618602	296.2	15.3	18.6
		IFNG	J00219	289.9	588	36.2
41531_at	transmembrane 4 superfamily member 1	TM4SF1	AI445461	278	800	200.6
61818_at			AI970348	265	32.3	5 4 6
35577_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin). member 7	SERPINB7	AF027866	262.3	26.1	5.6
34929_at	tumor necrosis factor receptor superfamily, member 8	TNFRSF8	M83554	255 9		0
33955_at	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, n35)	IL12A	M65291	250.2	18.4	14.6

Figure 12A

41096 at	S100 calcium hinding protein A8 (calgrapulin A)	C10048	41106134	1/0//	c	0 9
10000		0000	451021	4.64.7		
3982/ at	hypothetical protein		AA522530	245.1	38.4	14.6
41468_at	T cell receptor gamma locus	TRG@	M30894	245.1	2	1
35000_at	tumor necrosis factor (ligand) superfamily, member 9	TNFSF9	968800	232.3	2.9	3.1
33965_at	small inducible cytokine A1 (1-309, homologous to mouse Tca-3)	SCYA1	M57506	216.3	0	7.8
36116 at	thyroid hormone receptor interactor 10	TRIPIO	A IDODA14	215.0	56.7	7
1400 at		CSF2	M13207	210.9	0 1	
47855 at	,	11.19	AA151656	205.5	0	0.5
33789_at	small inducible cytokine A5 (RANTES)	SCYA5	AF088219	191.5	64.1	1.2
33513_at		SLAM	U33017	178.3	14.3	
58918_at			AA210892	176.1	24	34.8
41104_at	small inducible cytokine B subfamily (Cys-X-Cys motif), member	SCYB13	AF044197	171.2	0	2.3
	13 (B-cell chemoattractant)	,				
1334_s_at	colony stimulating factor 3 (granulocyte)	CSF3	X03656	167	1.2	7.2
31623 f at		MT1A	K01383	160.3	22.3	49.7
33364_at	similar to rat myomegalin		U51694	156	58.9	2.9
36296_at	lymphotoxin alpha (TNF superfamily, member 1)	LTA	D12614	154	62.8	28.5
72840_at	19A24 protein		AI638519	149.1	43.6	23.3
49076_at	SGRF protein, Interleukin 23 p19 subunit		AI796983	147.7	0.3	2.3
41870_at	lung type-I cell membrane associated glycoprotein		AF030428	143.7	0	1.2
34666_at	superoxide dismutase 2, mitochondrial	SODZ	X07834	141.3	63.1	42.3
32114_s_at	adenosine A2a receptor	ADORA2A	S46950	137.9	31	27.9
48919_at	potassium inwardly rectifying channel, subfamily J, member 2	KCNJZ	AA393850	130	11.2	13.1
63335_at	sorting nexin 10		AI285531	127.4	55.8	74.2
48753_at	PPAR(gamma) angiopoietin related protein		N57259	126	7.9	14.7
37319_at	insulin-like growth factor binding protein 3	IGFBP3	M35878	125.2	7	1.3
46468_at			AI735586	122.3	4.7	0.2
1548_s_at	Interleukin 10	110	U16720	121.9	4.3	3.2
57440_r_at			AW014801	120.2	4	10.2
84995_at			AA769482	117.4	12.2	9.9
50978_at	putative secreted ligand homologous to fix1	hfjx	AI338625	117.2	3.8	3.3
609 f at	(metallothionein 1B (functional)	MT1B	M13485	116.3	11.1	20.1
63066 at			AA001735	113	12.6	9.6

58957_at	hypothetical protein FLJ20637		AI620475	1089	42.7	28.3
36070_at	KIAA1199 protein		AL049389	108.4	0	6.0
33282_at	ladinin 1	LAD1	U42408	107.2	2.4	4.4
36454 at	carbonic anhydrase XII	CA12	AF037335	103	0	1.1
70594_at			AI819198	102.7	8.4	2.5
82795_at			AI793037	102.4	0	1.4
31622_f_at	metallothionein 1F (functional)	MT1F	M10943	101.8	13.1	32.6
33055_at	cytochrome P450, subfamily VIIB (oxysterol 7 alpha-hydroxylase), polypeptide 1	CYP7B1	AF029403	99.5	17.6	1.2
70097_at	indoleamine-pyrrole 2,3 dioxygenase	ODNI	AI302268	99.5	29.8	39.9
73341_at			AA678425	99.2	1.2	0
59805_f_at			AI636743	98.2	2.6	9 9
38909_at	cytochrome P450, subfamily XXVIIB (25-hydroxyvitamin D-1-alpha hydroxylase), polypeptide 1	CYP27B1	AB005038	98.2	17.2	2.9
87651_at			AI800110	95.3	10.5	
75146_at			AL047300	94.9	18.8	0.5
76710_at	cardiotrophin-like cytokine; neurotrophin-1/B.cell stimulating factor-3		AI040033	92.7	4.7	4
32984_s_at	chloride channel Kb	CLCNKB	230644	92.3	1.0	I.C.
1004_at	Burkitt lymphoma receptor 1, GTP binding protein	BLP1	X68149	92	0.2	115
56246_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	AI765775	91	6.2	11.3
1911_s_at	growth arrest and DNA-damage-inducible, alpha	GADD45A	M60974	88.7	5	2.7
38428_at	matrix metalloproteinase 1 (interstitial collagenase)	MMP1	M13509	87.8	0	0.3
37407_s_at	myosin, heavy polypeptide 11, smooth muscle	MYH11	AF013570	87	17.5	7
45237_at	superoxide dismutase 2, mitochondrial	SOD2	AA142976	84.4	32.6	17.7
1549_s_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4	SERPINB4	U19557	81.2	0.7	1.1
1693_s_at	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	TIMP1	D11139	79.8	-	6.0
60032_at	li		AI984197	79	0.2	6.0
	metallothionein 1E (functional)	MT1E	R92331	78.7	4.6	8.6
57711_at			AA576959	78.3	8.6	0.7
35844_at	syndecan 4 (amphiglycan, ryudocan)	SDC4	079206	77.4	5.8	20.7
85561_at			AL079435	76.5	7.7	9.0
40687_at	gap junction protein, alpha 4, 37kD (connexin 37)	GJA4	M96789	74	13.5	4.2

Figure 12C

69142_at			AI635522	72.4	7.8	8
69818_at	hypothetical protein FLJ22318		AI250747		0	
31540_at	tumor necrosis factor receptor superfamily, member 9	TNFRSF9	U03397	72.2	7.8	19.5
71013_at	interleukin-1 homolog 1		AI814314	71.5	4.1	2.3
41446_f_at	RNA helicase-related protein		H68340	71.4	10.1	21.9
47483_at	similar to rat myomegalin		AI659612	71.1	8 6	11.8
42204_at			AI219461	70.7	4.8	2
544_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2	876638	70.6	13.3	7.8
668_s_at	matrix metalloproteinase 7 (matrilysin, uterine)	MMP7	L22524	70.6	1.3	
73455_f_at			l	70.4	8.2	8.5
63675_at			AI680833	69.2	1.3	1.2
49438_at			AI535730	68.4	21	15.8
1006_at	matrix metalloproteinase 10 (stromelysin 2)	MMP10	X07820	67.5	2.4	3.6
59185_at			AA926689	66.3	1.8	1.1
41475_at	ninjurin 1	NIN 1	U91512	65.2	35.7	16.7
1036_at	interleukin 15	1115	U14407	64.7	16.6	22.1
77244_at	bHLH factor Hes4		A1380603	64.7	15.4	23.6
53126_at	NK homeobox (Drosophila), family 3, A	NKX3A	AI557413	63.8	2.8	12.5
51232_at	hypothetical protein FLJ20764		A1684508	62.7	4.1	2
1519_at	vets avian erythroblastosis virus E26 oncogene homolog 2	ETS2	J04102	61.9	3.6	4.4
49140_at			AI244908	61.5	3.8	4.4
34974_at	disintegrin protease		Y13323	61	1	1.5
53649_at	snail 1 (drosophila homolog), zinc finger protein	SNA	AA613301	8.09	0.3	1.8
45333_at	p53-induced protein PIGPC1		AI525592	59.9	9.0	0.5
44289_at	NY-REN-18 antigen		AA587445	59.8	23.1	1.9
51474_at			AA127641	58.7	2.4	7.4
48377_at			AI347073	57.3	2.1	11.6
37163_at	DKFZP586C1619 protein		AL050374	56.3	9.1	10.6
42302_at			AI082042	55.4	14.7	1.9
58391_at	testis zinc finger protein		AI798147	55.2	2.9	20
37954_at	annexin A8	ANXA8	X16662	55.1	0	0.8
34582_at	solute carrier family 1 (glial high affinity glutamate transporter), member 2	SLCIA2	U01824	55	0	1.2
906_at	signal transducer and activator of transcription 4	STAT4	L78440	54.6	10.3	5.9

Figure 12D

Time: Response of Dendritic Cells to a... Inventors: Nir Hacohen, et al.

10/05 91		MARSKS	01449/	230	4.5	1,1
T			AI246590	53.8	0 0	11
T	En domain containing 1	EHD1	AI986040	53.8	000	21
04003 at			N47335	53.7	2.3	4 0
47.287 at			AI475473	53.7 53.5	0.0	8.2
48676_at			010010	0.00	2.5	6.9
	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	SERPINB2	Y00630	52.6	0 0	
	kynureninase (L-kynurenine hydrolase)	XYNU	A1148772	7.0 E	0.00	
_at	Branzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB	M17016	52.3	9.1	15.3
at			H15072			
at	NCK adaptor protein 2	NCKO	A1034EE	21.8		13.9
222_at ex	exostoses (multiple) 1	14CAZ	A1934552	51.7	5.9	6.9
		EVII	3/9639	50.9	2	8.6
	KIAA1031 protein		AL109695	50.6	4.8	5.8
	antigen identified by monoclonal antihody MRC OX 2	0.01	A1138605	50.6	24.1	4.6
		MOAZ	X05323	50.5	7	
	vascular endothelial prowth factor		AI821392	20	4	
		VEGF	AF022375	49.9	11.8	8.6
Γ	Dannexin 1		AI358871	49.8	6.0	0.4
Ī	adipose specific 2	PANX1	AA115920	49.5	3.9	
at	. t		Al381790	49.3	1.4	
Ī	Serine (or cysteine) proteinase jobilator plada A (alaka		N58182	49.2	1.3	21.8
	antiproteinase, antitrypsin), member 1	SERPINA1	X01683	48.8	2.5	2.4
<u>.</u>		S100A12	D83664	70.0		
1583 at tu	tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B	M32315	488	0 %	ا ف
T			A1830607	177	7 (ol.
Т	regulator of G-protein signalling 16	RGS16	U70426	46.6	0.0	1.
T	prostagiandin E synthase	PTGES	T03380	46.5	0,0	1
7	retiriord acid marced 3	RAI3	AI990405	46.5	200	
54565 at			AI129310	45.7	0.8	200
58667 at			AA149736	45.6	8.7	10.3
Τ	dual spacificity phosphaton E		AA442239	45.4	0.4	5.5
		1 4 4				,

56561_at			W37880	43.8	0 11	[10]
53970_at	dual adaptor of phosphotyrosine and 3-phosphoinositides		AF150266	43.8	9.5	m
84364_at			AA665185	43.3	3.1	1.7
75246_s_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	SLC1A3	W26838	43.1	7.2	4.8
45647_s_at			AW005111	42.5	1.5	1.7
38131_at	prostaglandin E synthase	PTGES	AF010316	42.1	0	1.2
43524_at	KIAA1170 protein		C14031	42.1	18.4	7.2
42363_r_at	STAT induced ST,		AI680350	41.7	5.3	5.8
48822 s at	adenylate kinase 3	AK3	AW015546	41.5	6.1	0.5
35694_at	mitogen activated protein kinase kinase kinase 4	MAP4K4	AB014587	41.4	2.7	0.6
37225 at	KIAA0172 protein		D79994	41.4	3.6	10.9
33849_at	pre-B-cell colony-enhancing factor		002020	41	8.3	16.3
34439_at	absent in melanoma 2	AIM2	AF024714	40.9	18.1	16
58737_at			N27438	40.2	2.4	4.3
44640_at			W30985	40.2	11.6	8.4
64333 s_at	pyrophosphatase (inorganic)	ЬP	AW009649	39.9	10.9	5
41654_at	adenosine deami	ADA	X02994	39.7	4.1	3.2
40456_at	up-regulated by BCG-CWS		AL049963	39.4	1.8	0
34022_at	GRO3 oncogene	GRO3	M36821	39.3	1.9	1.4
53609_at			C14904	39.3	13	22.8
48014_at			N54957	38.8	5.2	2
54147_at	pyruvate dehydrogenase kinase, isoenzyme 4	PDK4	AI763378	38.3	4.5	9.0
68652_at			AI431778	38	3.8	0.6
67259_at			R56235	37.9	0	6.3
1343_s_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3	SERPINB3	968998	36.4	0	0.3
43456_at	serine/threonine protein kinase MASK		AI299952	35.5	2.6	C
52729_at	CD44 antigen (homing function and Indian blood group system)	CD44	1 ~	35.3	3.3	9.0
64170_at			AI609751	35	3.2	0.5
32686_at	prostaglandin E receptor 3 (subtype EP3)	PTGER3	960980	34.9	2.2	2.2
53261_at			AI337231	34.9	10.4	1.6
53100_at	hypothetical protein FLJ10307		AA747448	34.8	5.3	1.3
33730_at	retinoic acid induced 3	RA13	AF095448	34.7	1.2	4.6

Figure 12F

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	member 3) 	-))
52255_s_at	collagen, type V, alpha 3	COL5A3 A198422	221	33.9	2.1	3.9
55353_at		AA76097	161	33.6	6.9	9
46760_r_at		H38.	110	33.5	9.1	5.8
36780_at	clusterin (complement lysis inhibitor, SP-40,40, sulfated	CLU M25915	915	32.9	5	8.7
	glycoprotein 2, testosterone repressed prostate message 2, apolipoprotein J)				<u>.</u> .	
51026_at	hypothetical protein PR00813	N30257	257	32.6	3.3	0
36543_at	coagulation factor III (thromboplastin, tissue factor)	F3 J02931	131	32.3	6.6	4.2
66529_at		AA843926	3926	32.2	3.6	8.6
55063_at	glutamate decarboxylase 1 (brain, 67kD)	GAD1 AL042399	399	31.4	5	
49664_s_at		AW001427	1427	31.3	0.1	1.4
32518_at	zinc finger protein 259	ZNF259 AF019767	1926	30.5	2.7	0
42524_at		R37337	337	30.1	6.4	3.6
47076_at		06928W	969	29.9	2.6	3.4
64911 s at	hypothetical protein FLJ11305	AA85411	1113	29.8	3.8	
75742_at		A187061	1917	29.7	1.4	
38994_at	STAT induced STAT inhibitor-2	AF037989	686	29.2	6.3	1.8
67764_r_at		AA004879	1879	59	4.4	11.8
32863_at	similar to calcium/calmodulin dependent protein kinases	AL023754	3754	28.7	7.3	1.9
36139_at	DKFZP586G0522 protein	AL050289	289	28.5	1.5	20.1
53799_at	hypothetical protein similar to mouse Dnajl1	AA628434	3434	28.3	5	
40098_at	EH domain containing 1	EHD1 AF001434	1434	28.1	9.0	3.9
42769_at		N46441	441	27.9	0.7	0.4
51278_at		A1139543	9543	27.7	2.8	2.6
49670_at		W96225	225	27.7	2.1	
40268_at	FOS-like antigen 2	FUSL2 X16	902	27.6	1.7	2.1
47971_at	ferritin, heavy polypeptide 1	FTH1 192243	243	27.6	6.3	8.0
54491_at		AA043562	3562	27.5	c	3.1
48105_at	latexin protein	A1672094	2094	27.4	6.5	6.0
53380_at	hypothetical protein DKFZp434P0531	AI73272	727	27.4	5.9	4.9
56500_at	junctional adhesion molecule	AI241578	1578	27.4	3.9	
65628_at		AW02317	3171	27.4	1.6	3.4
38617 at	ILIM domain kinase 2	LIMK2 D45906	906	27.3	4.4	/

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34777_at	adrenomedullin	ADM	D14874	0.40	i o	-
49249_s_at			44533079	2.72		1.
44115_at	hypothetical protein from EUROIMAGE 588495		AAAB650A	27.1	8.7	2.5
56641_at	liver-expressed antimicrobial peptide		VI0277277	27.1	3.1	3.8
52958 at			122/22/	/7	10.1	2.5
38970 s at	Nefactoriated factor 1		N03458	26.5	0.8	0
44344 at	HOB histone family member		AJ011896	26.4	7.6	4.2
40.40K at	complement company, illetituel L	H2BFL	AA557205	26.4	3.9	0.5
52665 at	complement component 1, s subcomponent	C1S	J04080	26.3	5.6	7.9
75700 at			H16258	26.3	9.0	26
40/09 at	hypothetical protein from EURUIMAGE 1955967		AI807170	26.2	0.8	PIC
5010F 24	in the contract of the contrac		AI953847	25.7	8.6	128
39942 at	riniocholdrial solute carrier		AI862097	25.7	4.2	2
55750 at	Dasic leucine Zipper transcription factor, ATF-like	BATF		25.6	6.3	100
37300 at			AA292201	25.6	8	6 1
37 300 at	tissue lactor patriway innibitor 2	TFP12		25.5	C	
35362 at		MYO10	AB018342	25.1		1 2 1
33/30 at	AUP-fibosylation factor-like 4	ARL4	073960	24 9		1 0
7/// at	cystatnionase (cystathionine gamma-lyase)	CTH	A1955061	24.8	300	t C
30/49 at			AI653230	24.7	4	- C
			A!826091	24.6		
30/02 at			T55716	24 5		
1265 g at	protein tyrosine phosphatase, non-receptor type 2	PTPN2	M25393	24.4	6.4	1.0
39931_at	dual-specificity tyrosine-(1)-phosphorylation regulated kinase 3	DYRK3	Y12735	24.3	0.2	1.9
36564_at			01727/10			
36175_s_at	human immunodeficiency virus type I enhancer-binding protein 2	HIVEP2	AL023584	24.2	9./	2
7,000			:	i i	`	
48964 at			AI629027	24.2	17.0	C
39133 at			AA131626	24.1	2	7.7
- T	chloride intracellular channel 4	CLIC4	AA675919	200	7.7	0.7
at	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	LILRA3	AF025527	23.9	2.9	1.5
			A1249019	737	C	
32186_at	solute carrier family 7 (cationic amino acid transporter, y+	SI C7A5	M80244	23.6	2.3	٥
	system), member 5			0.0.	n. n	Z.3

Figure 12H

88550_at	hypothetical protein FLJ12929		AI468004	23.6	4.9	
54744_at			AA582287	23.5	8	
37032_at	nicotinamide N-methyltransferase	LWZZ Ω	U08021	23.4	0	1.5
34481_at	vav 1 oncogene	VAVI	AF030227	23.3	0	
39839_at	cold shock domain protein A	CSDA		23	1.1	
1779 s at	pim·1 oncogene	PIM1	M16750	23	3.5	9.9
34770_at	mitogen-activated protein kinase kinase kinase 8	MAP3K8	Z14138	22.9	9.0	3.3
88906_at	KIAA1442 protein		AL110312	22.8	0	1.8
54782_at			AI281068	22.7	9	1.1
38582_at	serine protease inhibitor, Kazal type 1	SPINKI	AI961220	22.6	9.0	10.6
44906_at			AI916646	22.6	0.7	2.1
84601_at			AI469960	22.6	2.9	7
889_at	integrin, beta 8	ITGB8	M73780	22.5	2.1	1.2
56979_at			AA133395	22.5	3.4	3.4
35036_at	complement component C1q receptor		U94333	22.4	1.2	0.9
68355_at			AI655376	22.2	0	0.7
49364_at			AL041551	22.2	1.7	2.7
47544 at			AA741324	22.1	4.8	5.3
80151_at			AA031832	22	0.7	0.3
36453_at			AB018254	21.9	1.1	0.3
38272_at			AF038844	21.7	2	
40606_at	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR		U88629	21.6	4.4	2.6
69197_r_at			AA508552	21.6	6.1	
1508 at	lintegrin, alpha 9	ITGA9		21.2	0	0.4
91587 at			AI554946	21.1	4	1.9
53757 at			AA131524	21.1	1.8	3.6
36933_at		NDRG1	D87953	21	2.3	0.5
1776_at		RRAD	L24564	20.8	0	1.2
39071_at	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	ITGAV	M14648	20.8	1.6	1.3
1237_at	immediate early response 3	IER3	\$81914	20.8	4.7	
41242_at	UDP-N-acteviglucosamine pyrophosphorylase 1	UAP1	AB011004	20.7	1.9	1.2
47500_i_at	c-myc promoter-binding protein		AA805337	20.6	7.1	2.8
44370_at			AI589469	20.6	0.3	2.5
64247_at			H40631	20.6	4	3.1

Figure 12I

48311_at			AI458231	20.6	3.8	1.3
43901_i_at			AI435160	20.5	8.7	2
39623_at	Norrie disease (pseudoglioma)	NDP	X65724	20.5	0.8	0.3
36560_at	KIAA0481 gene product		AB007950	20.4	1.2	0
62502_at	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR		C75510	20.4	4	2.1
56409_at			W72194	20.3	0.3	1.5
46567_at			AI732347	20.3	1	0.1
33291_at	RAS guanyl releasing protein 1 (calcium and DAG regulated)	RASGRP1	AF081195	20.2	2.4	2.7
33157_at	ated 1	INSM1	M93119	20.2	4.5	6
39143_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-	NFATC1	U08015	20.2	1.8	0
	dependent 1					
90629_at	cyclin K	CCNK	X84721	20.2	0.8	0.1
63969_f_at	clusterin (complement lysis inhibitor, SP 40,40, sulfated	CLU	AI982754	20.2	33	3.5
	glycoprotein 2, testosterone repressed prostate message 2, apolipoprotein J)		-		-	
61130_at			AI674404	20	3,3	1.9
39640_at	glutamine-fructose-6-phosphate transaminase 2	GFPT2	AB016789	19.9		4.4
53995_at	hypothetical protein		AI346913	19.8	1.1	4
54310 at			AA975511	19.7	1	2
64449_at			AI810399	19.7	5.7	3.4
40388_at	discs, large (Drosophila) homolog associated protein 1	DLGAP1	AB000277	19.6	2.1	0.1
84220_at			AI373122	19.6	0.1	1.1
32965_f_at	heat shock 70kD protein 1B	HSPA1B	l	19.5	0	2.2
38010_at	BCL2/adenovirus E1B 19kD-interacting protein 3	BNIP3	AF002697	19.5	5.8	0.2
34039_at	lymphocyte antigen 94 (mouse) homolog (activating NK-receptor: NK-p46)	LY94	AJ001383	19.3	0	0.8
32640_at	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	M24283	19.2	5.5	1.4
88541_at			AI800735	19.2	0.2	C
63742_r_at	KIAA0635 gene product		AA910186	19.2		3.4
45602_at			AA195108	19.2	1.3	2
38112 g at	chondroitin sulfate proteoglycan 2 (versican)	CSPG2	X15998	19.1	1.3	4.6
51771_at			AA284560	19	2.9	1.5
54759 at			AI291314	18.9	3.7	1.5

44744_at	solute carrier family 12 (potassium/chloride transporters),	SLC12A7	AI816843	18.9	1.9	0
48740 s at	neringer / novel retinal pigment epithelial gene		AI973108	18.7	5.4	4.1
53831_at	hypothetical protein DKFZp434F2322		A1632223	18.6	2.7	0.3
49626_at	Alg5, S. cerevisiae, homolog of		AA425251	18.6	4.7	3.8
39616_at			AL050227	18.5	0	4.8
1125_s_at	CD44 antigen (homing function and Indian blood group system)	CD44	L05424	18.5	9.0	
53497_at	integrin, beta 8	ITGB8	AI129512	18.5	2	9.0
61428_at			AW014148	18.5	6.0	0.4
1702_at	interleukin 2 receptor, alpha	ILZRA	X01057	18.4	0.2	1.8
48766_at	hypothetical protein FLJ23231		AA011633	18.3	2.1	2.2
36918_at	guanylate cyclase 1, soluble, alpha 3	GUCY1A3	Y15723	18.2	3.1	3.6
89756_at			AI768334	18.2	0	6.0
64285_at			AI050855	18.1	1.9	1.6
44972 at			AA999894	18.1	2.5	9.9
61778_at	sterile alpha motif and leucine zipper containing kinase AZK		N95341	17.4	0.5	0
59009_at			AI982723	17.4	1	0.2
43478_at	hypothetical protein FLJ20373		AW021103	17.4	9.0	5.2
58180 <u>a</u> t	KIAA0942 protein		AI073412	17.4	0.2	5.1
45561 <u>a</u> t			AI991958	17.2	0.4	1.2
35702_at	hydroxysteroid (11-beta) dehydrogenase 1	HSD11B1	M76665	17.2	3.2	2.5
182_at	inositol 1,4,5 triphosphate receptor, type 3	ITPR3	001062	17.1	0.2	6.3
55588_at	hypothetical protein FLJ13868		AI814485	17.1	3.4	1.7
76847_at			AI951161	17	1.9	3.4
70591_at	hypothetical protein FLJ21162		AL046389	17	0.4	0.3
56331_at	hypothetical protein FLJ20559		AA478923	17	3.7	1.4
64403_at			AA195829	16.9	0.2	0.7
64769_at			AI298599	16.8	5.1	2.9
32668_at	single-stranded-DNA-binding protein		AL080076	16.7	4.5	3.8
38797_at	KIAA0062 protein		D31887	16.6	0	2.3
58242_at	solute carrier family 21 (organic anion transporter), member 11	SLC21A11	AA053855	16.6	2.5	0
54819_r_at			AI720898	16.6	6.1	1.3
48556_at	HIV TAT specific factor 1	HTATSF1	AA581365	16.4	6.4	4.2

Figure 12K

55692 at	hypothetical protein FLJ11656		W22924	16.4	4.3	7.0
/500/_at			AI079327	16.3	33	0.1
80084 at	- 1		AI889019	16.3	2 2	100
35275_at		AP1G1	AL050025		0.0	0.0
49353 at	hypothetical protein FLJ20216		A1927837	16.1	0.00	0.00
745_at	transcription elongation factor A (SII), 2	TOFAS	1_	10.1	0.0	
55081_at	hypothetical protein bA395L14.2	2000	L	13.0	4.9	1.2
40767_at	tissue factor pathway inhibitor (lipoprotein associated coagulation	TFP	M59499	15.6	3.3	0 (
- 1	inhibitor)			?		7.7
70631_at			1000311	, ,		
73800_at			47000014	10.4	1.1	
80408 at	ribosomal protein L37a	410	A1030347	15.4	2.3	0.9
64879 at		RPL3/A	AA961504	15.2	0.3	0
51923 at		HS6ST	AA206625	15.2	0.2	0
7756A at	aprilinguality Alliane 1	SPHK1	AI769914	14.8	m	1.6
77007 at			AI694316	14.7	0.5	000
/0034 at			AW007125	14.6	- 3	1.3
44008 at			AI921877	14.6	7 - 7	5.1
34/26 at	calcium channel, voltage-dependent, beta 3 subunit	CACNB3	U07139	14.5		1.3
44/28 at			AI819734	14.5	1 10	0.0
	proline-rich protein with nuclear targeting signal		1103105	1 1 1 0		6.2
42537_at			AA281239	1 7 7	2.7	3.4
79494_at			777012	0.4.5	0.3	0.3
54077 at	hypothetical protein FL 110430		1//813	14.2	6.0	1.7
1440 s at			W18181	14.2	6.0	6.5
72541 at			X83490	14.1	2.6	2.8
ч	NY.RFN.45 antigen		A1652865	14	1.7	1.6
57579 at			AW001803	14	1.1	0
87957 r at			AI680721	14	4.6	4.6
٦ [.			AA513538	13.9	9.9	3.6
58935 5 34	hypothotical protein MCCEaca		AA160156	13.9	1	C
71889 at	Hypothetical protein MigCo3663		AW008462	13.7	1.1	25
37303 24			AI968055	13.7	0.7	90
88783 at	Tiany (Dissiplina)-Hormolog	HRY	L19314	13.6	0	0.6
45606 at			AI961740	13.6	1.8	0.5
13000 at			AA846692	13.6	0	0.2
30403 S at	adenosine monophosphate deaminase (isoform E)	AMPD3	U29926	13.6	2.6	0.1

Figure 12L

Niglutaryi-Coenzyme A synthase 1 (soluble)
rowth factor beta polypentide (simian cardoma
(similari sarconia
differentially expressed in adenocarcinoma of the lung

Figure 12M

48656 at			A1393886	12.3	0.6	90
63033 r at	complement CIr like proteinase precursor,		N91560	12.3	0.0	Sil
51545_at			AA160945	121	1 1	
50320 g at			A1/07833	177	1.1	7.7
58412 at	retinal degeneration B heta		2007640	12	3.8	5.
87114 at			AA80/60/	11.9	0.2	
56252 24			AW001674	11.9	1.8	0.5
30232 at			AA493229	11.8	2	
10493 at			AI393100	11.7	24	
50544 at	- 4.		N30562	117		C
33/6/at	Ineurofilament, heavy polypeptide (200kD)	NEFH		11 6		0.0
81351_at			AA527332	116	ο α	
/6515_at	ŔΙ		AA777011	11 6	י ע	
3619/_at	chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1	Y08374	11.7	5 -	
46538_at			AA913703	1111	7.7	o o
1084_at	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg	ARI 2	Magade	11.0	7.7	2.2
		7100	06700141	11.3	. i	7.5
	KIAA0477 gene product		1071701	-		
48486 at	Notch (Drosophila) homolog 2	CLOTO	000100	11.3	0.0	
81844 at	92.2.7	NOICHZ	AW024960	11.3	1.1)
84950 at			N92/24	11.2	1.8	
64937 at	noneve protein 2		A1681868	11.2	0	1.6
38763 at	Sorbitol dehydrogenase		AA044732	11.2	0.5	0.9
44868 s at		SORD	L29254	11.2	0	0.4
1919 at	vay 1 opcogene		AA917734	11.1	4.8	1.9
58697 r at		VAV1	X16316	11	0.4	
54961 r at			K6/3/0	11	3.1	2.7
53442 at			AA203620	10.9	4.9	1.1
	KIAA0623 gene product		K99605	10.9	3.1	8.1
			AB014523	10.8	1.4	1
Ī.	CASP2 and BIPK1 domain containing and all the		AA035/36	10.8	1.3	6.4
.]	Containing adaptor with death domain	CRADD	U84388	10.7	0	0
	core binding factor, runt domain, alpha subunit 2; translocated to,	CBFA2T3	AB010419	10.6	1.5	1.3
36451_at			AI743299	10.6	6	2.3

Figure 12N

entors:

			10.0	7.0	0.1
		R06655	10.6	0.2	0.7
kinesin family member 3B	KIF3B A	AB002357	10.4	1.2	0.8
	A	AW021631	10.4	0.5	2.9
ADP-ribosylation factor-like 4	ARL4 A	AI142552	10.4	1.4	3.2
guanine nucleotide binding protein (G protein), gamma 2	GNG2 A	AA738022	10.4	0.2	0.7
CD44 antigen (homing function and Indian blood group system)	CD44	M59040	10.3	0.4	0
	4	AW044646	10.3	9.0	0.5
KIAA0833 protein	1	AI796797	10.3	0	1.2
bone morphogenetic protein 6	BMP6	M60315	10.2	0	2.3
	4	AI660548	10.2	4.2	8
ADP-ribosylation factor-like 1	ARL1	128997	10.1	1.4	0.1
KIAA0833 protein	4	AB020640	10.1	0.5	1.8
integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	ITGB3	M35999	10.1	1.4	1.8
spermine synthase	SMS	AD001528	10	1.2	1.1
	1	AI808640	6.6	1.8	0.7
		R05809	6.6	0.4	0
PCTAIRE protein kinase 1	PCTK1	X66363	9.6	0.8	0.2
carboxylesterase 1 (monocyte/macrophage serine esterase 1)	CES1	107765	8:6	5.5	0.3
	4	AA487503	9.6	6.0	18
	,	AI913562	8.6	2.4	1.5
	/	AI686521	8.6	1.4	1.5
hypothetical protein FLJ11336		R51067	8.6	3.1	1
s_at RAB9, member RAS oncogene family	RAB9	A1934576	8.6	4	2
hypothetical protein LOC57333		AI797684	8.6	0	0.7
	4]	AA281494	9.8	0	2
small protein effector 1 of Cdc42		H10816	9.7	4.8	4.9
		F36583	9.7	2.1	2.9
61116 g at hypothetical protein, estradiol induced	1	AA442301	9.7	6.0	0
	SLPI	X04470	9.6	9.0	2.1
85092 g at lets homologous factor	EHF /	AI554809	9.6	0.3	0
protein tyrosine phosphatase, non-receptor type 1	PTPN1	M33684	σ	2 1	3.5

Figure 120

69629 at			AI744711	9.5	0	1.4
70377 at			AI753158	9.5	1.4	1.9
38942 r at	AD024 protein		W28610	9.4	9:0	1.8
39976 at	hypothetical protein from EUROIMAGE 783647		AL050087	9.6	4.1	5.9
77831_at	phosphodiesterase 4D, cAMP-specific (dunce (Drosophila):	PDE40	AI093171	9.4	1	0
50932 at			AI745136	9.4	1.6	2.9
54146 at			AA167624	9.4	1.1	2.7
40919 at	somatostatin receptor 2	SSTR2	M81830	9.3	1.5	2.9
34800 at	DKFZP58601624 protein		AL039458	9.3	0	0.1
91992 at	novel Ras family protein		AI382139	9.3	1.2	1
53398 at	transcription factor BMAL2		AA127950	9.3	2.3	0
76024 at			AI052586	9.3	2.2	1.7
47069 at	hypothetical protein FLJ20185		AA533284	9.3	1.3	1.6
46303 at			AA524250	9.3	9.0	1.7
47943 at			AI916838	9.5	0.3	1.6
61263 at			A1568596	9.5	3.5	0
46260 at	claudin 1	CLDN1	AI452474	9.5	2.9	2.4
90218_at			N50080	9.5	1.5	0
33452 at	plasminogen activator, tissue	PLAT	M15518	9.1	0	3.2
37338_at	phosphoribosyl pyrophosphate synthetase associated protein 1	PRPSAP1	D61391	6	1.4	0
63357_at			AI290954	6	0.2	0.4
47414 at			W91949	6	0.1	9.0
41202_s_at	conserved gene amplified in osteosarcoma		AF000152	8.9	1.5	0
86806_at			AA962815	8.9	2	1.4
56372_at			AI078177	8.9	0.4	1
39878_at	protocadherin 9	РС РС Р	AI524125	8.8	0.4	1.8
40458_at	signal transducer and activator of transcription 5A	STAT5A	U43185	8.8	6.5	1.9
33377_at	vitronectin (serum spreading factor, somatomedin B, complement S-protein)	NTV	X03168	8.8	1.7	2.8
83381_at	artemin	ARTN	AI695822	8.8	0	2
59830_at			AA995120	8.7	2.3	1.3
72917_at			W19971	8.7	0.1	0
45564 s at			AI290237	8.7	1.4	0

Figure 12P

.ntors:

Figure 12Q

miventors:

65088_at	hypothetical protein FLJ21313		AI378584	7.8	2.1	2.9
51247_at			AI264314	7.8	0	0.3
77899_at			N30618	7.8	8.0	0.4
35410_at	small inducible cytokine subfamily B (Cys.X.Cys), member 6	SCYB6	U81234	7.7		2.2
	(granulocyte chemotactic protein 2)					
41971_at	proline serine threonine phosphatase interacting protein 2	PSTPIP2	AA102566	7.7	6.0	0.7
63360_at	membrane spanning 4-domains, subfamily A, member 7	MS4A7	AI829939	7.6	6.0	0
51242_at			A1123826	7.6	0.8	1.4
54916_at			AI459123	7.6	0	0.3
38748_at	adenosine deaminase, RNA specific, B1 (homolog of rat RED1)	ADARB1	U76421	7.5	0	0
51208_at	metal-regulatory transcription factor 1	MTF1	N46867	7.5	2.1	1.2
77081_at			AI792789	7.4	0	0
85493_at			AI553724	7.4	0.5	0.5
76387_at			AA772692	7.3	1	1.6
90462_at			AA806207	7.3	2.2	3.1
54413_at			W72267	7.3	1	1.1
79207_r_at			A1939637	7.2	3	2.2
43697_at			AA504249	7.2	3.3	3.4
70204_at			R70880	7.2	0	0
49811_s_at	mitochondrial solute carrier		AA906314	7.2	8.0	1.3
82344_at			AI373048	7.1	0	0
82114_at			AA745458	7.1	0.8	0
51807_r_at			R38998	7	1.5	1.9
54016_s_at	uncharacterized hypothalamus protein HT011		AI248306	7	0.7	0
62125_at			N31710	7	0	0
46665_at	hypothetical protein FLJ20369		A1949392	7	0.2	0
91124_i_at	leukemia-associated phosphoprotein p18 (stathmin)	LAP18	AA156060	7	0	0
85911_r_at			AI285486	7	0.7	2.7
41402_at	DKFZP56400823 protein		AL080121	8.9	0	0
73989_at	spendent,	CLEUSF5	AI653660	8.9	0	0
	lectin, superfamily member 5			•		
86814_at			AI620731	8.9	9.0	0.8
72050_at			AI147202	8.9	0.5	0
44827_s_at	44827_s_at hypothetical protein STRAIT11499		AW016331	6.8	0	0

Figure 12R

37040 24	mingen activated protein kinase 8	MAPK8	AI052039	8.9	1 9	7.0
37042 at	I-mia domain-containing protein		AF054589	6.8	C	
81999 r at			AA877462	αυ	2 1	V C
41266 at	integrin, alpha 6	ITGA6	X53586	6.7	1.7	4.0
73.400 at			AA765781	6.7	0.0	
			AI820621	6.7	3.0	7.0
0/141 at			A1267607	9.9		7 %
22212 at	- 1:		W18190	9.9	80	9.0
52313 at	tropomyosin Z (beta)	TPM2	M12125	6.5	C	0.0
72594 1 at			AL042362	6.5	1.7	80
00000			AI984040	6.4		7.0
27517 at	2 11.14.2		AI476732	6.4	0.3	
41015 at		HMGCS1	X66435	6.3	0	0.7
52043 at	Process Aim activated, alpha 1 catalytic subunit	PRKAA1	AB022017	6.3	0.3	2.7
72408 at			AI217191	6.3	0.1	0
65148 at	hypothetical protein El 120130		AA923345	6.3	0.8	
3752A at	sering (through kings) 17k (1		AI860687	6.3	0	C
33707 at	۔ اے	STK17B	AB011421	6.2	1.1	1.4
B - (2)	Priospiroripase Az, group IVC (cytosoiic, calcium-independent)	PLA2G4C	AF058921	6.2	-1	1
78954_at			4400000			
68619_at			AA420590	6.2	0.3	0.6
54428 at	tensin	1	A1204439	6.2	3.7	1.4
35086 at	fls485	INS	AW00/778	6.2	1.2	2.1
32111 at	Chromodomain protein Y chromosome like		AB024705	6.1	0	6.0
37610 at	Pin Fi	CDYL	AL050164	6.1	0.8	0.4
76530 at	hypothetical protein FI 120639		AI765280	6.1	0	0
37244 at	tern		AI / 49464	6.1	1	0
'	(apidata) (aliolesterase)	UCHL3	AA746355 j	9	0.3	0
46999_at	oxidoreductase UCPA		A1096201A		į	
91718_at	chromosome 11 open reading frame 1	C1500E4	MEDCOF	٥١٥	9.0	0
49301_at	porcupine	1	M00093	٥١	0.2	0
50534_at	Small nuclear ribonucleoprotein polypeptide G	Oddino	AA23417F	٥		0.8
48745 s at	hypothetical protein FLJ12438	פועאוס	AAZ341/5	9	0.8	0.5
46323 at			M3/3240	٥	6.0	0
2000				•		

Figure 12S

25000 24		SCNIB	L10338	5.9	10	E
33990_at			AB007947	5.9) m
30034 at	B1G family, member 2	BTG2	U72649	0.5	0	0.0
5/364_at			Ľ			0.3
			AF052169			o c
	chromosome 21 open reading frame 18	C210RF18	AB004848	2.8	-	5
55555 at			AI872476		100	
38038_at	lumican	LUM	U21128		10	
68048 at			AA701259	5.7		0.0
43395 s at	UnaJ (Hsp40) homolog, subfamily B, member 5	DNAJBS	AW006148	5.7	0.1	0.5
1956 24			W07089	5.7	2.1	
63251 c at	vitel aviali leticuloendothellosis viral oncogene homolog	REL	X75042	5.6	4.1	ıc.
46727 at			AA904828	5.6	1.3	9.0
57000 f at	2001400		A1146850	5.6	6.0	
35182 f at	hypothetical professed allugell 3 (Hyaluronidase)	MGEA5	AI453779	5.6	0.1	
74006 at	האסמונים הוסופון בכיוסאלה		W25874	5.5	0	
55280 at	Distative ME DMA mothyltransferra		AI984623	5.5	0.7	
73601 at	Paracre no Division in an Sterase		AI016585	5.5	5.1	10,
71516 r at			AI885677	5.5	0	0.2
31633 7 at	aino finger protein OEO mestidans		Z40202	5.5	0.3	2
41275 at	1, 500,00	ZNF259P	295118	5.4	0	0.2
2045 s at	hemocoletic cell kinaco	E2F5	U31556	5.4	0	0
48436 at	יינין וטיטטופנוט ניפון אווומאפ	HCK	M16592	5.4	0.8	9.0
75064 at	NON2 protein		AI922968	5.4	0.1	2.4
51151 i at	hypothetical protein		AA910520	5.4	0.7	1.
1 "			A1983052	5.4	1	0.3
54799 at	glutaminase	- 1	N71632	5.4	0.3	4.4
57042 at	Similar to Caenorhabditis alegans protein 04001 o	SIS	W/2090	5.4	0	
49298 at	S cache and cickain protein 04201.9		W74749	5.4	1.6	
86004 at			AW021968	5.3	9.0	0
830 at	Tax1 (human T.cell lankamia virus taxa la kindin		AA767895	5.3	0.5	0.7
39950 at	acid sohingomyelinase like abasahadiasta	TAX1BP2	U25801	5.2	0.8	3.6
119 at	replication protein A2 (20kg)		Y08136	5.2	0	6.0
38397 34	polymerses (DNA discreted)	RPA2	J05249	5.2	0.5	9.0
יים ו	DOINT BY BY CONTROLLED TO BE 12 4	2	00.00			

Figure 12T

04300 at			AI004417	5.2	2 0	0.0
87493_at			AI 042667			2.0
47430_at			165857	5.5) † C	
48765_s_at	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	COX7A2		5.2	000	0
32735_at	KIAA0931 protein		AB023148	5.1		100
34/19_at	glutaminase	GLS	2	5.1	• 0	
3802/ at	fibulin I	FBLN1	X53742	5.1	6.0	0.50
4/832 at	-		AA100654	5.1	0	
88155 at	HZB histone family, member B	н2ВFВ	AI125923	5.1	0	9.0
00023 at			AI590115	5.1	9.0	C
32113 at		AIMI	U83115	5	2.4	
32002 at	KIAAU1/U gene product		AL041663	S	0.1	
40400 at	nypotnetical protein		AI889499	S	0	C
09029 at	otein FLJ10521		AI913628	2	9.0	9.0
40304 at	ancient conserved domain protein 4		Ai655884	5	6.9	5.7
בייסכים			AI884621	25		0.5
5365/ r at	non-kinase Cdc42 effector protein SPEC2		AI825880	5	2.2	2.4
			AA187437	2	Ĉ	200
3343/_at	homolog of yeast SPB1		AJ005892	4.9	1 2	2.0
36610 at	KIAAUU29 protein		D21852	4.9	6.0	
84588 at			AI691077	4.9	29	6 7
43690 at			AA019641	4.9	0.0	0.4
81083 at			AI248920	4.9	13	0.0
22655 at			AA479835	4.9	0.8	60
35303 st			X87613	4.8	1.1	6.0
52303 at	Illoquiti illoquedo Berre I	INSIG1	928960	4.8	2.6	0
64152 at			AI377910	4.8	9.0	0.4
76989 31			AA703523	4.8	0	0.4
64577 at			AI333655	4.8	0	0.3
610 34			H60064	4.8	2.1	2.9
52287 at	azz, receptor, surrace	ADRB2	M15169	4.7	6.0	2
81262 at	organially acid coeffyine A ligase 5		AA514342	4.7	0.8	0
89955 at			AI280818	4.7	9.0	0.2
27775 at			AW020975	4.7	-	0
46610_at			AL043934	4.7	α ς	

33198 at binder of Arl Tw	4ri Two		AA206524	46		
bbb9U at			Н92909	4 6	C	
4/4/1_at			AA916868	2 4		o (
44643_at			ACCC21A	0.4.	D.4	0
55264 at hypothetical pro	al protein SBBI67		400001	4.0	0	
47359 at			W/993/	4.6	0.5	
80778 at			AA887112	4.6	0	0
33283 at arrestin hote 2	C ***		AA179496	4.6	0	С
1		ARRB2	AF106941	4.5	80	
50042 at turnor necrosis	rosis factor receptor superfamily, member 6	TNFRSF6	Z70519	4.5	0	
Ī			AI243147	4.5	C	
63924 at transporting ger		ARHC	AI860379	4.5		100
SECTE 24	ii beta zb, transportin		AI885873	4.5	0	0.6
87673 at			AI652445	4.5	9.0	0.4
84407 7 2+			AI982610	4.5	9.0	0.0
54067 at			AI032906	4.5	9.0	
3400/ at			AI982669	4.5	0	
1			AA433928	4.5	0.5	0
25007 at HIORIGALIINE OXIG	le Oxidase A	MAOA	AA420624	4.4	C	
64001 at			AC004940	4.4	0.5	α
80370 at			AI762686	4.4	ō	
70379 at			AA907150	4.4	6.0	0.0
74047 i at			AI744361	4.4	1.2	o
- '			AW023188	4.4	С	200
83888 7.34			H48142	4.4	0	
33900 at follistatin like 3	· ·		AI031837	4.4	0	0.8
1	mitogen activated protein kinger 8	FSTL3	U76702	4.3	0	5.7
_	protein: Colai accosited	MAPK8	L26318	4.3	0.7	90
			AC002400	4.3	6.0	0.4
91181_at uncharacterized MDS031	erized hematopoietic stem/progenitor cells protein		AW044698	4.3	0	0
57414_at			00707000			
78392_at			112005	6.4	E. 1	
85068 at			102025	4 3	0.2	0.3
80554 c at			AIU329/2	4.3	0	0
2000			AW004040	4.3	6.0	С

Figure 12V

85293_at			AI468014	7.3	-	
70302_at			A1222295	0 0	-	
43246 at			NEGERO	t -	1.0	0.3
42700_i_at			106200			
T.	activating transcription factor 6	1	- 1		6.0	0.5
40012		AIF6	`	4.2	1.4	0.1
2504F 24	solute carrier larrilly 3 (mositor transporters), member 3	SLC5A3	~	4.2	1.6	0
30240 at	coagulation factor v (proaccelerin, labile factor)	F5	M16967	4.2	0	40
38005 at	nucleotide-sugar transporter similar to C. elegans sqv.7		AJ005866	4.2	0.5	0 5
56231_at			AA151678	4.2		0
33///_at	Inromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)	TBXAS1	D34625			
73576_at			00000010			
91474_at	hypothetical protein FLJ10339		777530	7.4	0.3	0
63369 at			177338	4.2	8:0	0
53933 at			A1830095	4.2	0.7	0.4
72060 5 34			AI525818	4.2	0	0.3
2000 S AL			AA199856	4.2	6.0	C
39027 at	early endosome antigen 1, 162kD	EEA1	L40157	4.1		0 6
64298 r at		ARRBZ	AW002000	4.1	80	
52656 s at		ABCA1	AW019972	4.1	0.7	70
46122 at	NY-REN-58 antigen		W52480	4	2.0	
46/36_at	ring finger protein 3	RNF3	AI301953	4 1	i -	
77905_r_at			AI287423	1 4	1 5	7.0
33004 g at	\rightarrow	NOKO	A1275502	-	5 0	
41447_at	KIAA0990 protein	KIAA0990	AB023207	1	0.0	0.0
34823_at	dipeptidy/peptidase IV (CD26, adenosine deaminase complexing protein 2)	DPP4	X60708	4	0.4	0.6
56854_f_at			A1742034		0	
90417_at	ribosomal protein S6 kinase, 90kD, polypeptide 5	PPCGKAG	41382101	1	·. 1 ·	J.0
74763_at	cold shock domain protein A	AUSO III	A1001577	1		0
77232 at		COSO C	//CT00IH	4	0.5	1
63270 at			AI683999	4	0	0.2
85864 at			AA027103	4	0	2.6
73460 jat			AW023438	4	0.5	0.3
-1 (H52268	4	0.2	0.8
מסטטט מו			R12560	4		0
62876_at			AI393573	4	C	

Figure 12W

Al494647		0.0 0.3 0.7 0.0 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
BTF3L1 TRAF4		0.0 0.7 0.0 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.2 0.2 0.2 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
BTF3L1 TRAF4		0.3 0.7 0.7 0.1 0.1 0.1 0.1 0.1 0.2 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3	000000000000000000000000000000000000000
BTF3L1 TRAF4		0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
BTF3L1 TRAF4		0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 		0.0 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.2 0.2 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3	0.27
1-		0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	000000000000000000000000000000000000000
1 4 + 1 + 1 + 1 + 1 + 1 + 1		0.02 0.03 0.01 0.01 0.01 0.01 0.01 0.01 0.01	0.0000000000000000000000000000000000000
 		0.3 0.1 0.1 0.1 0.9 0.1 0.9 0.1 0.1 0.1 0.1 0.1	000000000000000000000000000000000000000
		0.7 0.1 0.7 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1	0.0000000000000000000000000000000000000
		0.1	0.1
		0.7	0.88
		0.1	0.8 0.0 0.0 0.0 0.0
		0.1 0.9 0.1 0.1 2.8	0.8
		0.00 1.00 0.1 0.00 2.88	0.7
	m m m m	0.9	0.7
	m m m	0.1	0.7
	m m	2.8	000
	8	2.8	O
L)	
	3.6	0.4	C
N98652	~	0.3	5 -
AA075666	, m	500	0.7
WREDSE			
IGSEA ABOTZE	5		0.2
1	i m		0.0
			'
AI808755	55 3.9	0.7	0
AI378890	3.9	0.8	4.0
AA0587	3.8	9.0	0.8
LAIR2 AA133246	3.8	0	0
AA496024	33		2
AI675886	6		9
PPP1R6			
LAMC2	i m		1.8
004914	91 38	Cu	
TNFRSF11B TNFRSF11B LAIR2 OO LAMC2	0087 0087 0087 0087 0087 0087 0087 0087		

Figure 12X

80967_at			AA703048	3.7	1	0.8
75265_at			AI821772	3.7	0.2	0.3
83640_at			AI948598	3.7		9.0
88805_at			AI761186	3.7	0.3	9.0
43120_at myeloid/	myeloid/lymphoid or mixed-lineage leukemia3	MLL3	AI640514	3.7	1	0.8
34397_at acid-indu	acid-inducible phosphoprotein		AF069250	3.6	6.0	0
59119_at			AL038787	3.6	ō	0
68570_at			AA496390	3.6	0.3	0.2
81370_r_at			AA578920	3.6	0.7	0.7
	hypothetical protein FLJ20727		AW000901	3.6	1.1	0.5
53354_at			AI668938	3.6	0	0
61314_at KIAA020	KIAA0203 gene product		AL043152	3.6	9.0	0
51817_at			AI991014	3.6	0.2	0.3
53573_f_at			AA573272	3.6	2.7	3.9
41233_at DnaJ (Hs	DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6	AB014888	3.5	0.5	0
at	Fc fragment of IgG, low affinity IIa, receptor for (CD32)	FCGR2A	M31932	3.5	0	0
74390_at			AI740774	3.5	0.5	9.0
76759_r_at			AI224653	3.5	1.1	
gat	hypothetical protein DKFZp761A052		AW003291	3.5	=	0
69337_at			AI925894	3.5	9.0	0
59619_at			AW007238	3.5	0.1	0.5
78473_at			AW051926	3.5	0.7	9.0
87678_at			AI270326	3.5	6.0	0
75923_at			AI356228	3.5	1	0
	hypothetical protein		AI650829	3.5	6.0	0.3
aţ	glutamate receptor, metabotropic 1	GRM1	U31216	3.4	0.5	0.9
	aldehyde dehydrogenase 8	ALDH8	U37519	3.4	0	2.1
78618 at			AI889955	3.4	0.3	0.5
54720_at			AA493420	3.4	10.4	2
56662_at			AI627666	3.4	0.2	0
67593_at			A1033153	3.4	0.5	9.0
at			AA019910	3.4	1.6	0.2
at	hypothetical protein FLJ10698		AI951927	3.4	0	0.5
45751 g at			AA528592	3.4	8.0	0
72954_at			AA883059	3.4	0.7	8.0

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37819_at	hypothetical protein		AF007130 I	8		
40069_at	supervillin	IIAS	AF051850	3 2 6	0	
41523_at	RAB32, member RAS oncogene family	RAB32	1	3 6 8		10
38037_at	diphtheria toxin receptor (heparin binding epidermal growth	DTR	1	9.00		130
00000	Tactor-like growth factor)					
80698_at			AI051390	3.3	0	O
81813_at			AI732902	3,3	С	
77275_at			AI693524	3.3	0.50	
84163_at			AI802667		0.8)
48527_at			AI394438	3.3	0	IC
64083_at			AL044092	3.3	1	C
46126_at			AI498592	3.3	0	80
39004_at	hypothetical protein FLJ22512		AI432190	3.2	0.0	
32249_at	H factor (complement) like 1	HFL1	M65292	3.2	60	000
40034_r_at			D86864	3.2	0.8	0
84187_s_at	KIAA0729 prote		A1952956	3.0	α	-
63106_at			AA521504	3.0	5 6	0.1
59594_r_at			A1632101	3.5		1
61697_at	ankyrin repeat, family A (RFXANK like), 2	ANKRAZ	A1829903	3.5	2	
57337_s_at	hypothetical protein FLJ12389 similar to acetoacetyl-CoA synthetase		AA640793	3.2	0.4	0.1
51995_at	cysteine knot superfamily 1, BMP antagonist 1	CKTSF1R1	AA912445	3.0		
46583_at			A1640524		0	0.0
46652_at			AA524036	3.5		0.0
76844_at	hypothetical protein FLJ20608		AI797782	3.5		0.0
37274_at	biotinidase	BTD	AF018631	3.5		0.0
44801 s at	hypothetical protein FLJ21080		AI769154	3.2	0.3	t α
/8889_at			H53956	3.2	0 6	5
31884_at	hypothetical protein		L40399	3.1	0 0	
40049_at	death-associated protein kinase 1	DAPK1	X76104	3.1	0 7	
452_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c. member 1	SMARCC1	U66615	3.1	6.0	0
35703_at		PDGFA	X06374	3.1	1 2	0
362 at		70400	1	1.0	7.7	0.0
200		アスト	215108	3.1	-	0.5

Figure 12Z

81672 at			W38444	3.1	6.0	0
82436_at			AI242023	3.1	0	0.5
86391_at			W90335	3.1	1	0
68575_at			AA993965	3.1	0.2	0.1
89640_f_at			AI422384	3.1	0.4	0.7
72876_at			A1970209	3.1	0.3	0.7
45334_at hypothetical protein, clone	otein, clone		AI628609	3.1	0	0
	Telethon(Italy_B41)_Strait02270_FL142					
44027_at			AI472026	3.1	0.7	0.2
62168_at caspase 4, apopto	ptosis-related cysteine protease	CASP4	AI246018	3.1	6.0	0.2
57230_at			N98637	3.1	1	0.3
55067_at KIAA1450 protein	ein		N32192	3.1	2.5	0.7
35218 at programmed cell death 10	ell death 10	PDCD10	PDCD10 AF022385	m	6.0	0
34827_at unc-51 (C. eleg	unc-51 (C. elegans)-like kinase 1	ULK1	ULK1 AF045458	e	0.3	0.5
33167_r_at adenylosuccinate	ate synthase	ADSS	X66503	3	0.1	0.2
52207_at protein phosph	protein phosphatase 4 regulatory subunit 2		W87465	m	0.8	1
88879_at			AI378857	e	0	0.8
67251_at			AI379741	m	0.2	0.5
70798_at			AI400344	m	0	0.4
85190_at			AA737437	m	0.7	0
86047_at			AA689588	ĸ	0.3	6.0
46229_at			H23103	e	0.8	0
86346 at			AA528523	č	ć,	C

Figure 12AA

affyID	Gene Name	Gene Symbol	GBA	Score_Ecoli	Score_Candida	Score_Influenza
			AF026941	484.1	612.9	1149.5
35061_at	small inducible cytokine subfamily B (Cys.X-Cys), member 11	SCYB11	AF030514	655.1	844.8	729.7
909_g_at	interferon induced protein with tetratricopeptide repeats 2	IFIT2	M14660	320.5	145.5	573.3
431_at	small inducible cytokine subfamily B (Cys-X-Cys), member 10	SCYB10	X02530	152	390	545.7
1214_s_at	interferon, beta 1, fibroblast	IFNB1	V00535	433.9	0.1	
61371_at	cyclin-E binding protein 1		AA555023	204	148	479.5
1715_at	tumor necrosis factor (ligand) superfamily, member 10	TNFSF10	U37518	8.99	179.7	463.3
49148_at			AA947472	182.2	52	423.6
425_at	interferon, alpha-inducible protein 27	15127	X67325	565.9	754	421
41048_at	phorbol:12-myristate:13-acetate-induced protein 1	PMAIP1	D90070	159.8	8.6	408.5
908_at	interferon induced protein with tetratricopeptide repeats 2	IFIT2	M14660	22.9	34	384.9
39945_at	fibroblast activation protein, alpha	FAP	009278	1.1	1	279.2
38299_at	interleukin 6 (interferon, beta 2)	1L6	X04430	1566.4	101.3	2
51972_at	ubiquitin specific protease 18	USP18	AA143794	114.4	158.3	
1107_s_at	interferon-stimulated protein, 15 kDa		M13755	159		2
1403_s_at	small inducible cytokine A5 (RANTES)	SCYA5	M21121	232.1	9.06	
1666_at	interferon, type 1, cluster	1FN1@	J00210	2.7	0	191.9
37219_at	monokine induced by gamma interferon	MIG	X72755	261.6	704.2	
675_at	interferon induced transmembrane protein 1 (9.27)	IFITM1	J04164	112.7	140.9	173.6
37944_at	GTP cyclohydrolase 1 (dopa responsive dystonia)	GCH1	U19523	505.4	330.9	169
84893 at			AI446168	83.4		160.2
91313_at			AA131041	84	77.5	157.1
38584_at	interferon induced protein with tetratricopeptide repeats 4	IFIT4	AF026939	179.4	153.2	148.6
48864_at	interferon, alpha-inducible protein 27	1F127	A1991845	216.4	274.9	141.4
40159_r_at	neutrophil cytosolic factor 1 (47kD, chronic granulomatous	NCF1	M55067	160.7	91	
	disease, autosomal 1)		•			
70458 i at			AI654525	120.3	174.3	127.2
1369_s_at	interleukin 8	1L8	M28130	2300.5	32.6	122.1
62330_at			AI075407	185.9	169.1	121.9
269_at	2:5'oligoadenylate synthetase-like	OASL	L40387	19.8	6.9	119.4
71174_r_at	KIAA1682 protein		AI921158	67.8		115.6
1520_s_at	endothelin 1	EDN1	105008	4444		113.7
41677_at	interleukin 15 receptor, alpha	IL15RA	AF035279	278		111.4
41384_at	receptor-interacting serine-threonine kinase 2	RIPK2	AF117829	46.7	26.8	104.9

Figure 13A

1736_at	insulin-like growth factor binding protein 6	IGFBP6	M62402	50.4	Ī	0.00
33304_at	interferon stimulated gene (20kD)	115G20	188964	207.0	0 00	104.8
38388_at	2',5'-oligoadenylate synthetase 1 (40.46 kD)	OAC1	01011	27.75	2007	103.7
52615_at		1000	M1 1610	38.7	54	103.7
39081 at	metallothionein 2A	* ATTOW	MA340319	472	188.4	94.9
	. 1 4	IVI I ZA	AI547258	92.5	37.3	94.1
	homolog phosphodiesterase E4)	PDE4B	L20971	232.3	51.8	92.7
36892_at		ITCA7	00.000			
1097 s at	chemokine (C-C motif) recentor 7	1194/	AF032108	0.5	0	92.6
47013 at) (CR)	L31584	276.6	100.6	88.3
36927 at	hypothetical protein expressed in actachlact		AA121732	0.1	3.2	86.3
71839 at	The state of the s		AB000115	53.4	60.4	83.5
89884 at	metallothiopein 24		AA251131	111.4	76.5	82.8
62493 24		MT2A	AI991852	138	45.1	82.3
50591 24			W68034	1.7	0	ν.
17637			N95225	42.1	4.1	808
1401			AW052044	0	C	79.8
1491_dl	pentaxin related gene, rapidly induced by IL 1 beta	PTX3	M31166	827.3	σα	2.0
32814 at	Interferon induced protein with tetratricopeptide repeats 1	IFIT1	M24594	50 5	70.7	0 32
70460 r at			AI654525	48.9	2.06	7.37
44399 at			H11732	1 2	20.5	73.7
13/2 at	tumor necrosis factor, alpha induced protein 6	TNFAIP6	M31165	573.0	27.7	75.4
63335_at	sorting nexin 10		A1285531	10.0.0	0.7.7	75.1
51546_at			A1400001	12/.4	22.8	74.2
49117 at	interferon induced protein 75, 52kD	15176	A1436361	113.1	77.9	73.9
89899 at	myxovirus (influenza) resistance 2 homolog of musico	11/3	AI/43445	26.5	24.4	71
2002 s at	BCI 2 related protein 1	MXZ	AW001846	54	64.3	70.9
1914 24	Ovelin A1	BCL2A1	U27467	547.8	65.2	70.5
	ou bui	CCNA1	U66838	57.6	16	70.3
36776 at	Ilymphowde activation and 3	IFITM3	X57352	49.6	74	6 69
27017	minocyte activation gene 3	LAG3	X51985	13.2	148 7	69.7
3/014_4	Injaxovirus (influenza) resistance 1, homolog of murine (interferon. MX1 inducible protein p78)	MX1	M33882	53.6	82.5	69.2
879_at	myxovirus (influenza) resistance 2, homolog of murine	MX2	M30818	61.1		
48856_at	plastin 3 (T isoform)	PI 53	V10001V	1000	10	69
57699 at			A 1 1 2 2 0 0 F	42.8	2.1	68.4
87002 i at			AA133285	12.1	31.2	65.3
. 1			[AI270476	14.8	28.7	63.7

Figure 13B

Т	0 U	RBBP6	X85133	16.5	28	615
at plastin 3 (1 isotorm)		PLS3	M22299	37	C	60.4
37013_dt growtii lactor receptor-bound	ound protein 10	GRB10	D86962	19	3.9	50.3
030/0_dt			AI825713	36.1	32.1	60.3
74230 at			T93893	3.6	10.2	250
יייייייייייייייייייייייייייייייייייייי			AI692445	15.4	6.3	28
TZA IIIStone family, mer		HZAFO	L19779	64.6	21	57.1
tuillor hecrosis lactor (Nr superfamily, member 2)	TNF	X02910	201.2	47.5	57
73/21_dl			AI733197	16.5	116	56.6
nollino (December 1			AI742057	87.7	54.8	55
penno (prosopina) nom		PELI1	AL043980	85.4	6.2	54 5
Email inducible exterior		IRF7	U53831	49.2	41.5	54.1
Silian maccinia cytokille	subtantity A (Cys-Cys), member 20	SCYA20	U64197	943.4	28.3	53.8
Ī			AI470600	0.7	0.1	53.5
	ntnase z (prostagiandin G/H	PTGS2	004636	495.3	26.7	53.1
27000 S. at UNIZEDSOGUDZZ protein			AW008790	85.4	αV	500
Ę,			AI161358	45.6	13.2	52.3
(phosphoinositide bindir	nain-containing, tamily A ig specific) member 4	PLEKHA4	AA521373	23.6	0.2	49.9
guanylate binding protei	n 1, interferon inducible, 67kD	GBP1	M55542	72.1	V 0V	000
31023 Tat metallothionein 1A (functional)		MT1A	K01383	160.3	22.3	707
4			AI936516	93.7	5 -	101
chromosome	tetratricopeptide repeat gene, X	XLO	AF000993	10.2	4.6	48.9
			AI823649	69	7 L Z	707
SZU03 at CAMP responsive element mod	t modulator	CREM	568134	7.7	85.5	40.7
			AI040220	0.8	σ	47.3
(monocyte chemotactic	subfamily A (Cys-Cys), member 8 protein 2)	SCYA8	Y16645	17.3	63.9	47.1
49103 at			N47894	2.2	14.6	47
48080 at hypothetical protein El 120037			S62138	11.6	25	46.1
t Icyclin.denendent kinase	inhibitor 10 (nE7 King)		AI566481	10.4	12.6	45.7
1 at thyptophanyl-BNA synth	(VI) (VO), NIDZ)	CUKNIC	U22398	0.3	5.2	45.6
The proping of the sylini		WARV	C000UA	001		

2		AI307804	AI307804
		Al347618	Ai347618
46.9 13.9		AI916948	A 916948
4.3		M27826	M27826
71 20.1		AA897516	
95.8 38.5		AA101125	AKAP2
68.5 51.1		D28915	d, hepatitis C-associated microtubular aggregate
37.3		AA580047	
90.7		M93311	
0.4	li	AA609509	H3F3B AA609509
15.4 14.3		AI743005	AI743005
11.6 20.2		S62138	
141.3 63.		X07834	S0D2 X07834
119.6 44.8		X70326	X70326
98.3 63.		AA766831	
34.3		X57522	
19.4 20.3		AF059/34	HESA1 AF059/34
2.1		K61847	K61847
37.5		AA651720	
		AI302268	INDO AI302268
29.7 55.3		AA902134	
8.11 11.8		X57985	
		X75918	2
91.3 36.9		M34455	INDO M34455
4.4		AA897644	AA897644
31.4 36.2		AB007447	AB007447
68.8		AI760613	AI760613
12.4	1	AI810266	AI810266
289.9		J00219	IFNG J00219
		AI807018	
53.5		L06797	CXCR4 L06797
3.6		AB023182	AR033182

Figure 13D

36085_at	guanine nucleotide binding protein (G protein), alpha transducing GNAT1 activity polypeptide 1	GNAT1	X63749	9	2.4	35.8
74402_at			A1924226	0	60	35.7
78482_at			AA705165	62.7	3.6	35.7
56608_at	endogenous retroviral protease		AW007800	2.7	1.6	35.5
56922_at			AA211158	32.7	18.2	35.1
36488_at		EGFL5	AB011542	0	0	35
38389_at	: 1 (40-46 kD)	OAS1	X04371	36.5	71.8	35
39263_at		OAS2	M87434	26.7	28	34.8
56879_at	3-O sulfotransferase 3B1	HS3ST3B1	AA780067	9.79	2.5	34.8
58918_at			AA210892	176.1	24	34.8
35302_at	nuclear RNA export factor 1	NXF1	AJ132712	6.9	8.3	34.6
55625 at			N21579	2.2	3.6	34.4
63347_at	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related)		AA745981	E	1.7	33.9
81887_at			AI766826	27.8	10.9	33.8
86168_at			AA745606	2.2	9.9	33.8
57761_at			AI313253	161	50.6	33.7
45256_at	pre-B-cell colony-enhancing factor		AI271460	35.1	7.1	33.4
37406 at	microtubule associated protein, RP/EB family, member 2	MAPRE2	X94232	0	0.1	33.3
53588_at			AI967984	29.5	4.3	33.3
1580_f_at	interferon, alpha 4	IFNA4	M27318	0.5	0	33.1
32775 r at	ramblase 1	PLSCR1	AB006746	81.8	68.4	32.6
31622_f_at	metallothionein 1F (functional)	MT1F	M10943	101.8	13.1	32.6
72808_at			A1640523	16.1	6.1	32.6
45164_at	19A24 protein		W74027	189.7	74.5	32.5
31850_at	systeine ligase, catalytic subunit	CCLC	M90656	1.3	7.4	32.4
35937_at	MHC class I polypeptide related sequence B	MICB	U65416	16.3	17.2	32.3
35682_at			AI133727	17.4	1.4	32.1
68328_at			AI475514	5.5	10.2	32.1
53809_at	lation initiation factor 5	EIF5	AA831658	1.4	2	31.5
54594_at	KIAA0668 protein		AA009571	78.6	23.3	31.3
39070_at	iila)-like (sea urchin fascin homolog like)	SNL	U03057	36.9	23.6	31
84661_at	protein 1; HQ0024c protein		AI436109	0	0	30.9
44825_at	RAD50 (S. cerevisiae) homolog	RAD50	AA126482	27.8	17.5	30.9

52878 at			141632502	60	12 01	0.00
1000			200500	5.0	15./	30.3
50061_at			AI742085	0	3.5	30.8
52085_at			AA210833	33.1	21	30.6
40639_at	SCO (cytochrome oxidase deficient, yeast) homolog 2	SCO2	AL021683	7.1	5.2	30.4
38908_s_at	REV3 (yeast homolog) like, catalytic subunit of DNA polymerase	REV3L	AL096744	0.3	0.2	30.2
	zeta					
38649_at	KIAA0970 protein		AB023187	14.2	7	30.1
38570_at	major histocompatibility complex, class II, DO beta	HLA.DOB	990E0X	84.2	55.5	30.1
37643_at	ımily, member 6	TNFRSF6	X63717	69	17.4	30
40852 at	tudor repeat associator with PCTAIRE 2		AB025254	20.7	18.9	29.9
52831_at			A 160811	14.7	0	29.8
53010_at			AI809925	28.6	4.2	29.8
73236 g at	guanylate binding protein 1, interferon inducible, 67kD	GBP1	AW014593	63.9	55.8	29.8
36094_at		TNNT3	M21984	11.6	0.2	29.6
2072_at		CDH12	L34057	20.9	3.1	29.5
56169_at			W55852	35	2.2	29.4
46187_at			AI344122	2.1	3.1	28.9
36223_at	splicing factor proline/glutamine rich (polypyrimidine tract- binding protein-associated)	SFPQ	AI827895	r	0	28.7
39114_at	decidual protein induced by progesterone		AB022718	68.6	26.6	28.6
44815_s_at			AA733119	92	11.1	28.6
36296_at	lymphotoxin alpha (TNF superfamily, member 1)	LTA	D12614	154	62.8	28.5
58957_at	hypothetical protein FLJ20637		AI620475	108.9	42.7	28.3
65867_at	FXYD domain containing ion transport regulator 6	FXYD6	AL043089	103.8	73.3	28.2
62495_f_at			AI433785	4.4	17.4	28.1
32114_s_at	adenosine A2a receptor	ADORA2A	S46950	137.9	31	27.9
38111_at	chondroitin sulfate proteoglycan 2 (versican)	CSPG2	X15998	71.2	4.1	27.4
92145_at			AI703103	21.9	13.4	27.4
43848_s_at			A1968465	9.1	8.8	27.3
669 s at	interferon regulatory factor 1	IRF1	L05072	9.05	35.4	27.2
53508_at			A1247103	124.7	84.6	27.2
39643_at	IA directed), gamma 2, accessory subunit	POLG2	U94703	1.2	0.1	27
595_at	tumor necrosis factor, alpha induced protein 3	TNFAIP3	M59465	65.1	11.4	26.6
42456_at			AA758732	1.3	2.2	26.6
63780_at	hypothetical protein FLJ11259		AA814195	51.4	19.6	26.4

C2EC1 -+						
٧Į.	Dilay (HSP40) Holfilolog, Sublamily B, member 4	UNAJB4	AI741503	18.5	4.6	26.4
39594_t_at	metallothionein 1H	MT1H	R93527	91.6	9.4	26.1
37187_at	GRO2 oncogene	GR02	M36820	785	32	26.1
74689_at	lymphocyte-activation gene 3	LAG3	AW003135	7.7	77.5	26.1
36398_at			W28729	16.1	1:1	25.02
33413_at	protein tyrosine phosphatase type IVA, member 1	PTP4A1	AF051160	α	0	25.0
190_at	nuclear receptor subfamily 4, group A, member 3	NR4A3	1112767	29.1	27.6	25.0
33113_at	Cbp/p300 interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	065093	5.8	0.4	25.7
40301_at			A1703188	3.0		0 30
64293_at			A1971000	7.6		23.0
41472_at	phorbolin-like protein MDS019		AI 078641	22.0	0.0	25.0
427_f_at	interferon, alpha 10	IFNA10	V00551	4.6		25.0
1370_at	interleukin 7 receptor	11 7R	M29696	1001	0.00	25.4
61368_at			N22849	0.00	30.00	25.3
48873_at	Gene 33/Mig-6		A1571452	0.00	0.0	25.5
44921_at			R42823	3.5	1 0	2.62
40004_at	sine oculis homeobox (Drosophila) homolog 1	SIX1	X91868	000	0 0	27 0
41992_at			A1002966	3 1	0 0	0.47
33236_at	retinoic acid receptor responder (tazarotene induced) 3	RARRES3	AFOGO228	000	24.7	24.9
35985_at	inchor protein 2	AKAP2	AB023137	7.5	200.00	24.0
37078_at	(TiT3 complex)	CD37	104132	4.9	1.7	24.0
81966_at			41199/18	21.0	10.0	24.5
45289 at	novel Ras family protein		01133410	31.6	19.8	24.4
35669 at	1.=		AA133240		3.8	24.3
40757 at	granzyme & (granzyme 1 sytotoxic T lymphopyte general)		AB014533	3.2	30.4	24.1
	serine esterase 3)	GZIVIA	M18/3/	5.6	1.3	23.9
81908_at			A1650444		0	000
62214_at	hypothetical protein FLJ1354		A1583960	2 7 7	28.0	23.9
39726_at	glucagon	909	104040	2:5	7.07	63.0
61738_at			A1475680	1.1	5 -	23.0
77244 at	bHLH factor Hes4		0000014	0.10	7.7	23.0
56023 at			A1300003	04.7	15.4	23.6
39168 at	Artlike transposable element	J + 1 V	A1041556	6.3	3.9	23.6
20100 at	historical activity	ALIE	AB018328	1	11.8	23.5
03342_at	hypothetical protein	hypoprotein	AA150254	31.6	2.4	23 ₫

0.11.0			AA513397	9	7.	23.4
34/59 at			U68494	3.9	7.2	23.3
76364_at			AA643507		171	23.3
6360/_at	hypothetical protein FLJ20360		AI923841		0.7	23.3
59451_at			AI800640	. r.	6.9	0.82
65615_at	KiAA0129 gene product		AA843533		γ α C	2.62
44057_at	hypothetical protein FLJ10633		AA708740			22.0
6/846_at			AI217382	4 8	0	000
43197_at			AA863064	60	0.0	9 00
53609 at			C14904	39.3	13	22.8
51104 at			AI937446	37.7	10.5	22.6
31330 at			AI681179	34	13.3	22.5
39630 at	nypotnetical protein		AA160474	7.2	2.8	22.5
30707 at	meranoma dinerentiation associated protein 5		AA134958	61.8	417	22.4
3238/ at	butyrate response factor 2 (EGF-response factor 2)	BRF2	U07802	2	0	22 2
1027 at			AI239840	8.2	0.5	22.2
1030 at	interieukin 15	115	U14407	64.7	16.6	201
62649 1 at			N35156	1.3	4.3	22 1
40320 at	7,744,7		R61533	0	0.5	22
63260 at	NIAMIOIU protein		AA411556	2	ō	22
03300 at			W81119	0	4.8	22
40419 at	erytirocyte membrane protein band 7.2 (stomatin)	EPB72	X85116	42.8	19	219
20021 c at	\neg		H68340	71.4	10.1	21.9
75051 S at	growth arrest and	GADD45B	N95168	11.8	7.1	21.4
55040 at			N49940	0.8	3.2	21.4
50310 at			AI701480	0	5.2	21.4
71370 f at			AA429326	5.8	19.9	21.3
41744 at	timor poerocia factor alaba indicata		T55845	0	0	21.2
1	tunior recuesta factor alpira inducible cellular protein containing leucine zipper domains; fundingtin interacting protein L; transcration factor III induced.		AF070533	56	45.9	21.1
35849 at	phosphatidylserine recentor					
63628 at	interletikin 7 recentor		AB01115/	0	6.0	21
62246 at		IL/R	AI655781	123.1	41.5	20.9
02.470 at			T92947	6.8	3.4	20.8
33407 at			141928767	1001		

Figure 13H

34214 at	KIAA0644 gene product		ABOLASAA	25	7.2	500
١	evadecan / (amphightean paydocan)	, CCC	1100000	2	2	7.07
33044 at	sylluctail + (alliplie)ytail, lyuuttall)	SDC4	9026/0	17.4	5.8	20.7
64683_at			AI681906	1.3	0.1	20.7
47643_at			H10322	0.5	2	20.7
35606_at	histidine decarboxylase	HDC	D16583	5.7	2 6	20 5
51141_at	protein kinase domains containing protein similar to		A1949781	1.3	7.1	20.5
	phosphoprotein C8FW))
37060_at			U79289	1.5	6.0	20.4
51161_at	ras homolog gene family, member A	ARHA	AI743085	20.9	5.2	20.3
86293_at			AI439642	7.4	2.3	203
1717_s_at		BIRC3	U45878	63.1	47.7	20.2
58867_s_at	s at immunoglobulin lambda locus	GL@	AI872510	ĸ	2.9	202
1005_at		DUSP1	X68277	44.6	0.2	20.1
36139_at	NI		AL050289	28.5	1.5	20 1
609 <u>f</u> at	metallothionein 1B (functional)	MT1B	M13485	116.3	11.1	20.1
40505_at	ubiquitin-conjugating enzyme E2L 6	UBE2L6	AA883502	29.7	38.7	20
33380_at	topoisomerase related function protein 4.1		AB005754	6.9	6.7	20
34595 at		MYHL	AF105424	10.9	1.8	20
58391_at	testis zinc finger protein		AI798147	55.2	2.9	20
60812_at	pyruvate dehydrogenase phosphatase		A1625803	0		19.9
48076_at	hypothetical protein		AI949434	24.1	7.5	19.9
55362_at			AI653767	4.6	182	19.8
33273_f_at	┪	IGL@	X57809	0.5	1.5	19.7
52905_at	Rag C protein		AI279898	26.9	14.5	19.7
41582_at	advillin		AF041449	1.7	0	19.5
31540_at		TNFRSF9	U03397	72.2	7.8	19.5
47090_at	' ` I		A1004667	37.2	45.7	19.5
41544 at	serum inducible kinase		AF059617	24.6	0.2	19.4
1173 g at				26.2	15.6	19.2
65031_at			AI142111	0.7	1.1	191
40700_at	nuclear body protein Sp140		U36500	3.7	13.3	19
34460_at	peripheral benzodiazepine receptor associated protein 1		AB014512	1.9	0.2	19
		OAS2	AI340262	25.2	27.3	10
38787_at	promyelocytic leukemia	PML	X63131	17.9	49.4	18.9
39755_at	X-box binding protein 1	XBP1	Z93930	15.7	2.1	18.8

Figure 13I

81333 at			AI350977	2.1	80	0
52183 at			AA243659	33.5	15.4	0,0
1737 2 d	\top		AA176915	0	0	18.7
1/3/_s_at	Insulin-like growth factor-binding protein 4	IGFBP4	M62403	26.2	7.2	186
40323 at	CU38 antigen (p45)	CD38	D84276	160.1	1028	20.01
#3033 at	ilypornetical protein		AA618602	296.2	15.3	
37701 at	المراجع المراج		AI658703	8.2	3.1	18.5
48416 at	hypothetical protein algualling 2, 24kD	RGS2	L13463	9.2	1.3	18.5
56103 at	INPOCINETION DOCIMONAL		AA082707	0	0	185
56244 at			H48444	0.3	9.0	18.5
36227 at			H64595	9.0	9.0	18.5
38631 at	filmor pecrosis factor alcha industrial		AF043129	63.4	21.8	18.5
41635 at	- 1	TNFAIP2	M92357	63.8	17.8	18.4
36019 at	Passociating protein		D14661	31.6	6.1	18.4
38369 at	Milase 19	STK19	L26260	25.5	9.0	18.4
62512 at	tration printary response gene (88)	MYD88	U70451	5.1	15	18.4
40447 at	Caicil		AI927692	9.7	7.3	18.4
18357 24	CCC	LPIN2	D87436	20.2	47.2	18.0
40337 at	ribosomai protein 528	RPS28	AA968694	0.2	irc	18.1
01,555 f 2t			AI381435	5.6	12	
2000 41	00 LQ		AI419764	3.1	3.5	101
33105 at	c		AB011152	71.4	27.4	10.1
1377	Subtamily 1, group H, member 3	NR1H3	U22662	13.2	181	2 0
13//_dt	nuclear factor of kappa light polypeptide gene enhancer in B.cells 1 (p105)	NFKB1	M58603	54.5	18.3	18
87811_at			44868517	000	,	
43186_at			71000000	2.53	1.1	18
51725_at			AAE01046	5.7	4.1	18
43939_at			AA321246	129.3	35.4	18
39221_at	e receptor, subfamily B (with TM	LILRB2	AF004231	62.6	9.7	18
86419 f at	and this dollaries, member 2				•	<u>)</u>
55776 at			AA837464	2.1	0.3	17.8
15237 24	0 000		W20082	16.8	26.9	17.7
#3777 at	utase Z, mitochondriai	SOD2	AA142976	84.4	32.6	17.7
39403_at	coatomer protein complex, subunit beta	COPB	AA402414		9-	177

Figure 13J

1			11000011	25	10.0	176
74567_at			A1424032		t (1 :0
79341 at			AA084622	7	12	1 / .6
	interferon, alpha 16	IFNA16	M28585	1.2	0.5	17.5
52591 s at	ne ligase, catalytic subunit	CCLC	AI971137	0	5.6	17.5
50049 f at			AA045236	0.7	9.0	17.5
	myelin basic protein	MBP	MI3577	2.1	2	17.4
49459 at		-	AA156784	25.2	18.2	17.4
35822 at	din	BF	L15702	1635.7	287.1	17.3
87415 at			W73083	22.7	4.8	17.3
44060 at	selenoprotein W, 1	SEPW1	AA625451	4.6	1.9	17.2
90375 at			N25135	0	0	17.2
52989 at			3143817	0.3	0.1	17.2
33499 s at	immunoglobulin heavy constant gamma 3 (G3m marker)	IGHG3	AF067420	5.9	3.8	17.1
39775_at	serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor),	SERPING1	X54486	41.5	67.8	17.1
	member 1					
58161 at			AA813728	9.7	1.5	17.1
49496 at			AA521168	1.1	7.4	17.1
58889 at			R45627	0.2	0	17
39517 at	hypothetical protein 23851		AF035313	20.5	14.3	16.9
39412 at	n 173	ZNF173	U09825	4.3	5	16.9
40390 at	se	SDS	760301	3.7	5.2	16.9
40686 at		NMB	AI985272	2.9	3.2	16.9
38342 at	KIAA0239 protein		D87076	4.2	10.8	16.9
60001 at			AA405241	9.0	2.4	16.9
			AI161358	14.7	5.7	16.9
35408 i at	zinc finger protein 44 (KOX 7)	ZNF44	X16281	3.8	1.5	16.8
35224 at			AF070569	7.9	1.9	16.8
50310 at			2805207	0	1.9	16.8
41475 at	niniurin 1	NIN)1	U91512	65.2	35.7	16.7
35868 at	d glycosylation end product specific receptor	AGER	M91211	3.2	1	16.7
34445 at	KIAA0471 gene product		AB007940	1.2	6.4	16.7
36575 at	rotein signalling 1	RGS1	S59049	31	46.9	16.7
61148 at			AA884400	1.5	1.5	16.7
37531 at	KIAA0210 gene product		D86965	1.6	0.7	16.6

Figure 13K

32026_s_at	PDZ domain containing guanine nucleotide exchange		AB002311	68.3	25.1	16.6
	factor(GEF)1					
49875_at			AI733353	6.3	6.3	16.6
56525_at	integral membrane protein 2B	ITM2B	N73873	7.7	9.0	16.6
48767_at	ALEX1 protein		AI693923	3.8	5.8	16.6
77840_f_at			AI720888	4.4	8.1	16.6
32595_at	G-rich RNA sequence binding factor 1	GRSF1	U07231	7.8	22.7	16.5
32253_at	acid dipeptide (RE) repeats	RERE	AB007927	0	3.9	16.4
39132_at	SWI/SNF related, matrix associated, actin dependent regulator of SMARCA5	SMARCA5	AB010882	7.1	3.9	16.4
	chromatin, subfamily a, member 5					
35099_at		APOL1	AF019225	8.3	7	16.3
32088_at	r 1 (JEM·1)	BLZF1	U79751	9.7	6.4	16.3
33849_at	pre-B-cell colony-enhancing factor		002020	41	8.3	16.3
35337_at	F-box only protein 7	FBX07	AL050254	8.6	8.5	16.3
33969_at	interferon, omega 1	IFNW1	X58822	3.6	1.5	16.3
38450_at	Sjogren syndrome antigen B (autoantigen La)	SSB	X69804	1.4	7.7	16.2
44126_at			W28501	73.5	28.6	16.2
46867_at			AI659243	0	0.7	16.2
64692_at			W30810	10.8	3.6	16.2
83553 f at			AA703100	9.9	1.9	16.2
37168_at	similar to lysosome associated membrane glycoprotein		AB013924	6.06	9.05	16.1
33035_at	ribosomal protein L34 pseudogene 1	RPL34P1	AL021397	7.5	0.1	16.1
38576_at	H2B histone family, member B	H2BFB	AJ223353	37.4	13.7	16.1
34439_at		AIM2	AF024714	40.9	18.1	16
1326_at	caspase 10, apoptosis-related cysteine protease	CASP10	U60519	7.2	18.6	15.9
81061_at			AI978710	0.5	6.0	15.9
59052_at	similar to aspartate beta hydroxylase (ASPH)		T83087	0	1.5	15.9
55915_r_at	hypothetical protein LOC54149		AI922520	5.2	13.7	15.9
69458_f_at			AI693465	5.6	2.1	15.9
62217_at			T81422	23.7	7.2	15.8
49438_at			A1535730	68.4	21	15.8
31345_at	airway trypsin-like protease		AB002134	4.6	2.7	15.7
35015_at	CD80 antigen (CD28 antigen ligand 1, B7·1 antigen)	CD80	M27533	61	26.5	15.7
42893_at			R16983	3.1	3.7	15.7
54398_at			AA679287	4.1	1.6	15.7

Figure 13L

88629 at			A1337136	42	125	157
36423_at	p8 protein (candidate of metastasis 1)		W47047	3.1		15.6
56307_at			AI862477	0	2.3	15.6
49241_at			AI376957	3.6	4.6	15.6
61074_at			AI817642	0.4	0	15.4
37137_at	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB	M17016	52.3	9.1	15.3
36760_at			U79277	1.2	6.0	15.3
65008_g_at	splicing factor (CC1.3)		AI539492	2.1	1.1	15.3
60190_at			A1668659	1.8	1.7	15.3
51032_at	ain) 26S subunit, ATPase, 2	PSMC2	AI754675	0	0	15.3
287_at	factor 3	ATF3	L19871	9.5	4.8	15.2
36097_at	immediate early protein		M62831	6.2	1.6	15.2
33814_at	protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs		AF005046	3.5	2.3	15.1
39660_at		DEFB1	AI309115	21.1	7.8	15.1
70682_at	YME1 (S.cerevisiae) like 1	YME1L1	AI832869	0.4	m	15.1
32344_r_at	channel, shaker-related subfamily,	KCNA4	M55514	0.3	0.8	15
50205_at		LEPR	N46838	5.2	5.1	15
44594_at	CGI-112 protein		AA570477	-	2.2	15
40434_at	podocalyxin-like	PODXL	U97519	3.7	1.4	14.9
45234_at			AA648522	7.8	11.3	14.9
1008_f_at	protein kinase, interferon-inducible double stranded RNA dependent	PRKR	U50648	2.6	1.7	14.9
49634_at			N51441	0	3.2	14.9
90424 r at			AI122603	11.7	1.2	14.9
38678_at	small nuclear ribonucleoprotein polypeptide E	SNRPE	AA733050	1.2	0.4	14.8
37064_at			U66048	3.4	2.8	14.8
73776_at			AI554044	18.6	13.5	14.8
53016_at	hypothetical protein FLJ20654		AL121389	1.2	1.8	14.8
920_at	natural killer tumor recognition sequence	NKTR	L04288	6.4	0	14.7
			AA203416	33.9	10.8	14.7
52111_at			H47347	1.3	1.5	14.7
48259_at			AI123757	3.7	2.4	14.7

Figure 13M

18753 at	0242010101010101010101010101010101010101		AW007698	10	1	14
636 24	i raygamma/ anglopoleum related protein		N57259	126	7.9	14
30 at			143338	-		:
3982/_at	hypothetical protein		44522520	1.1	7.0	14.
33955_at	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic	1124	MCE201	245.1	38.4	14.6
	lymphocyte maturation factor 1, p35)		162C0M	7.067	18.4	14.6
50246_at	hypothetical protein PRO2900		0000	,		
54579 at			A13921/8	2	3.2	14.6
52855 at			AI799534	0.1	5.9	14.6
55518 at	tachykinin 3 (nouromadin V. nourolinin L. 1.1)		AI885781	4.7	11.3	14 6
35718 at		TAC3	AA004764	13.1	4.2	14.6
74681 at	medicionimadea protein 41, 30KD	IF141	L22342	23	37.3	14.5
16655 at			AI018220	3.6	1 4	17.5
40033 at	transcription factor (SMIF gene)		AA131327	16.6	0	14.5
1761 24			AI769281	1.4	α-	2 2 2
01_41		PDGFRL	D37965	110	7 75	14.0
6/5 g at	small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-ie)	SCYA2	M26683	2.5	15	14.4
1586_at	insulin-like growth factor binding protein 3	IGFBP3	M35878	0 70		
38265 at	hypothetical protein DKFZp761B2423		A1538170	2.1.7	0 0	14.4
34375_at	small inducible cytokine A2 (monocyte chemotactic protein 1.	SCYA2	M2822E	/:/	0.8	14.4
100000	homologous to mouse Sig-je)		(2707)	7/	15	14.4
703 at			A1749656	878	Č.	
1027 3 41			U50527	82.5	t 04	14.3
20333 at			AA526392	0.7	7.00	14.6
0/5 at	٠.		AI949662	σ	10.1	14.6
30364 at	carboxypeptidase A3		AI082244	100	3.6	14.0
7407E 5 24	ĭ١٠	PPP1R5	Y18207	17	200	14.6
27.0	1	ZNF173	AWOO9746			1
/4566 at	insulin-like growth factor-binding protein 4	IGFBP4	A1440424	13.7	5.5	14.1
Seeds at			N52761	16.0	4.0.4	14.1
38935_at			V7277V	0.01		14.1
36059_at	low density lipoprotein receptor-related protein 4	I RP4	APO11540	2.4	2.3	14.1
55712_at			00011340			14
46522 at			A182141/	0.4	1.7	14
47533 at			AI021992	31.5	0.1	14
			110001V			

35488_at	small nuclear KINA activating complex, polypeptide 1, 43kD	SNAPC1	U44754	3.4	0.8	13.9
823_at	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)	SCYD1	U84487	3.9	1.1	
40755_at	MHC class I polypeptide-related sequence A	MICA	X92841	15.4	α	13.0
80773_at			H15073		σ	12.0
46526_at	hypothetical protein MGC5242		A1434025	14.2	0.01	13.9
56619_at			AIROR330	3.5	1.0.1	13.9
1089_i_at			M64936	0.1.0	0.7	13.9
48431_at	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid.	FUT4	A1970292	9	14.7	
47032_at			A1885390		CV	0 0 0
36934_at	hypothetical protein LOC57158		AI 035447	ς α	100	13.0
37049 g at	translocase of outer mitochondrial membrane 34		1158970	3.00	0.71	13.0
38750 at	Notch (Drosophila) homolog 3	NOTCH3	097669	233	4 4	13.6
56019 f at			AA992380	α -	1 7	13.6
32693_at	KIAA1040 protein		AB028963	4.4		12.0
36578_at	baculoviral IAP repeat-containing 2	BIRC2	U37547	18.6	4 9	13.5
37249_at	phosphodiesterase 8B	PDE8B	AF079529		2	12.5
3801/at	CD79A antigen (immunoglobulin-associated alpha)	CD79A	005259	0.3	0 2	12.5
143_s_at	TATA box binding protein (TBP) associated factor, RNA polymerase II, D, 100kD	TAF2D	075309		0	13.5
58182_r_at			NOON 1900	C		
51450 s at			AA121544	0 0	2 5	13.5
32533_s_at	vesicle associated membrane protein 5 (myobrevin)	VAMP5	AF054825	14.0	7.00	15.5
41052_s_at	calcium channel, voltage dependent, P/Q type, alpha 1A subunit	CACNAIA	079666	0.3	33.7	13.4
47899_at			AAOS6755	23.8	0.91	
84064_at			A1365233	0 0	10.0	13.4
64194_at	hypothetical protein FLJ10903		H14920		5.1	13.4
63746_i_at			AA279977	000	0.0	13.4
36729 g at	adrenergic, alpha·1D·, receptor	ADRAID	M76446	5.0	0 0	13.4
36674_at	small inducible cytokine A4 (homologous to mouse Mip-1b)	SCYA4	104130	30.3	13.7	12.3
44729 at	hypothetical protein FLJ13855		A1027524	28.8	10.5	12.0
51105_at	Rho guanine nucleotide exchange factor (GEF) 3	ARHGEF3	N57933	0	5.7	13.3

nventors.	1.4	11	1 1	ac	U	110	.11	, c	 .44

34308_at H2A histone family, member L 33527_at potassium inwardly-rectifying channel, subfamily J, member 3 45306_at BCL2-antagonist/killer 1 45302_at BCL2-antagonist/killer 1 45302_at BCL2-antagonist/killer 1 48919_at potassium inwardly-rectifying channel, subfamily J, member 2 68002_at potassium inwardly-rectifying channel, subfamily J, member 2 68002_at potassium inwardly-rectifying channel, subfamily J, member 2 68002_at potassium inwardly-rectifying channel, subfamily J, member 2 88861_at potassium inwardly-rectifying channel, subfamily J, member B (2233_at torson family 1, member B (torsin B) 4227_iat proteoglycan 4, (megakaryocyte stimulating factor, articular superficial zone protein) 32233_at torsin family 1, member B (torsin B) 4737_at torsin family 1, member of RAS oncogene family 48062_at interferon-induced protein 35 6459_at interferon-induced protein 35 6459_at interferon-induced protein 35 6459_at function) 68714_at 47447_at 47247_at 47200_at 6700_at 67		1	_			
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at at at at at at at at at at at at at a		KON 13	130106	110		13.2
at at a at a at a at a at a at a at a		2000	033130	0.0	2.9	13.2
at a a a a a a a a a a a a a a a a a a		BANI	016811	1.4	3.6	13.2
and the second s			AA742560	1.2	5.4	13.2
at at at at at at at at at at at at at a			R05527	0	0.1	13.2
at at at at at at at at at at at at at a		KLF4	U70663	0.2	0	13.1
at at at at at at at at at at at at at a	nel, subfamily J, member 2	KCNJ2	AA393850	130	11.2	13.1
at at at at at at at at at at at at at a			AA503803	21.9	17.2	13.1
at at at at at at at at at at at at at a			AI680122	0.7	00	13.1
at at at at at at at at at at at at at a			AA398118	2.4		13.1
a			D87119		0 0	13.1
at at at at at at at at at at at at at a	megakaryocyte stimulating factor, articular	PRG4	U70136	5.8	7 0	100
at at at at at at at at at at at at at a					<u>.</u>	2
at at at at at at at at at at at at at a)	TORIB	AF007872	ır	0 9	-
at at at at at at at at at at at at at a			44017037	0 0	0.0	21
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at at at at at at at at at at at at at a	amily	DAD1A	0/1470	13.8	1.0	13
at at at at at at at at at at at at at a		C - X - C	AI4/0340	0	0.1	13
at at at at at at at at at at at at at a		31711	AF044309	12.7	5.6	12.9
at at at at at at at at at at at at at a	in the state of th	11.135	U72882	24.3	35.4	12.9
at at RNA binding mot at r_at	lospilodiesterase 4 (putative	ENPP4	AB020686	10.3	1:2	12.9
at RNA binding mot at at r at			00000000			
at RNA binding mot at r_at at at			00000000	94.5	63.3	12.9
at	Osome	> VAGO	MI202829	3.6	3.6	12.9
72290 r at 56871 at		VINICA	AI9/1694	4.9	2.5	12.8
56871_at			AI420959	0	3.3	12.8
0000 at			AA814901	9.1	10.9	12.8
			AI953847	25.7	8.6	12.8
90850 + 3+			AI989871	29.1	26.8	12.8
á .			AI522161	2	C	10 g
homolog	n A·2) viral oncogene	SRC	AF077754	4.6	1.9	12.7
34898_at amphiregulin (schwannoma-derived growth factor)	growth factor)	AREG	M30704	4.4	0	7 2 1
85409_at			VI0E3670			15.7

Figure 13P

62480_at			DIAMEATA	2 1		
44978_at	Ac-like transposable element	AITE	A197919A	0.1	0 1	12.7
34476 r at	eniregulin		200700	7	C.,	12.7
38156 at	Myon family inhihitor	באבופ	030/83	36.5	0.8	12.6
100000	וומונסו	MOFI	U78313	0.4	0	12.6
31669 at		MLANA	U06452	4.2	0.3	126
38824 at	lat interacting protein (30kD)		AF039103	5.1	5.8	126
46133_at			W60263	34.8	34 9	126
3/6/4 at	aminolevulinate, delta., synthase 1	ALAS1	Y00451	6.6	3.7	12.5
53855 at			N36284	20.1	12.7	12.5
59008 1 at			AI815758	7	4.2	12.5
72959_at			T93073	1.4	32	125
3312b_at	INK nomeobox (Urosophila), family 3, A	NKX3A	AI557413	63.8	0.0	10 5
1894 f at			L27065	0.5	0.4	
1363_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	PPP2R2A	M64929	5.3	7.5	12.4
1788_s_at	dual specificity phosphatase 4	DUSP4	U48807	α ς:	35 6	100
38207_at			C Y Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z		0.55	17.4
1895_at	V-jun avian sarcoma virus 17 oncopene homolog	Z	104111	13.4	6.4	12.4
50825 at		NOC	J04111	2.1	2.3	12.4
53801 at			W23499	3.5	2.8	12.4
			AL045781	2.4	1.3	12.4
31300 at			AA827683	0	0	12.4
32228 at			AI242476	0.2	1.6	12.4
η.			AA005281	14 7	16.7	107
1435 f at	Interferon, alpha 21	IFNA21	V00540	0	0.5	123
35514 at	KIAAU861 protein		AA916905	1.6	0	12.3
33031_dt			AL079289	11.6	0.5	12.3
340 al	t-complex-associated-testis-expressed 1-like 1	TCTEL1	D50663	22.1	20.3	12.3
30032 at			AI871408	13.7	6.9	12.3
49130 at			W56900	1.1	7.4	123
48493 at	myosin 50	MYOSC	AA195002	6.0	3.8	12.3
/3/15 at			AI126206	4.6	1.9	12.3
28220 at			AA081874	6.0	0.0	10.3
46169 at			AI745624	5	4 5	123
5356/ at			AW003119	0	0.0	123
47128_at			AI341820	6		12.3

Figure 13Q

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39402_at	interleukin 1, beta	IL1B	M15330	468.5	30.5	12.2
35251_at	human immunodeficiency virus type I enhancer binding protein 1	HIVEP1	X51435	5.6	6.4	12.2
37558_at	IGF-II mRNA binding protein 3		0010			
54648 at			09/188	3.5	11.9	12.2
49321 at			AA810864	0.2	1.6	12.2
			A1161111	0.4	2.8	12.2
40088 at			AI624103	2.5	0.2	12.2
37129 at	neitonantido EE amida acentida		AI625805	2	6.2	12.2
38082 at	KIAAAASO orotein	NPFF	A1936758	1.9	1.2	12.1
65402 24			AB014550	3.7	m	12.1
45072 r at			R71414	0.8	3	12.1
50206 2+	2 1 1 2 2 2 2 2 2 2		AI033014	3.6	5.8	121
38888	appripagation aliams in the state of the sta	APOL3	T63428	20	24.4	12.1
37172 at	carbovnontidate D2 (closes)	LGI1	AF055636	1.1	0.1	12
7/1/2 at	cal boxypeptidase bz (piasma)	CPB2	M75106	3.1		12
4004/ at	Men blood group precursor (McLeod phenotype)	××	232684	2.3	18	12
5407E 2+	NAMORUS gene product		AI948512	17.5	18.7	12
75871 2+			N57875	8.6	4.9	12
13051 at			AI916641	0	7.2	12
27112 of			AW000885	2	1.5	121
3/112 at	Ciromosome b open reading frame 32	C60RF32	AB002384	0.2	0	11 9
39636 21	Sound of the control		AB020631	0	0.1	11.9
50000 at			AL079294	0.7	0.8	110
67222 at			AA741304	10.6	26.4	11.9
53130 at	of the production 10 (ferming)		AI219734	7.3	2.6	119
18-00 too	protein priospriatase 15 (formeny 20), magnesium-dependent, beta isoform	PPM1B	AW020971	10.6	7.4	11.9
37442_at			07503014	100		
38773_at	carbonyl reductase 1	1000	AL030370	0./2		11.8
67764_r_at		Tubo	AB003151	1.6		11.8
45420 at			AAU04879	59	4.4	11.8
47483 at	similar to rat myomegalin		AI / 69692	1.2	4.7	11.8
44241 r at			A1659612	71.1	9.6	11.8
53672 at			192908	0	1.6	11.8
5207 L at			AA055179	2.2	4.6	11.8
31346 91			AA282811	1.5	9.0	1.8

73420_at			A1858360	10.8	1 6	[0
33328_at			W28612		t a	11.0
1105 s at	T cell receptor beta locus	TRB@	M12886	5.2	5 6	11./
37228 at	polo (Drosophia)-like kinase	PLK	U01038	0.3	0	11.7
78072 at			AI743607	13.5		11.7
64566 at			N54523	1 1	2	117
5216/ at			AA151346	13.5	12.1	117
64020 ot			AI808804	1.3	4.3	11.7
74020 at			AL048962	2.5	6.1	11.7
47450 at			166087	0	2.4	11.6
56171 2t			T86276	1.1	1.5	11.6
51637 24			AI566128	2.3	0.4	11.6
1007 24			T62959	20.8	2.6	11.6
3602E 2+	burkitt lyfilpriorita receptor 1, GTP-binding protein	BLR1	X68149	95	0.2	11.5
3670E 24	Stiffingled trails-acting factor (50 kDa)		X82200	18.3	22.2	11.5
30703 at	protein kinase, AMP-activated, beta 2 non-catalytic subunit	PRKAB2	AJ224538	1.8	2.4	11
			N24659	6.9	1.1	11.
30341_at	phosphatidyiserine specific phospholipase Alalpha		AI765967	28.1	24.1	11.5
51037 at			AA085091	4.2	1.3	11.5
54242 at			AI377043	0	2.3	11.5
38517 24	interpretation to the state of		AA780058	1.5	1.1	11.5
11706 at	10	ISGF3G	M87503	10	6.3	11 4
36890 24	priospirolipase C, epsilon Z	PLCE2	AB029015	1.7	3.6	11.4
1633 g at	periplaniii	PPL	AF001691	3.4	5.6	11.4
27900 st		PIM2	U77735	32	15.7	11.4
3/ 303_at	(150kD), epilegrin)	LAMA3	L34155	9.0	1.2	11.4
63332_at			AA127696	0 0 1	,	
59283_at	hypothetical protein FLJ20035		AI 042790	17.0	11./	11.4
43463_at	ineuropilin 2	NDDO	ALO42/30	37.5	24.6	11.4
71530 at		7 (11)	1/1050IA	9.6	7.2	11.4
59941 at	phosphoprofein associated with GFMs		A193652U	0.2	1.3	11.4
42933 at	"		AI769545	21.2	7.6	11.4
77297 at			195101	15.3	4.8	11.4
16000 at			AL046564	4.6	6.9	11.4
40000 at			AA742293	1.3	c	, , ,

Figure 13S

47120_at			000000000	,		
106 at	runt-related transcription factor 3	0,74	AWUUSPSP	0	0	11.4
40930 at	Suffortranferace family 44 momber 1	RUNXS	735278	20.4	17	11.3
10000		SULT4A1	W25958	3.6	1.1	11.3
39000 41		CP	M13699	5.9	0	11.3
	KIAA0195 gene		D83779		000	11.0
39953_i_at			AR014528	0 0	200	11.3
40667_at	CD6 antigen	CD6	X60992	1.5	100	11.3
78498_at			70777	0.1	2.3	11.3
42720 at			A13/4080	1.3	9.0	11.3
62837 at			AI393/2/	9.5	3.2	11.3
43084 at			AI240359	0.8	4.2	11.3
60514 at	ATC (Jaran transfer of the second transfer of		AA424211	4.4	4.8	11.3
56246 at	Entra (raige turnor suppressor, prosophila) nomolog 2	LATS2	N69566	3.3	0.4	11.3
80915 at	transcription factor at:	PFKFB3	AI765775	91	6.2	11.3
53978 24			AI347001	38.2	44.7	11.3
305 EE 24			AW024692	4.5	1.2	113
30333 41	Tosphatase 10	DUSP10	AB026436	18.8	2 /	11.0
34200 at	preast carcinoma amplified sequence 2	BCAS2	AB020623	0.7	0 0	11.5
1891 at		MAP3K8	D14497	53.8	4 5	11.2
32410 at	Interieron, alpha 5	IFNA5	V00541	0.4	2.4	11.2
745 at	selectin L (lymphocyte adhesion molecule 1)	SELL	M25280	a c	25	11.0
4/939_at			AA102788	0,00	1 2 1	71.0
/3405_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	A1990466	3.1	5.8	11.2
53773 34	the contraction for the contraction of the contract)	1
7/361 at	tuitior rectosis ractor (rigand) superfamily, member 13b	TNFSF13B	AA682496	16.9	17.6	11.2
73536 f at			AI015772	1.2	0	11.2
35055 21	Ortochromo o like antimen		AA737775	1.8	O	11.2
1061 24	interleukin 10 moonton oleh		580864	0.7	0.2	1111
37678 34	mieneumii 10 leceptor, alpha	IL10RA	U00672	9.6	5.1	
370/0 at	putative transmerriprane protein		U23070	8.7	26	1111
3/301_al	priospnoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)	PIK3R3	706060	2.1	2.1	11.1
58452_at	sperm associated antigen 9	SPAG9	A) 079765	7 /		
	DKFZP434M098 protein		AI452715	t F	7.4	
40091_at	B-cell CLL/lymphoma 6 (zinc finger protein 51)	BCL6	1100115	t C	0.1	11.1
32606_at		BASP1	AA135683	26.0	9.71	7 7
				<u>.</u>		-

Figure 13T

16/682 at 70 18 18 18 18 18 18 18 1	46954 at			AA131894	3.1	3.1	
Nicosoc Nico	3683 21			167687	9	1.8	
Kurpate Nessage Additional part Nessage Additional part	0652 at			N56920	7	7	
KLF4 AIG2903F6 3.5 KLF4 AIG2903F6 3.5 KIAD1414 protein KLF4 AIG2903F6 3.5 KIAD1414 protein SAP18 U96915 8 Line and a control of the c	2032 at			N53764	0.1	0.3	
NAMA A Decirio	3032 dt	ŀ		AI653152	14.9	3.1	
SAP18 M499339 0.3		4	KLF4	AI290876	3.5		
SAP18 U96915 SECONTICHED POlypeptide, 18kD SAP18 U96915 SECONTICHED SECO	2531_at	KIAA1414 protein		A1499339	600	0	
Alignature Ali	3859 at	sin3-associated polypeptide, 18kD	SAP18	U96915	ς α	0 01	101
Cathepsin F	3443_at			(AI033001		0.41	01
CTSF AA102395 1.7 1 1 1 1 1 1 1 1 1	3701 <u>f</u> at			1700001		6.0	
CTSF AAT02395 0.3 1	9788 at			1000000	1:/	1.3	10.
V-myb avian myeloblastosis viral oncogene homolog V-myb avian myeloblastosis viral oncogene homolog V-myb avian myeloblastosis viral oncogene homolog V-myb avian myeloblastosis viral oncogene homolog V-myb avian myeloblastosis viral oncogene homolog V-myb avian myeloblastosis viral oncogene homolog V-myb avian myeloblastosis viral oncogene homolog V-myb avian myeloblastosis viral myeloblas	3846 at	cathensin F	10	AA102395	0.3	1.9	10.9
Integrin, beta 8 All SZKD, ribonucleoprotein solutions are autoantigen S.S.A.Ro) Integrin, beta 8 In	1854 at	w.mvh avian myoloblactoria vizal	20.07	AF071748	0.1	1.7	10.8
IFRD2 U73167 U7	3118 24	interferent relational designations of the property of the pro	МҮВ	M13666	8.0	0	10.8
AB020700 4.9	2720 at	31	IFRD2	073167	ō	9.0	301
Tribonuclease, KNase A family, 2 (liver, eosinophil-derived neurotoxin) Tribonuclease, KNase A family, 2 (liver, eosinophil-derived neurotoxin)	2000	1		AB020700	4 9	22	0.01
tr	0/ 00 /d	a)	RNASE2	X55988	3.5		10.8
2'-5'oligoadenylate synthetase 3 2'-5'oligoadenylate synthetase 3 2'-5'oligoadenylate synthetase 3 2'-5'oligoadenylate synthetase 3 2'-5'oligoadenylate synthetase 3 AA4135525 AA4135525 AA4135525 AA4135525 AA4135525 AA4135252 AA4135252 AA4135252 AA4135282 O'-3 ATP-binding cassette, sub-family B (MDR/TAP), member 1 OUP-N-acetyl-alpha-D-galactosamine:polypeptide N. ATP-binding cassette, sub-family B (MDR/TAP), member 1 ATP-binding cassette, sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/TAP), sub-family B (MDR/	5213 i at			AA046067	-	,	
2: Soligoadenylate synthetase 3 OAS3 AA058770 1.1 at Soligoadenylate synthetase 3 OAS3 AA453525 1.1 at Solute carrier family 4, sodium bicarbonate cotransporter, member 8 SLC4A8 AA453357 9.9 1 ATP-binding cassette, sub-family B (MDR/TAP), member 1 ABCB1 M14758 0.3 1 UDP-NacetyLalpha-D-galactosaminyltransferase 1 (GalNAc-T1) GALNT1 U41514 0 acetylgalactosaminyltransferase 1 (GalNAc-T1) AH911873 3.6 acetylgalactosaminyltransferase 1 (GalNAc-T1) AA922861 0.6 integrin, beta 8 AA605336 1.6 integrin, beta 8 AA632861 0.6 AA922861 0.6 0.6 AA922861 0.7 0.7	344 t at			AWOOAGGA	1	4 0	10.8
2'-5'oligoadenylate synthetase 3 OAS3 AA135525 1.1 at Solute carrier family 4, sodium bicarbonate cotransporter, member 8 SLC4A8 AA43357 9.9 1.1 ATP-binding cassette, sub-family B (MDR/TAP), member 1 ABCB1 M14758 0 UDP-N-acetylalpha-D-galactosaminyltransferase 1 (GalNAc-T1) GALNT1 U41514 0 acetylgalactosaminyltransferase 1 (GalNAc-T1) AH911873 3.6 integrin, beta 8 ITGB8 AA005336 1.6 integrin, beta 8 AB01873 1.6 0 Sjögren syndrome antigen A1 (52kD, ribonucleoprotein SSA1 M62800 8.6	207_at			AAAE0220	5		10.8
th AA453529 25.2 3 solute carrier family 4, sodium bicarbonate cotransporter, SLC4A8 AA453357 9.9 1 member 8 ATP-binding cassette, sub-family B (MDR/TAP), member 1 ABCB1 M14758 0 ATP-binding cassette, sub-family B (MDR/TAP), member 1 ABCB1 M14758 0 UDP-N-acetyl-alpha-D-galactosaminyltransferase 1 (GalNAc-T1) GALNT1 U41514 0 acetylgalactosaminyltransferase 1 (GalNAc-T1) AH911873 3.6 integrin, beta 8 AA005336 1.6 integrin, beta 8 A6222861 0.6 integrin, beta 8 A6222861 0.6 Sjogren syndrome antigen A1 (52kD, ribonucleoprotein SSA1 SSA1 M62800 8.6	1450_at	synthetase	6040	AA038//0	7	9.0	10.8
solute carrier family 4, sodium bicarbonate cotransporter, SLC4A8 AA453357 9.9 1 member 8 member 8 ATP-binding cassette, sub-family B (MDR/TAP), member 1 ABCB1 M14758 0 UDP-N-acetyl-alpha-D-galactosaminoyltransferase 1 (GalNAc-T1) GALNT1 U41514 0 acetylgalactosaminyltransferase 1 (GalNAc-T1) ABCB1 M14758 0 integrin, beta 8 AA005336 1.6 1.6 integrin, beta 8 AG222861 0.6 1.6 Slogren syndrome antigen A1 (52kD, ribonucleoprotein succontigen SSAI SSAI M62800 8.6	229 r at		CASS	AA135525	25.2	30.3	10.8
member 8 ABD 18282 0.3 ATP-binding cassette, sub-family B (MDR/TAP), member 1 ABCB1 M14758 0 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) GALNT1 U41514 0 acetylgalactosaminyltransferase 1 (GalNAc-T1) ARD 1873 3.6 integrin, beta 8 AA922861 0.6 integrin, beta 8 ARB 1875 1.6 Slogren syndrome antigen A1 (52kD, ribonucleoprotein sudoantigen SS-A/Ro) SSA1 M62800	545 at	1 >		AA453357	6.6	10.2	10.8
ATP-binding cassette, sub-family B (MDR/TAP), member 1 ABCB1 M14758 0 0 UDP-Nacetyl-alpha-D-galactosaminytransferase 1 (GalNAc-T1) GALNT1 U41514 0 0 acetylgalactosaminytransferase 1 (GalNAc-T1) AND (GalNAc-T1) AND (GalNAc-T1) 0 0 integrin, beta 8 ITGB8 AND (GalNAc-T1) 0 0 0 integrin, beta 8 AND (GalNAc-T1) 0 0 0 0 Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro) SSA1 M62800 8.6 8.6			SLC4A8	AB018282	0.3	1.5	10.7
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) GALNT1 U41514 0 0 acetylgalactosaminyltransferase 1 (GalNAc-T1) Algi1873 3.6 0 integrin, beta 8 AA005336 1.6 0 integrin, beta 8 AR922861 0.6 1. Slogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro) SSA1 M62800 8.6 8.8	75 at	te, sub-family B (MDR/TAP)	ARCR1	1414750			
acetylgalactosaminyltransferase 1 (GaiNAc-T1)	041_at	-D-galactosamine:polypeptic	GAI NT1	11/11/51/0	0		10.
Al911873 3.6 0	1, 000	acetylgalactosaminyltransferase 1 (GalNAc-T1)	j	410140	5	0	10.7
AA005336	000 at			AI911873		9	-
Integrin, beta 8 1.0	042 at			44005336	5 -	0.0	10.
Integrin, beta 8	220_at			A A G C C C C A A	0.0	.O.	10.
137.5 3 137.5 3 Siogren Syndrome antigen A1 (52kD, ribonucleoprotein SSA1 M62800 8.6	896_at	integrin, beta 8	ITCBS	1007660		1.6	10.
Sjogren syndrome antigen A1 (52kD, ribonucleoprotein SSA1 M62800 8.6 autoantigen SS.A/Ro)	672_at		000	A1034832		31.7	10.
Siogren Syndrome antigen A1 (52kD, ribonucleoprotein SSA1 M62800 8.6 autoantigen SS.A/Ro)	985_at			AIG1/103	1.2	0.2	10.
autoantigen SS-A/Ro)	126 at	Singren syndrome antigen A1 (50kD ribonishoppistein	, , ,	96/6/08	0.1	9.0	10.
	150-41	Joseph Symbolic angent At (JZAD, Tibolidolebprotein Jautoantigen SS:A/Ro)	SVAI	M62800	8.6	8.2	10.6

37163_at	DKFZP586C1619 protein		AL050374	56.3	9	10.6
32082_at			AL049229	4.5	1.8	10.6
31443_at			S76346	2.4	1.5	10.6
90878_at			179248	1.1	1.9	10.6
56889_at	dual specificity phosphatase 10	DUSP10	N36770	14.2	4.1	10.6
43592_at	chondroitin 4.0-sulfotransferase 2		AA449104	0.5	6.1	10 6
88354_at			H18944	2.5	1.6	10.6
40097_at	n factor 1A, Y chromosome	EIF1AY	AF000987	1.6	3.2	10.5
529_at	dual specificity phosphatase 5	DUSP5	U15932	45	12.1	10.5
35340_at	forming oncogene (derived from cell line NK14). RAB8	MEL	AI819948	0	6.9	10.5
	homolog					
39119_s_at	natural killer cell transcript 4		AA631972	22.5	34.2	10.5
44895_at			H00995	1.1	1.8	10.5
50829 at			AA706818	4.8	10.8	10.5
78020_at			AI470127	3.3	0.7	10.5
58222_at	neural precursor cell expressed, developmentally down-regulated	NEDD1	R71348	1.1	1.3	10.5
59516_at	KIAA1268 protein		AA210695	141	113	10.5
65531_at	hypothetical protein FLJ22794		AA948676	6	5.2	10.5
45453_at			AW000995	1	3.5	10.5
46317_at	collagen type I receptor, thrombospondin	CD36L2	W07476	8.0	88	10.5
	sosomal integral membrane protein II)		_			
40492_at	KIAA0826 protein		AB020633	0.2	1 7	10.4
	scription complex, subunit 4	CNOT4	U71267	4.7	4	10.4
·v _i	9	IFNA6	X02958	0.4	0	10.4
36315_i_at	KIAA0919 protein		AB023136	0.5	0.4	10.4
33979_at	e, RNase A family, 3 (eosinophil cationic protein)	RNASE3	X55990	3.8	0	10.4
36914_at		CTSO	X77383	8.0	1.4	10.4
41045_at	secreted and transmembrane 1	SECTM1	U77643	37.2	67.4	10.4
61150_at			AA894558	0.5	0.3	10.4
43363 s at			AI978590	5.1	1.9	10.4
65331_at			AW009884	1.9	2.5	10.4
43269 at	KIAA1554 protein		AA424170	7.6	12.5	10.4
/19/3 r at			AI089044	9.3	5.3	10.4
86326 g at			AA488988	13.1	0	10.4

71701 24			ODATACIA			
17.21-01			AI34/466	5	0.3	10.4
32882_at	sterol O-acyltransferase 2	SOAT2	AF059203	1.2	0	10.3
33828_at	SWI/SNF related, matrix associated, actin dependent regulator of SMARCE1 chromatin, subfamily e, member 1	3MARCE1	AF035262	0	1.4	10.3
40696_at	receptor (TNFRSF) interacting serine threonine kinase 1	RIPK1	U50062	10.9	2.9	10.3
31590 g at	gamma-aminobutyric acid (GABA) B receptor, 1	GABBR1	AL031983	4.9	6.0	10.3
37921_at	neuronal pentraxin l	NPTX1	U61849	1.3	3.6	10.3
55551_at			AI766561	10.6	7.1	10.3
90167_at			AI684439	æ	2.3	10.3
62528_at	hypothetical protein FLJ20073		AA741307	51.4	23.4	10.3
54565_at			AA149736	45.6	8.7	10.3
1203_at			D17357	17.8	5.2	10.3
35096_at	igh affinity aspartate/glutamate	SLC1A6	U18244	7.7	4.1	10.2
	transporter), member 6					
41784_at	DKFZP564B0769 protein		AL080186	0	0.3	10.2
39802 at	small inducible cytokine A7 (monocyte chemotactic protein 3)	SCYA7	X72308	1.8	15	10.2
37275_at		GABPB1	U13045	6.5	3.9	10.2
602_s_at		HSD17B1	M29037	0	0.7	10.2
38782_at		GTF2H1	M95809	0.4	2.1	10.2
66524_at			AA830101	0.4	0.5	10.2
.62288_at			A1336854	6.4	3.1	10.2
76762_at			AI246590	53.8	8.9	10.2
44947_at			AA047365	1.7	2.3	10.2
53595_at	AD:015 protein		6006EN	9.0	3.4	10.2
78732_f_at			A1094933	4.2	9.3	10.2
78728 g at			AA425815	1.1	4:0	10.2
35113_at	in transporter), member 1	SLC22A1	X98332	16.2	1.8	10.1
40457_at	splicing factor, arginine/serine-rich 3	SFRS3	AF038250	0.4	0.7	10.1
1449_at	pain) subunit, alpha type, 4	PSMA4	D00763	8.3	6.2	10.1
37018_at		H1F2	A1189287	26.1	2.3	10.1
	hypothetical protein FLJ11286		AI862559	9.2	10.4	10.1
61181_at			AA063523	2.9	3.1	10.1
43131_at			R00030	2.1	9.6	10.1
65678_at			AA461084	8.4	9	10.1
76802_at	core promoter element binding protein	COPEB	AI355637	æ	0.3	10.1

1 000		AI741209	5.6	4.3	10.1
		AI799784	2.7	9.0	101
		AI247356	9 5	0.3	101
		AA825923	0.00	2.0	10.1
ubiquitin conjugating enzyme E2L 3	UBF213	A 1000519		100	1.0.1
interferon, alpha-inducible protein (clone IFI-6.16)	G1P3	1122970	1100	2.4	019
KIAA0615 gene product		AB014515	13.5	0.0	215
hypothetical protein FLJ11149		AE038172		1.	2 .
nuclear antigen Sp100	SP100	M60618		1.0	10.
myeloid cell leukemia sequence 1 (BCL2-related)	MCL1	108246	10.4	3.0	10
		AW006763	100	000	
hypothetical protein FLJ11264		AI692513	4.7	D C C	10
		AA291194	3.1	2 4	10
		AW026509	11.0	5 2 2	
		AA194980	40.7		101
KIAA0442 protein		AB007902	0.7		0
heat shock transcription factor 4	HSF4	D87673	4 1		
transgelin	TAGLN	M95787	C	2 4	00
trefoil factor 3 (intestinal)	TFF3	AI474125	2.3	0.1	9.0
		AA682849	2.9	α.	00
61840_s_at catenin (cadherin-associated protein), delta 1	CTNND1	A1863000	5.3	4.5	000
_s_at hypothetical protein FLJ13171		AW001604	6.4		00
		AI066588	3.5	2.5	0.0
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitropsin), member 8	SERPINA8	AI208913	23.9		9.9
		A1334284	α	3.7	
		AL042923		χ. α	0.0
tumor necrosis factor (ligand) superfamily, member 8	TNFSF8	L09753	0.5		000
- 1	TLL2	AB023149	2.5	20	0.0
BCL2-associated X protein	BAX	L22474	4.1	4 6	80
exostoses (multiple) 1	EXT1	879639	50.9	100	80
growth arrest and DNA damage inducible 34		U83981	23.2	1.9	96
KAB5B, member RAS oncogene family	RAB5B	X54871	2.8	2.5	86
CD48 antigen (B-cell membrane protein)	CD48	M37766	15.4	21.6	86
		20300444	o o		

20000			AI740855	1.7	1.2	9.8
71001 at			W04199	0	0.8	9.6
71984 at	hynathetical protein El 120647		AI478759	7	14.4	9.8
81915 at	ocyte-associated protein 4	CTLA4	AI733018	0	19.5	8.6
44310 at			AA521497	0.4	2.6	9.8
51839 at			AA284279	1.6	3.3	8.6
63087 24	inhighting Cytochrome Cyteductase (6.4kD) subunit		AI480328	29.8	8.6	9.8
87258 at			N53015	4.1	14.9	8.6
39541 at	KIAA1237 protein		W52003	2.7	7.1	9.7
	hypothetical protein P15-2		AL031387	8.2	4.5	9.7
34638 r at	ase I (class I), alpha polypeptide	ADH1	M12963	1.8	0.2	9.7
40372 at			N67059	0.2	0.1	9.7
49372 at			R08912	2.6	3.3	9.7
45/0/ at			R51079	4.0	6.0	9.7
13760 at			AA397579	1.4	9.0	9.7
61207 at			N54899	4.3	3.4	9.7
46712 at			W63773	13.2	2.4	9.7
51508 3			T92882	13.7	7.2	9.7
32053 at	cyclin T2	CCNT2	AF048731	4.2	6.0	9.6
33841 at			R48209	0.1	1.8	9.6
34376 at	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	PKIG	AB019517	5.4	2.2	9.6
37729 at	exportin 1 (CRM1, veast, homolog)	XP01	Y08614	1.5	2.4	9.6
45379 at	٠l		AI659019	6.4	5.8	9.6
59479 at			W44692	1.2	0.8	9.6
63066 at			AA001735	113	12.6	9.6
44055 at			AA133979	0	6.8	9.6
54025 at			H16294	6.6	2.6	9.6
58459 s at			AA150805	0	6.0	9.6
46961 r at			T91186	6.9	8.3	9.6
1-			AI819225	0.2	0	9.6
1	H2B histone family, member H	Н2ВГН	280780	8.6	0.3	9.5
32206 at	Г		AB007920	2.4	1.4	9.5
36866 at	testis-specific ankyrin motif containing protein		D78334	2.1	2.4	9.5
33823_at	CD36 antigen (collagen type I receptor, thrombospondin	CD36L2	D12676	16.8	30.9	9.5
	receptor)-like 2 (lysosomai integral memorane protein il)					

56373_at	UDP-Gal:betaGlcNAc beta 1,4. galactosyltransferase, polypeptide B4GALT5	B4GALT5	AA133969	42.2	ю. б	9.5
77832 f at			A1638850	0.8	1.9	9.5
٦ [-			T59016	0	2.4	9.5
74034 at			AW002600	8.6	2	9.5
63781 r at	CHMP1 5 profein		AI368368	1.8	1.7	9.5
75181 at	zinc finger protein 281	ZNF281	AA121673	5.1	5.9	9.5
5/501 at			AI253196	0	O	9.5
54301_at			AI400414	15.6	6	9.5
57722 at			AI492902	0.2	5.8	9.5
37027 at	AHNAK nucleoprotein (desmovokin)	AHNAK	M80899	7.7	4.7	9.5
35298_at	eukaryotic translation initiation factor 3, subunit 7 (zeta, אבי אבי ארבי).	EIF3S7	U54558	₹ <u>₹</u>	9.7	9.5
25527 24	KIAA0514 gene product		AB011086	2.7	0.2	9.4
	alvoorotein Ib (platelet), alpha polypeptide	GP1BA	J02940	30.9	9.1	9.4
33003 at	om noi	ICAM5	U72671	2.7	1.3	9.4
32134 at			AL050162	2.8	1	9.4
39650 c at	30650 s at IKIAA0435 gene product		AB007895	1.6	1.9	9.4
36053 at	Cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	CDKN2C	AF041248	0	0	9.4
36814 at			AB029032	0.3	2.9	9.4
890 at	Inhiguitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	M74524	1.2	4.2	9.4
61191 at			AI539443	3.9	14.2	9.4
44122 at	transcriptional regulator protein		AI074024	2.4	2.7	9.4
46065 at			N23366	0	2.3	9.4
			AI634580	15	16.9	9.4
	DNA segment on chromosome X (unique) 9928 expressed	DXS9928E	AI697939	21.5	20.6	9.6
	sednence		AA216639	1.7	0.1	9.4
32163 L at			AA167191	0.4	0	9.4
44212 at			2884969	1.1	1.3	9.4
12010 12010	١.		1122897	7.9	5.1	9.3
40063 at	nuclear containt to protein	BID	AF042083	9.9	4.2	9.3
1200 04		PCTK2	X66360	0.4	0.1	9.3
1666 di	spermidine/speri	SAT	AL050290		12	9.3
34304 S at	Sperification of a point of a poi	PLXNC1	AF030339	18.3	38	9.3
32133 at						

cyclin-dependent kinase-like 1 (CDC2 related kinase) ineuroblastoma, suppression of tumorigenicity 1 H4 histone family, member H hypothetical protein hypothetical protein, clone 2746033 angiopoietin 2 soluble adenylyl cyclase delta-like homolog (Drosophila) cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) Cdc42 effector protein 3	CDKL1 NBL1 H4FH ANGPT2 DLK1 CMAH	X66358 D28124 AA700227 R43774 R43805 AA180163 N32748 W81697 W44483 AA126461 AF004327 AL035122 U15979	11.7 19.1 19.1 1.7 1.7 1.7 1.7 1.7 1.7 1.7 1.7 1.7 1	0.7	0 0 0
	18L1 14FH 14FH 14FH 14FI MAH	D28124 AA700227 R43774 R43805 AA180163 N32748 W81697 W44483 AA12641 AF004327 AL035122	11.7 19.1 1 2.1 1 4.2 6.9 6.9 4.8	31.1	8.6
	I4FH NGPT2 NGPT2 NGAH	AA700227 R43774 R43805 AA180163 N32748 W81697 W44483 AA126461 AF004327 AL035122	19.1 1.2.1 4.2 6.9 4.2	31.1	5.0
	I4FH NGPT2 NGPT2 NAAH	R43774 R43805 AA180163 N32748 W81697 W44483 AA126461 AF004327 AL035122	2.1 4.2 6.9 4.2 4.2	1.10	
	HFH NGPT2 ILK1 MAH	R43805 AA180163 N32748 W81697 W44483 AA126461 AF004327 AL035122 U15979	2.1 4.2 6.9 6.9 4.8		6.0
	I4FH NGPT2 ILK1 MAH	AA180163 N32748 W81697 W44483 AA126461 AF004327 AL035122 U15979	6.9	0.10	5.0
	I4FH NGPT2 ILK1 MAH	N32748 W81697 W44483 A4126461 AF004327 AL035122 U15979	4.8	0.0	0.0
	NGPT2 LK1 MAH	W81697 W44483 AA126461 AF004327 AL035122 U15979	4.8	2 2	0.0
	NGPT2 LK1 MAH	W44483 AA126461 AF004327 AL035122 U15979	4.2		
	NGPT2 LK1 MAH	AA126461 AF004327 AL035122 U15979		4.0	0.0
	NGPT2 LK1 MAH	AF004327 AL035122 U15979	α α	2 0	0.0
	LK1 MAH	AL035122 U15979	0.50	ò	0.0
	LK1 MAH	U15979	1 7		2.6
	MAH	0,000	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		9.6
		D86324	10.9	17.0	9.6
					į
		AF094521	5,5	2.1	00
		U55989	1	C	
		AI300111	7.7	49	00
		N32169	13	2.4	0.0
		T98171	3.6	3.7	0.0
		AA535914	15	1,51	7.0
		H82526	23.6	1:01	9.6
		AW051767	2	7 -	9.6
		AI 040635	16.7	100	9.2
desert hedgehog (Drosophila) homolog	Ŧ	U59748	60	4.4	9.6
		AA226513	0.0		0.0
	BO	X84746	3.6	0.3	9.1
acetylgalactosaminyltransferase; transferase B, alpha 1.3. galactosyltransferase)					
	ERPUD1	AF055001	1.4	3.4	9.1
related to the N terminus of tre		D13644	0.0	α	0
nger protein, 1	KRN1	U41315	2.1	4.2	9.1
forkhead box C1	OXC1	AF078096	2.9	0.7	9.1
	E (Drosophila) homolog p (transferase A, alpha 1.3 N. minyltransferase; transferase B, alpha 1.3. ferase) nducible, endoplasmic reticulum stress-inducible, omain member 1 I terminus of tre nger protein, 1	redgehog (Drosophila) homolog od group (transferase A, alpha 1.3.N. alactosaminyltransferase; transferase B, alpha 1.3. syltransferase) syltransferase) rike domain member 1 n-like domain member 1 to the N terminus of tre d box C1 FOXC1	E (Drosophila) homolog (transferase A, alpha 1-3.N- minyltransferase; transferase B, alpha 1-3. ferase) nducible, endoplasmic reticulum stress-inducible, HERPUD1 omain member 1 I terminus of tre nger protein, 1 FOXC1	AA535914 AA535914 B2526 AW051767 AW051767 AU040635 1 AU04065 1 AU040635 1 AU04	E (Drosophila) homolog AHS55914 15 1 E (Drosophila) homolog DHH AM051767 0 P (transferase A, alpha 1.3.N-minyttransferase; transferase B, alpha 1.3.ndicible, endoplasmic reticulum stress-inducible, and cible, endoplasmic reticulum stress-inducible, herePUD1 AA226513 0.2 I terminus of tre D13644 0.2 I terminus of tre MKRN1 U41315 2.1 I foxc1 AF078096 2.9

Figure 13AA

1,001	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					
41021_S_dt	41021 s. at Biyceroi-s-phosphate denydrogenase Z (mitochondrial)	GPD2	U36310	16	10.7	9.1
5810/_at			AA984220	1.5	1.1	9.1
89202_at			AI347361	28.3	30.4	9.1
48374_at			W87470	5.1	1.4	9 1
63968_at			A1979124		C	50
83253_i_at			H11766	14	1 4	0
47343_at			AI655198	2.4	2	100
53670_at			AA664156	4.7	17.4	9 1
64794_at			AA120764	2.6	2.9	9 1
42056_at			AA282541	1.8	1.6	9 1
48964_at			AI629027	24.2	17.2	9.1
41455_at	KIAA0712 gene product		AB018255	0.7	0.1	6
31847_at	highly charged protein		X59131	2	2.4	σ
32319_at	factor (ligand) superfamily	TNFSF4	AL022310	1.2	1.4	6
0000	transcriptionally activated glycoprotein 1, 34kU)					
36282_at	- 1		AF054994	1.4	6.4	6
1452 at	LIM domain only 4	LM04	U24576	5.7	1.5	6
33952_at			U71601	0.4	0.8	6
1512_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	DYRKIA	D86550	6.9	2.9	6
37578_at	actin filament associated protein		D25248	0.7	20	σ
51307_at			AI589165	0.2	1 0	0
48417_r_at	hypothetical protein PRO2849		AA636101	0	0.2	10
74628 g at	NICE-5 protein		AI986085	0	2.5	6
65626_at			AA059458	96.4	20.4	6
46172_at			AI142832	9.7	6.8	0
47823_r_at			AI452659	C	C	O
43640_at	sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 5	SIRT5	N55168	1.1	3.2	0
61789_i_at	ne (prosome, macropain) 26S subunit, non ATPase, 11	PSMD11	H05559	0.3	0.2	6
58560_f_at			AA810101	1.7		σ
31722_at	ribosomal protein L3	RPL3	AL022326	4.9	3.9	0
38546_at	ssory protein	ILIRAP	AB006537	2.5	1.5	8.9
1754_at	death-associated protein 6	DAXX	AF006041	3.1	3.1	8.9

33365_at	KIAA0945 protein		AB023162	0.2	0.2	68
1354_at	neurotrophic tyrosine kinase, receptor, type 2	MTRK2	U12140	1.7	9.0	8
465_at	HIV-1 Tat interactive protein, 60 kDa	HTATIP	U74667	9	2.8	8.9
33135_at	solute carrier family 19 (folate transporter), member 1	SLC19A1	U17566	1.6		68
45748_at	SAR1 protein		AI143121	15.6	1.9	6.8
59870_at			AI003552	2.3	1.1	8.9
91329_at			A1669284	0	0	8.9
59548_at			AI732248	3.3	4	8
32156_at	poliovirus receptor-related 2 (herpesvirus entry mediator B)	PVRL2	AF044968	23.4	5.9	8.9
80897_at			R63836	1.8	1.7	8
74908_at	interferon-induced protein 35	IF135	AW026462	19.7	35.8	8.9
53157_at			AI092930	1.2	1.1	0 &
35310_at			D45288	9.4	5.5	8.9
38227_at	microphthalmia-associated transcription factor	MITE	AB006909	8.9	2.2	80,
34057_at	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	SLC28A2	U84392	2		8.8
34066_at	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	Н6РД	AJ012590	e	1.3	8.8
39210_at	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	FUT4	M58597	2.8	6.2	8.8
1048_at	retinoid X receptor, gamma	RXRG	U38480	1.7	0.8	80
56968_at	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)	MEF2D	AL118605	3.4	5.6	8.8
56459_at			AI821762	6.0	9.0	8
77121_at			AI733322	2.4	2.1	8,8
59865_at			AI003502	Е	2.5	8.8
47484 at			H17489	32.5	22.9	8.8
61149_at			AA888887	2.2	2	8.8
46069_at			W45330	5.2	3.8	8.8
65262 <u>r</u> at			H29209	0.5	1.8	8.8
42350_r_at			N71364	2.3	4.1	8.8
82421 i at			AI554417	4.1	6.2	8.8
85192 r at			AI351062	9	2.5	8.8
45326_at	hypothetical protein PR02577		N21414	0.1	2.2	8.8
52425_at	KIAA1376 protein		AA164405	1.4	0	8.8

50804 at	L-kynurenine/alpha-aminoadipate aminotransferase		AI798980	60	2 5	8
45099_at			N92526	9 1		ο α
55830_at			AANSAGRE	101		0.0
47870_r_at	hypothetical protein DKFZp761C169		AW003245	22.0		\$ 0
54940_at			R49669	200	100	0,0
38788_at	promyelocytic leukemia	PML	M82827	25.1		0.0
42130_at			AAAOOERO	107	20.3	0 0
48182_f_at			T91299	t Q	1	000
84483_f_at			A1459092	100		0 0
36493_at	lymphocyte-specific protein 1	I SP1	M33552	7.1	6.0	X) C
44688_at	RelA-associated inhibitor		AA614049	7.7	1.1	X 0
41432_at	ribosomal protein S6 kinase, 90kD, polypeptide 5	RPS6KA5	AF090421	П	000	0 0
39269_at	replication factor C (activator 1) 3 (38kD)	RFC3	107541	5.0	0.0	0.7
33016_at			AI052224	110	5	000
39710_at	P311 protein		130551	4.7	1.4	χ.
32254_at	vesicle-associated membrane protein 2 (synaptobreyin 2)	VAMP2	0.50521	0.0	32	8.7
34745 at			ALU30223	Σ.Τ	7.7	8.7
35675 at	Vinexin beta (SH3.containing adaptor males 1)		AF070570	38.1	14.3	8.7
36,050	יוי		AF037261	4.8	2	8.7
30409 at	dystroprevin, alpha	DTNA	U46744	1.1	0.1	2
30/80_at	ភ :	CLU	M25915	32.9	ıc	ζα
	glycoprotein 2, testosterone-repressed prostate message 2,)	ò
10 20000	applipation of			-		
36280_at	KIAA1U/1 protein		AB028994	2.5		ν α
694 at	mucin 5, subtype B, tracheobronchial	MUCSB	X74955	13	40	ν. α
64989 r at			AA482282	3.2	80	ν.α
53410 at	tumor susceptibility gene 101	TSG101	AA553646		2 3	ς α
51896 at			AL038511	3.6	4 4	200
75031_at			AW051699	7	V C	7.0
5/84/ at			R48461	20	3 6	0.0
63288_at			R12689		0.7	000
51155_at			A10/3660	2.0	4.6	\%.
41742 s at	tumor necrosis factor alpha-inducible cellular protein containing		ALO43009	19.8	6.2	8.7
!	leucine zipper dates upita materiale centural protein containing leucine zipper datamains; Huntingtin interacting protein L; transcration fartor IIIA.interaction existen		AF061034	24.3	28.1	8.7
57739 at	hypothetical protein El 10010E					
31/35 at	hypothetical protein FLUZUL95		A1949010	4	ι C	7 0

45855_at			AI872417	3.4	3.3	8.7
45889_at			AW024527	0	0	8.7
57194_at			157670	0	2.6	8.7
64344 at	lysosomal associated membrane protein 1	LAMP1	AI984264	1.8	0.8	8.7
44093 at	hypothetical protein FLJ13441		W28327	S	8.8	8.7
39917_at	gamma-tubulin complex protein 2		A1961040	2	9.0	8.6
40552_s_at			AL049987	0	0	8.6
33439_at	transcription factor 8 (represses interleukin 2 expression)	TCF8	D15050	4.1	2	8.6
37026_at	core promoter element binding protein	COPEB	AF001461	6.9	5.7	8.6
41503_at	KIAA0854 protein		AB020661	23.1	10.5	8.6
36472_at	N-myc (and STAT) interactor	IMN	U32849	7.8	12.1	8.6
36130_f_at	metallothionein 1E (functional)	MT1E	R92331	78.7	4.6	8.6
237_s_at	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha	PPP2CA	M60483	7.6	S	8.6
	isotorm					
59414_at			AI480103	0.8	0	8.6
47510_r_at			AI924696	1.9	1.9	8.6
62256_at			R50614	0	1.8	8.6
90421_at	conserved gene amplified in osteosarcoma		AA633203	36.5	35.1	8.6
70516_at	leucine-rich protein mRNA		AI817736	14.2	6.4	8.6
59630_g_at			AA143009	1.2	0.5	8.6
69142_at			A1635522	72.4	7.8	8.6
43958_at			AI499157	0	6.0	8.6
47655_at			AI022328	6.4	6.5	8.6
43031_at			AL045916	0	1.8	8.6
60116_r_at			N59866	1.8	1.1	8.6
55412_at			AI768697	3.1	1.6	8.6
49792_at			AI298555	2.7	2.4	8.6
55423_f_at	- 1		AA001367	1.1	6:0	8.6
39013_at	APG5 (autophagy 5, S. cerevisiae) like	APG5L	Y11588	1.6	1.2	8.5
36734_at	small proline-rich protein 2A	SPRR2A	M21302	1.2	0.8	8.5
39744_at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 3	DDX3	AF000982	e	1.5	8.5
40088_at	nuclear receptor interacting protein 1	NRIP1	X84373	15.6	6.6	8.5
31522 f at	CI.	H2BFG	580779	5.4	2.5	8.5
34709 r at	stromal antigen 2	STAG2	275331	7.4	1.8	8.5
1241_at	protein tyrosine phosphatase type IVA, member 2	PTP4A2	U14603	0	9.0	8.5

89894_at			A1991103	1.4	3.4	X
59266_at			AI272654	1.2	1 7	0 00
79512_at			AI248270	6	2.5	0 0
70238_at			AA521399	3.9		000
64176_at			AI650542	10.3		8
51092_at	putative zinc finger protein NY-REN-34 antigen		AI950095	21.1	14.6	8.5
73455_f_at			H72723	70.4	8.2	8.5
55974_at			AI732621	0.8	6.0	8.5
56435_at	hypothetical protein FLJ20625		AA573749	6.7	5.9	8.5
64508_s_at			A1968969	7.4	6.4	8.5
64739_at		DOK2	AI828929	8.8	8.3	8.5
41374_at	2	RPS6KB2	AB016869	1.5	0.4	8.4
39084_at	enolase 3, (beta, muscle)		X56832	1.2	3.2	8.4
40621_at		PAWR	U63809	0.2	1.1	8.4
40641_at			AF038362		6	8
33455_at		ALDOB	X02747	0		8.4
36484_at		GALNT3	AI935146	12.9	7.	8 4 8
)	-
41283_at	tein H3 (2H9)	HNRPH3	AF052131	1.3	0.4	8.4
32629_f_at	, subfamily 3, member A1	BTN3A1	U90552	10.8	6.6	8.4
34318_at	JM4 protein		AJ005896	2.9	2.7	8.4
40738_at	CD2 antigen (p50), sheep red blood cell receptor	CD2	M16336	0.8	1	8.4
566_at	promyelocytic leukemia	PML	M79462	6.1	9.9	8.4
66442_f_at			AA774820	1.1	0.2	8.4
60305_at			A!015280	4.3	e	8.4
60723_at	1001		AA744550	1	6.0	8.4
61140_at			AI768092	1.1	0.2	8.4
47215 r at			AA129058	4.9	2.9	8.4
84319_at			AI684171	0	ō	8.4
44640_at			W30985	40.2	11.6	8.4
33489_at	trefoil factor 2 (spasmolytic protein 1)	TFF2	U47292	1	0	8.4
44602_at			AA156238	0.3	1.1	8.4
45922_at			AI560775	2.6	4.6	8.4
45225 at	ATPase, Class I, type 8B, member 2	ATP8B2	AA142939	9.1	1.6	8.4
52750_at			AI632711	1.6	0.4	8.4

40907 at			AA043502	6.4	6.5	83
31970 r at	protein phosphatase, EF hand calcium binding domain 2	PPEF2	AF023456	0.7	9.0	8.3
32480_at		HOXC4	X07495	16.6	2.1	8.3
1783_at	ras association (RaIGDS/AF-6) domain containing protein JC265		M37190	1.7	0.5	8.3
37360_at	lymphocyte antigen 6 complex, locus E	LY6E	U66711	13.4	13.6	8.3
38740_at	butyrate response factor 1 (EGF response factor 1)	BRF1	Z9067X	2.5	0.8	8.3
39230_at	similar to APOBEC1		AL022318	4.4	11.8	8.3
46806_at			R66690	3.8	0.4	8.3
76551_at			A1125848	1.6	1.1	8.3
45486_s_at			AW021213	1.4	8.0	8.3
59347_at			R25153	0	1.5	8.3
67975_at			AA934126	8.0	6:0	8.3
52535_s_at	cyclin-dependent kinase inhibitor 1B (p27, kip1)	CDKNIB	AI680672	9.1	3.9	8.3
51084_at	SUMO-1 activating enzyme subunit 1		AI339364	2.5	1.2	8.3
49943_at			AI681558	11.3	3.8	8.3
44051_at	SMC4 (structural maintenance of chromosomes 4, yeast) like 1	SMC4L1	AI338462	1	1.6	8.3
55361_at			AI821565	4.3	6.5	8.3
56080_at			AI703473	13.1	12.8	8.3
56697_r_at			AI791520	7.1	8.2	8.3
85630_at			AI086384	0	0.3	8.3
1357_at	ubiquitin specific protease 4 (proto oncogene)	USP4	U20657	5.7	3.4	8.3
32859_at	signal transducer and activator of transcription 1, 91kD	STAT1	M97935	3.2	18	8.2
33847_s_at	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	CDKN18	AI304854	6.6	5	8.2
36860_at	KIAA1064 protein		AB028987	1.1	1.2	8.2
77757_f_at			AA806526	3.2	2.3	8.2
42764_at			AI459108	0.1	0.1	8.2
58370_at	hypothetical protein DKFZp761A052		AW003291	0.2	0.4	8.2
87874_at			169727	4.7	4.4	8.2
54990_at	hypothetical protein		AW009586	16.3	9	8.2
53468_at			AI149508	0.2	0.3	8.2
64394_at	cadherin 12, type 2 (N-cadherin 2)	CDH12	AI476284	0.4	9.0	8.2
45074_at			N69656	3.6	2.2	8.2

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48081_at	myristoylated alanine-rich protein kinase C substrate (MARCKS, 180K-1)	MACS	AA131320	18.7	7.3	8.2
53756_f_at			AA709471	11.3	0.7	8.2
88927_at			AA889052	3.8	2.2	8.2
2055_s_at			M34189	2.8	1.5	8
33538_at	myelin gene expression factor 2		H96671	1.1	0.5	8.1
_	WW domain containing oxidoreductase	WWOX	U13395	2.8	1.9	000
1909_at	B-cell CLL/lymphoma 2	BCL2	M14745	12	6.6	8.1
33997_at			AL049449	1.6	0.7	8.1
82887_at			AI760827	0.5	5.7	8.1
81659_at			AI928037	0.3	1.8	8.1
			W56309	6.3	9.2	8.1
	leucine aminopeptidase		AF034175	10.1	15	8.1
63921_at			AI683528	1.4		8
64804_r_at			T40707	6.3	3.1	8.1
73574_at			AI290214	4.8	3.7	8
50365_at			AI760821	1.1	3.5	8
49939_at	KIAA1201 protein		AL042980	2.3	3.4	8.1
52355 g at			AW003924	1.6	3.8	8.1
84963 <u>r</u> at			R42423	4.9	2.9	8.1
36954_at	KIAA0218 gene product		D86972	7.4	39	0
65827_at		STUB1	A1630895	7.2	6.3	8
214_at	msh (Drosophila) homeo box homolog 1 (formerly homeo box 7)	MSX1	M97676	1.2		8
34981_at	potassium voltage gated channel, shaker related subfamily, member 5	KCNA5	M55513	1.8	1.3	8
31418_at	high-mobility group (nonhistone chromosomal) protein 17-like 1	HMG17L1	Z97055	3.4	4.3	8
1826_at		ARHB	M12174	0	0	oc o
32940_at	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis, chromosomal region, gene 1	AMMECR1	AJ007014	8.4	1:1	0
32288 r at	like receptor subfamily C, member 3	KLRC3	AJ001685	9.0	0.5	0
34699_at	protein	CD2AP	AL050105	20.4	12.9	8
259 s at	(in alpha (TNF superfamily, member 1)	LTA	M16441	13.8	2.9	8
34573_at	ephrin-A3	EFNA3	U14187	9.0	0	∞

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41500 24	6 h					
41000 at	iibroblast growth factor 18	FGF18	AA022949	1.6	0	8
3/294_at	B-cell translocation gene 1, anti-proliferative	BTG1	X61123	34.3	15.2	8
37980_at	CBF1 interacting corepressor		U03644	4.1	9.1	8
66332_at			R43566	1.6	1.9	8
79145_at			W72060	12.5	α C	
79520_at			AW022213	18.4	0 00	
63382_at	interferon consensus sequence binding protein 1	ICSBP1	AI073984	53.5	35.7	0
72361_at			A1885066	0	0	OC.
87585_at			AA565209	2.9	1.1	0
61745_r_at			N76044	5.1	2.7	0
44422_r_at			D59337	6	3.3	α
65898_at	potassium channel modulatory factor		AI743396	2.1	-	0
59454_at	serine/threonine kinase 17a (apoptosis-inducing)	STK17A	AI806790	2.1	2.3	ά
63663_at			AA649208	-	C	
80940_f_at			AI147061	0 1	0 0	0
37684_at	solute carrier family 21 (organic anion transporter), member 9	SLC21A9	AB020687	84		
1084_at	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg. Abelson-related gene)	ABL2	M35296	11.3		7.9
32137_at		JAG2	AF029778	90	,	7.0
40496_at	complement component 1, s subcomponent	C1S	104080	26.3	T U	0.7
629 <u>a</u> t	interleukin 9 receptor	IL9R	L39064	0.02		0.7
35328_at			AF055023	6.0		7.0
1885_at	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	ERCC3	M31899	0		7.9
38301_at	adenosine kinase	ADK	1150196	4	-	7
57406_at			AI240813	1.4	2.3	6.7
50546_at			AA761629	2.8	2.4	7.9
42582 at			N22508	1.2	2.3	7.9
44718_at			AA577672	9.9	5.7	7.9
82992 r at			AI565735	1.3	1	7.9
5/00/ at			AA904435	2.3	1.1	7.9
55421_at			AA995447	2.6	1.2	7.9
33023 41			H14337	0	3.5	7.9
89024_at			AI720099	6.0	0.3	7.9

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64543 at			AIGGRES7	2.5	1/0	0 7
45541 s at			AW015697	5 -	1100	0.7
			A12CF 45	7 1	3.0	6.7
40 VCV33			A1350548	7.5	3.2	7.9
55454 at			U55967	1.8	2.3	7.9
51179_at	brefeldin A-inhibited guanine nucleotide exchange protein 2		AI741843	5.1	2.9	7.9
45731_at	HSPC003 protein		AA581878	6.4	9	7 9
57261_f_at	_	RPLP0	AA588862	4.4	4 1	7.0
34502 g at	\neg	RUNX2	L40992	C	0	7 8
39691_at	SH3·containing protein SH3GLB1		AB007960	c	0.7	7.8
40836_s_at	j	MTA1L1	W26677	1		0.7
33243_at	TNF-induced prot		AF099935	19.9	2.5	ν / ν
33295_at	Duffy blood group	FΥ	X85785	0.5	0.0	α / Δ
634 at	protease, serine, 8 (prostasin)	PRSS8	141351	ر ا	0 0	7 0
37551_at	KIAA0211 gene product		D86966	0.5	80	α /
56927_at			W49628	4.3	4 5	ν / ν
77706_at			AA641972	493	50	7 8
39768_at	2',3'-cyclic nucleotide 3' phosphodiesterase	CNP	D13146	23.7	0 6	α / α
63202_at			AI218553	0	280	2 / 2
83013 <u>ı</u> at			AI400387	1.1	0.8	78
60460_at			N95430	1.6	0.8	7.8
86261_at			AA017070	15.5	12.3	78
69/08_at			A1689617	1.6	1.6	7.8
46207_at			A1640326	1.5	0	7
63124_at			AA631399	3.6	1.7	7 8
87419 r at	7		AI679413	2.6	60	7 8
41190_at	tumor necrosis factor receptor superfamily, member 12	TNFRSF12	U83598	0.7		7.7
0.00				•	'	
31510 s at	H3 histone, family	H3F3B	Z48950	3.5	1.3	77
40979_at	- 1	C140RF3	AJ243310	0.4		7.7
39093_s_at	- 1	BRD4	Y12059	32	C	7.7
41592 at	_		AB000734	4 9	2	7.7
40386_r_at	teratocarcinoma-derived growth factor 3, pseudogene	TDGF3	M96956	1.2	0.3	7.7
34002_at	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta- isomerase 2	HSD3B2	M77144	1.6		7.7
38278_at	modulator recognition factor		M62324	5.3	2.9	7.7

cincors.	4	iiuco	11011, 0	

5056/_r_at			AA780080	9.0	1.7	7.7
49458_at			AA921835	4.5	1.1	7.7
47206_at			AA984304	0	2.8	7.7
62857_at			AI784540	1.3	0.4	7.7
71584_at	X-box binding protein 1	XBP1	AA503434	2.5	0	7.7
83201_at			AI984360	1.4	3.2	7.7
82126_at			AA831700	0.8	0.1	7.7
64460_at	M-phase phosphoprotein homolog		AI823360	6.0		7.7
45298_at			N66638	9	2.8	7.7
44808_at			AA455864	2.5	3.9	7.7
87497_f_at			AI832016	27	21.1	7.7
47018_at			AI168404	0	0.8	7.7
56668_at			AI806747	0.4	2.3	7.7
36050_at	Н	ZNF313	AL031685	9.0	0.5	7.6
39041_at	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate	DLAT	Y00978	0	3.7	7.6
	dehydrogenase complex)					
32217_at			AF052105	12.6	6.3	7.6
33754_at	thyroid transcription factor 1	TITF1	U43203	2.3	0.3	7.6
34312_at	nuclear receptor coactivator 2	NCOA2	AI040324	4.5	3	7.6
1562 g at		DUSP8	U27193	2.9	3.7	7.6
36066_at	KIAA0828 protein		AB020635	5.7	2.4	7.6
36103_at	ytokine A3 (homologous to mouse Mip.1a)	SCYA3	D90144	13.1	6.1	7.6
36943_r_at	pleiomorphic adenoma gene-like 1	PLAGL1	U81992	8.1	5.8	7.6
37195_at	cytochrome P450, subfamily XIA (cholesterol side chain cleavage) CYP11A	CYP11A	M14565	2.9	1.1	7.6
40681_at	integrin, beta-like 1 (with EGF-like repeat domains)	ITGBL1	AB008375		0.4	76
47202 at			AA116061	-1	1.2	7.6
53862_at			AA447888	0.1	0.7	7.6
62431_at			AI197909	7.1	7.9	7.6
62866_at			AI274114	1.4	1.8	7.6
55217 i at			AA886955	2.2	0	7.6
81583 <u>f</u> at			AI243475	38.1	2.1	7.6
44920_at			AI914925	12.7	4.8	7.6
43312_at			R10159	2.8	2.6	7.6
68447_at			Ai809257	0	1.4	7.6

52546_at	hypothetical protein FLJ20530		91577744	2.1	2 5	1
50853 at			010001	1.2	6.3	0./
10000			AI299/19	0.8	0.4	7.6
45693 at			H24387	7.5	5	7.6
	erythropoletin	EPO	AF053356	2.8	1.9	7 6
52107 g at	CGI-90 protein		A1800674	5.5	62	7.6
35009_at	low density lipoprotein-related protein 2	LRP2	U33837	1.5		7 7
35386_at	acetylcholinesterase (YT blood group)	ACHE	AI825097	0 0	7.7	7 7
32294 g_at	luteinizing hormone/choriogonadotropin receptor	HCGR	M63108	0 6	3.0	7.5
1338_s_at	cytochrome P450, subfamily IIA (phenobarbital inducible),	CYP2A6	X13930	13		1,5
)	1 .	?
32353_at	ma (Fletcher factor) 1	KLKB1	M13143	1.5	0	7 5
37162_at	ment, single copy, probe pH4 (transforming sequence,	D10S170	872869	1.4	12	7.5
	thyroid·1,			<u> </u>	1	?
1317_at	hage stimulating 1 receptor (c-met-related tyrosine	MST1R	X70040	0.8	2	7.5
	kinase)) :	<u> </u>	?
38735_at	KIAA0513 gene product		AB011085	0.3	1.5	7 5
35638_at	or, runt domain, alpha subunit 2; translocated	CBFA2T1	D43638	2.4	0	7.5
.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	D-related					
40344 at		NLGN1	AB028993	1.3	2.3	7.5
37535 at	element binding protein 1	CREB1	M27691	1.3	19	75
38436_at	KIAA0252 protein		D87440	0.2	2 8 6	7.5
38485_at	drogenase (ubiquinone) 1, subcomplex unknown, 1	NDUFC1	AA760866			5 7
		•		J.	<u>.</u>	0.7
38772_at		CYR61	Y11307	0.4		7.5
38319_at	CD3D antigen, delta polypeptide (TiT3 complex)	CD3D	AA919102	9.0	0.4	7.5
66366_at			AI695056	0	9.0	7.5
/3/03_at			AA777616	7	4.7	7.5
51193 at			R14888	2	2	7.5
82251_at			AI819034	0.5	0.7	7.5
44833 s at	heat shock 70kD protein 8	HSPA8	AI986374	2.2	2.1	7.5
48210 r at			AA251543	5.1	5.9	7.5
72200 c			AI041279	3.2	2	7.5
72092 T at			AA677864	4.9	3.4	7.5
40052 dt			AA063037	2.1	3.3	7.5
42007_at			AA210684	1.9	3.1	7.5

			W/X740		4.0	<u>.</u>
3/101 at			3038358	0.3	0.5	7.5
72546 at			AI033943	1.3	1.4	7.5
40074_at	methylene tetrahydrofolate dehydrogenase (NAD+ dependent).	MTHFD2	X16396	0	0	7.5
1785 at	retinoblastoma-binding protein 2	RBBP2	S66431	5.9	2.4	7.5
1/65 at			A1982669	3.1	6.8	7.5
"\~	KIAA0461 protein		AB007930	3.1	3.3	7.4
30050 at	KIAA0610 protein		AB011182	2.2	5.1	7.4
40053 at	KIAA0573 protein		AB011145	0.1	3.1	7.4
38187 at	N.acetyltransferase 1 (arylamine N-acetyltransferase)	NAT1	D90041	0.5	0.5	7.4
	۾ ڇار	HLAE	X56841	2.6	2.5	7.4
31524 f at	v. member K	HZBFK	280782	4.5	1.4	7.4
33879 at	2		U79528	3	0	7.4
33454 at			AF016903	2.2	3.1	7.4
3/333 at	KIAADO63 gene product		AL021707	2.3	1	7.4
32530_at		YWHAQ	X56468	4.8	2.9	4.7
26176 24	activation protein, titera polypopituo	TBCC	U61234	2.6	3.8	7.4
37681 at	matrin 3	MATR3	AB018266	1.4	0.3	7.4
71107 at	syntanhilin		AB002372	0.8	0	7.4
10 0000	Charot. Levden crystal protein	CIC	L01664	0	1.7	7.4
50009 at	~		AI273692	8	3.3	7.4
18738 at			AA421131	3.9	1.1	7.4
67068 at			AI298437	0.3	2.4	7.4
49312 at	ICGI-102 protein		AA747303	4.4	3.2	7.4
51474 at			AA127641	58.7	2.4	7.7
44306 at			AA707318	3.8	e	7.6
69439 at	hynothetical protein MGC5356	İ	AI655792	7.9	4.2	7.7
88792 at			AI681436	0.4	1.8	7.4
71483 at			AI937154	0.1	0.8	7.4
74482 at			AW025586	1.2	8.3	7.4
43738 at			AA565834	3.6	2.9	7.4
50228 at	Themoglohin gamma (3	HBG2	AA992592	0	4.3	7.4
30250 01			41016311	2	4 2	,,

	CGI-34 protein		AW016801	1 7		
at at fat at at at at at at at at at at at at a	בויסו לו סומון		100010		5	7 2
at at fat at at at at at at at at at at at at a			AA528059	12.9	101	1/
at at at at			N48679	0.6	17	1.7
at fat at at fat			N21600	0.4	1.4	
at fat at at	ribosornal protein 520	RPS20	AA479427	62	100	1.7
f at at at f at			AA394228	46	1 6	1.7
			W37770	0.71		7 7
$\overline{}$	TTI protoin		H60827	2		7.4
\neg			AL041780	5.9	2.9	7 4
	apolipoprofein 3		AI879381	6.9	6.9	7.4
1	Chart accordated sector	APOL3		10	17.1	7.3
7 -	kinesin heavy chain member 2	SFIPC	J03553	2.2	2	7.3
	1 like demonstrate	KIF2	Y08319	13.3	24.6	7.3
Τ	mannosidase alpha class 14 momber 2	EDIL3	U70312	2.3	0.2	7.3
T		MAN1A2	AF027156	2.3	0	7.3
	ocuri, garactostue birturig, soluble, 3 binding protein (galectin 6 binding protein)	LGALS3BP	L13210	10.5	19.8	7.3
37587_at rec	recoverin	PCV1	1,000			
7996_s_at dy	37996_s_at dystrophia myotonica-protein kinase	TANK T	343833	1.1	1.1	7.3
2021 s at cv		DISTRA	L08835	0	0	7.3
8 at		CCNET	M73812	0.4	0	7.3
	Deptidylprolyl isomerase A Cyclophilip A)		AA706942	2.2	2.8	7.3
		PPIA	A1952127		1.6	7.3
86833 r at			R01845	2.2	0.4	7.3
1	DNA segment, single conv. probe pH4 (transforming segment)	0110	H68862	4.7	3.1	7.3
	thyroid-1,	0/1801/0	H15313	0	0	7.3
	protein 1, alpha	HSPCA	100001			
at	ubiquitin A-52 residue ribosomal protein fusion product 1	10000	AA133001	3./	2	7.3
51842 at		2000	AI802408	0	9.0	7.3
49837 at			AI570531	15	2.9	7.3
67827 f at			AI209180	3.4	2	7.3
\top	Orotein phosphatase 10 magazine algebra		AA525067	1.4	0.2	7.3
	The state of the s	PPM1D	U78305	1.1	0.1	7.2
31985_at			AL049228	43	7.0	7.0

Figure 13NN

34931 21	KIAA0940 protein		145003157			r
10000			AB02315/	0.8	0.9	7.7
39920_r_at	CIQ-related factor		AF095154	1.8	0.1	7.2
317_at	protease, cysteine, 1 (legumain)	PRSC1	969550	2.5	8.6	7.2
32779 s at	inositol 1,4,5-triphosphate receptor, type 1	ITPRI	U23850	2.2	2.1	7.2
40428 i_at			AW043812	0	0.3	7.2
1065_at	nase 3	FLT3	U02687	2.2	1.8	7.2
32628_at	zinc finger protein 161	ZNF161	D28118	3.7	3.5	7.2
1953_at	vascular endothelial growth factor	VEGF	AF024710	28.4	6.2	7.2
1106_s_at	alpha locus	TRA@	M12959	6.0	1.2	7.2
37994_at	fragile X mental retardation 1	FMR1	X69962	1.00	CI	7.2
63350_at	hypothetical protein FLJ20707		N66569	1.7	0.4	7.2
81276_at			N63894	3.5	5.5	7.2
81726 at			AI885498	15.1	10.7	7.2
77922_at			AA884304	17.6	0.5	7.2
50868_at			AW021051	1.2	11.4	7.2
43524_at	KIAA1170 protein		C14031	42.1	18.4	7.2
82383_r_at			AI215733	0.5	0	7.2
44000_at			AA534378	2.8	2.8	7.2
63142_at	hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit		C16964	0.4		7.2
50146_at			AI819320	1.9	3.1	7.2
44567_at			A1992275	1.4	0	7.2
51024_at			AI400509	13.3	17.3	7.2
45220_at			AA150501	9.0	2.2	7.2
45608_at			AI202327	11.7	4.7	7.2
84373_at	fragile X mental retardation, autosomal homolog 2	FXR2	AI703341	2.2	1.1	7.2
47844_at			AA131302	1.7	2.5	7.2
58848_at	d protein kinase kinase 2	MAP2K2	AI809489	2.8	8,5	7.2
64267 f at	lated protein interacting protein (duo)	HAPIP	AI962617	9.0	2.7	7.2
47113_at)	KLF5	AI815057	31.5	41.2	7.2
	hypothetical protein FLJ20279		AA039793	0	m	7.2
9			AI201082	1.9	0.2	7.2
1280 at			225424	0.1	0	7.2
193/ at			M26460	0.8	0	7.2
60690 at			AA203328	4.2	4.4	7.2
					i	

40 TXT 7			A1086392	ľ	6 3	-
1000	ωį	ADCY7	025538	7.0	0.5	1
32854_at	_		ABO1 4506	2.7	3.1	,
45509_g_at			H45672	2.4	2.5	7.7
39422_at	KIAA0477 gene product		CCO50004	0		
1252_at	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis		M73547	23.8	0.7	7.1
37925 r at	apolipoprotein M		A 1205030	C		
33922 at	_	PRDM2	1117838		Σ. σ	
3/429 g at	netrin G1		A1140857	2 6	0 0	, ,
33492 at			AI624840	4 7	φ.	, ,
36535 at	mirrofibrillor	ADM	D14874	27.2	0.00	7
844 at	profein phoenhateed 1 200 letter 1	MFAP1	U04209	5.8	5.1	7
408 at	GRO1 propaga (malanament)	PPP1R1A	U48707	9.0	0.5	7
15-00	Cross of Constant of Standard activity, alpha)	GR01	X54489	486.7	11.5	7.1
39476_at			249995	00	9	ľ
20334_at	basic transcription factor 3	BTF3	AI798775		10.0	7 1
62375 at			AI792267	3.1	0.3	7
53959 at			AI521162	1.4	9.0	7 1
81541 at	natiliral killer cell recentor 284		AW009031	1	1.1	7.1
	.1:7		AI871467	2.3	3.8	7.1
54857_at	ancient conserved domain protein 4		AA534572	3.1	1.6	7.1
43281_at			AI636759	9.6	8	7.1
			AA481181	3.5	5.5	7.1
44265_at			AA460146	0.7	1.1	7.1
53439 at			H10709	1.9	3.9	7.1
54166 at			R97957	4.3	2.7	7.1
41985 at			AI082750	4.3	1.9	7.1
48940 at			AA143802	2.6	1.6	7.1
53155 at			AA773807	0	4.3	7.1
41641 at	GPI.anchored metactacic acconiated protoin bomola		AA608559	5.7	4.4	7.1
40264 p at			AJ223603	1.6	0	7
	T 2V1					

Figure 13PP

mivelitors.	

40109_at	serum response factor (c-fos serum response element-binding	SRF	103161	0	1.7	2
	transcription factor)					
1478_at	IL2 inducible T cell kinase	ITK	L10717	9.7	4	7
34776_at	Cdc42 effector protein 4; binder of Rho GTPases 4		W27541	8.6	0	7
36116_at	thyroid hormone receptor interactor 10	TRIP10	AJ000414	215.9	56.7	7
1052_s_at	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	M83667	15.2	3	7
38127_at	syndecan 1	SDC1	248199	0.1	0.1	7
			AI791208	41.5	10.4	7
50855_at			AA789332	0	8.4	7
59187_at			AA970451	1.6	1.9	7
60417_r_at			AI081821	5.7	3.3	7
75201_f_at			A1688900	5.5	11	7
77231_at			AI761622	4	3.1	7
59299_at			Н98190	3.3	3.3	7
91636_at			AI652725	886.7	27.7	7
83074_at			AI817967	2.3	6.0	7
62624_at			AL043110	ō		7
86090_at			T69814	3.3	1.9	7
68084_at			AI916367	2.7	1.1	7
59627_at	hypothetical protein FLJ10628		AA885169	2	5.5	7
70209_at			AI761629	6.4	1.3	7
49600_at			AI936984	3.5	3.9	7
49485_at	PR domain containing 4	PRDM4	W22625	3.5	1.7	7
42867_at			AI701798	2.4	2.3	7
64174_at			AI127460	11	8.6	7
83561_at			W26087	8.2	2.8	7
56273_at	hypothetical protein FLJ20514		AA534400	m	0	7
72462_f_at			H40456	1.4	0.4	7
78727_at			AA425815	0	0	7
38712_at	membrane protein CH1		AL035291	6.7	6.1	6.9
34966_at	T brachyury (mouse) homolog	1	AJ001699	1.1	0	6.9
32755_at	actin, alpha 2, smooth muscle, aorta	ACTA2	X13839	3	4.3	6.9
34175_r_at			AL049242	9.0	0	6.9
678_at	lalkaline phosphatase, placental (Regan isozyme)	ALPP	104948	3.4	1.1	6.9
32429 f at	zinc finger protein 33b (KOX 31)	ZNF33B	D11958	0	1.4	6.9

 	- Auconion,	

30/02 at	61 x00-1	TBX19	AJ010277	α		2
35359_at	KIAA0235 protein		D87078	0 0		6.9
36888 at			AB020648		100	37.0
37664 at	developmentally regulated GTP-binding protein 2	DRG2	X80754	7.5	0.0	9.0
38814_at	ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J	АТР6Ј	AF038954	1.6	4.1	6.9
48025_at	NCK adaptor protein 2	NCKO	0.00			
46778 at		20081	AI934552	51.7	5.9	6.9
47818 at			AA129377	2.4	3.8	9.9
57619 at	hypothetical protein 61 110076		A/968249	2.4	4.9	6.9
58549 at	5		W63595	2.5	0.1	6.9
59341 at			190987	0	2	6.9
85019 at			AI311917	5.4	2.4	6.9
49339 s at	reticulocalbin 1		F02458	4.2	3	6.9
67857 at	teredecapitat, Littliana calcium binding domain	RCN1	AI817760	29.7	11.9	6.9
57101 at			AA425402	0.2	0.3	6.9
46697 at	protein kinase AMD activition of any or any		AI242202	0.3	1.2	6.9
44763 at	Process will sectivated, Barnina 2 non-catalytic subunit	PRKAG2	AA115330	1.3	7.5	6.9
80665 r at			AA280886	9.3	3.8	6.9
47287 at			AI963771	2.1	1.9	6.9
62582 at			AI475473	53.5	2.5	6.9
53334 at			AI821408	4.1	2	6.9
64490 at	CGL141 protein		H12612	3.3	1.1	6.9
54060 at			A1692654	1.9	2.3	6.9
47159 at			AI523569	2.7	3.5	6.9
56683 i at			AL119027	1.8	8.0	6.9
61180 f at			AA639553	1.6	2.3	6.9
89276 at			AA024934	0.7	0	6.9
46727 at			AI810946	2.4	0.2	6.9
46093 at	hypothetical protein El 120173		AI146850	3.8	3.1	6.9
46218 at	Violation Violation		AA513748	5.3	3.2	6.9
32125 at			W22908	2.6	1.3	6.9
176 at	profession photospates 2 manustration in the interest		AA928996	e	3.8	8.9
5-0	isoform	PPP2R5C	U37352	0	0	6.8
33700_at	sprouty (Drosophila) homolog 2	CDDAD	AF020042			

33881_at fal 35568_at ad 32529_at tra 36949_at ca 3736_at pra 3736_at pra 58284_at Ki. 50807_at 76062_at 50807_at	N 2 a 5					
t t	ylate cyclas membrane nediate co	FACI 3	44977580	0		
at		ADCYAP1R1	D17516		2.1	8 9
t			X69910	21.7	23.9	6.8
t	casein kinase 1, deita	CSNK1D	1170171			
t	protein-Lisoaspartate (Diaspartate) Oimethyltransferase	PCMT1	0431/1	0 0	0.7	6.8
ŧ	KIAA0304 gene product		0.1007041	0.0	2 -	6.8
ω[] ω			AA9474E9	2.7	1.7	6.8
] a			AA128061	1.7	2.1.0	8.9
			AAO20898	0.0	1.7	8.9
			R94508		7.7	0.0
\dashv	T-cell lymphoma invasion and metastasis 2	TIAM2	AI126294	416	25.5	0.0
20229_s_at			AI361218		2.9	8 9
76700 at			AI091533	1.6	2.7	89
55030 at			AI221251	1	1.9	8.9
59357 at			AA233120	6.1	7.4	6.8
			AI433468	0	0	6.8
58473 at			H09073	3.2	2.9	6.8
48085 at			AA020010	1.2	2.7	6.8
49645 r at			T99531	0	2	6.8
46673 at			N66472	4.9	4.3	6.8
44884 at			H18113	0	1.4	6.8
61409 at			AA039908	4.1	7.3	6.8
78387 at			AA442889	4.4	2.3	6.8
Γ	dynein axonemal light polypeptide 4		AI244/57	9	3.9	6.8
, t		UNAL4	AL008583	4.2	-1	6.8
T			AA206524	4.8	2.3	9
j ;	٦		A1189200	9.9	2	6.8
	or symmase (phosphatidate cytidylyltransferase)	CDS1	060808	0.1	8.9	6.7
Ī	n homologous to Zfp.36 in mouse	ZFP36	M92843	4.9	0.5	6.7
40000 at IDN	UnaJ (HSp40) homolog, subfamily C, member 4	DNAJC4	AW024467		0.5	6.7

Figure 13SS

34295_at	ubiquitin specific protease 15	115915	AB011101	100	- 1	1
36600_at	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	PSME1	L07633	15.9	19.1	6.7
37230_at	KIAA0469 gene product	KIDANAGO	86070004			
37368 at	• •	00t0CHV14	AD00/930	13.3	1.2	6.7
	dependent 4	NFA C4	AA292277	3.6	F	6.7
38091_at	lectin, galactoside binding, soluble, 9 (galectin 9)	1 GAI S9	749107	3.0	7 7	
37941_at	myosin-binding protein C, fast-type	MYBPC2	X73113	3 4	, ,	0.7
38254_at	KIAA0882 protein		ABOSOGO		J. 0	0.7
66311_r_at			AB020009	-	x 0	6.7
66515_at			AA707328	0.0	1.0	6.7
58890_at			T89102	8	7	7.0
49388 at	chromosome 8 open reading frame 2	C80RF2	W23473		5 6	7.0
5/6/2 at			AI743880	0	0	6.7
91032_at			AI791640	0.3	ic	7.7
80124 at			AA643238	0.6	0	6.7
86332 at			AI523641		0.1	6.7
22931 at			AI819394	9.0	6	6.7
ျ			AI990273	2.7	88	6.7
49291_r_at	hypothetical protein FLJ23445		N30264	9.0	2.5	6.7
51496 at			R63923	2.6	1	6.7
45948 r at			R98767	4.6	4 1	6.7
53540 at			AI168683	4.8	3.7	6.7
31033 at			AI122787	3.8	4.8	6.7
45001 41			N90348	4.5	5.5	6.7
65715 at			AW001342	4.8	2.5	6.7
13770 at	inclear receptor coactivator I	NCOA1	AL079440	2.5	5	6.7
31680 at			AA082768	0.5	0.2	6.7
			M55630	14.3	5.5	6.7
53083 24			AA534354	0	0.8	6.7
33134 at	١,		3147616	3.1	0	6.7
15578 5 24	aueliyiate cyclase 3	ADCY3	AB011083	5.8	0	6.7
20061 24			N26243	5.5	1.8	6.7
33001 at	Joone marrow stromal cell antigen 2	BST2	D28137	5.5	9.7	9.9

Figure 13TT

, , , , , , , , , , , , , , , , , , , ,	 	,	

		AGXT	X53414	2.3	1.2	9.9
37883_i_at	hypothetical pro		A1375033	ř	2	0 3
31508_at	upregulated by 1,25-dihydroxyvitamin D-3		\$73591	0	0.10	0.0
1044 s_at	E2F transcription factor 5, p130-binding	E2F5	U31556	233	0.4	9.0
33872_at			AB018329		0	9.9
37240_at	histidyl tRNA synthetase like	HARSL	U18937	25	000	9 9
793_at	placental growth factor, vascular endothelial growth factor related protein	PGF	X54936		2.9	9.9
40299_at	G-protein coupled receptor		AF091890	0		
35335_at	Rho associated, coiled coil containing protein kinase 2	ROCK2	AB014519	3 - 7	5.0	0.0
35219_at			AI 050202	α ς	7.70	0.0
36899_at	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	SATB1	M97287	 6.4	8.4	9.9
36573_at	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	DDXBP1	U78524	3.7	α	
1217 g at	protein kinase C, beta 1	PRKCB1	X07109	6.5	0 4	0.0
1779_s_at		PIM1	M16750	23	0 0	0.0
40691_at	zinc finger protein 274	ZNF274	U71598	2	5 0	0.0
34060 g at	_		AA586695	0 00	? -	9.0
38805 at	(G-interacting factor (TALE family homeobox)	TGIF	X89750	6.2	4.4	6.6
50713 at			H73401	5.8	4.1	9 9
60685_at			AA292534	т	1.9	9'9
51300 of			AA621958	0.7	2.9	9 9
75652 at			AI392609	1.9	1.6	9'9
73032 at			AI983437	24.3	2.9	9.9
02061 24			AI378639	0.5	0	9.9
502901 at			AI286142	1.1	2.6	99
30100 at			AA548518	1.2	0	99
69128_at	Utype (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9	CLECSF9	AI968491	7.5	4.9	6.6
50352_at			AA151706		20	
61328_at	C-terminal binding protein 1	CTBP1	A1970615	000		0.0
87416_r_at			T91504		0 9	9.0
48098_at	glucose regulated protein, 58kD	GRP58	AA478520	2.6	0 0	0.0
84995 at			44760400	11.		0.0

040/2-41			AI339915	0	0.6	99
48573_at	zinc finger protein 161	ZNF161	AA452188	3	1.5	9.9
44972 at			AA999894	18.1	2.5	9.9
55673_at	RAB-8b protein		AI807023	16	13.1	9.9
48960_at			AI191934	1.4	1.5	9.9
63037 s_at			AI653002	2.4	1.1	9.9
46454 at			AA401446	0.1	0.4	9.9
49843_at			AI082569	2.2	3.3	9.9
59805_f_at			A1636743	98.2	2.6	9.9
51938_at			N33202	4.0	0	9.9
44110_at			AI762752	2.9	9.9	9.9
44127 at			AA604375	4.3	2.8	9.9
31559_at	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	SLC13A2	U26209	8.0	0	6.5
40082_at	fatty-acid-Coenzyme A ligase, long-chain 2	FACL2	D10040	16.9	11.5	6.5
118_at	prostaglandin E receptor 4 (subtype EP4)	PTGER4	L28175	2.7	1.2	6.5
34237_at	HBS1 (S. cerevisiae) like	HBS1L	AB028961	6:0	9.0	6.5
38660_at	cytochrome c oxidase subunit VIa polypeptide 2	COX6A2	F27891	0.4	1.3	6.5
34708_at	ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen)	FCN3	D88587	0.7	9.0	6.5
37218_at	BTG family, member 3	BTG3	D64110	9.7	8.7	6.5
40698_at	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	CLEUSF2	X96719	0.3	8.4	6.5
38326_at			M69199	64.6	20.8	6.5
58024_at			N32301	0	1.2	6.5
82892_at	hypothetical protein FLJ12567		AA192481	2.9	2.3	6.5
56894_at	RAB38, member RAS oncogene family	RAB38	N29070	2.6		6.5
56930_at	integrin beta 1 binding protein (melusin) 2	ITGB1BP2	AI568769	1.1	1.1	6.5
56991 at			AI927199	4.7	1.2	6.5
42486 at			AI004422	3.4	4.1	6.5
66819_at			AA984073	3.4	1.6	6.5
67223 at			AI003757	6.9	7.8	6.5
51643_at			AL036254	6.9	3.9	6.5
49903 at	KIAA1404 protein		W72798	7.5	3.2	6.5
89178_at			AI741934	0	7.2	6.5

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60815_at			AA601208	0.4	1.2	6.5
65544 at	hypothetical protein FLJ12799		AA524503	1.2	2.5	6.5
71661_at			A1174651	9.1	5.4	6.5
59273_at	hypothetical protein FLJ11729		AI681511	2.3	2.4	6.5
46767_f_at			N95476	1.4	3.2	6.5
50083_at			A1669535	0	2.2	6.5
43190_at	mel transforming oncogene (derived from cell line NK14) RAB8 M homolog	MEL	AA211355	8.0	1.1	6.5
55342_at			AA010697	1.1	4.7	6.5
55873_at			AI674683	0.1	E. T	6.5
54077_at	hypothetical protein FLJ10430		W18181	14.2	6.0	6.5
57543_at	bromodomain adjacent to zinc finger domain, 1A	BAZ1A	AA112166	8.3	6.2	6.5
42109 at			AA435715	1.5	4.3	6.5
55540_at			A1806973	2.8	1.2	6.5
42245_r_at			AA461492	1.6	2.2	6.5
55542_at			AI735416	0	0.2	6.5
60022_f_at			AA584560	2.2	0.7	6.5
52341_at			3052895	0.5	1.3	6.5
75000_at			AI735440	25.9	12.1	6.5
7657_f_at			A1371706	0.2	0.4	6.5
37037_at	procollagen proline, 2-oxoglutarate 4-dioxygenase (proline 4-	Р4НА1	M24486	2.1		6.5
	hypothetical protein DKFZp761H221		AI547243	4.6	3.7	6.5
ţ	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH- NDUFS8 coenzyme Q reductase)	NDUFS8	AW021179	6.4	5.3	6.5
1373_at	transcription factor 3 (E2A immunoglobulin enhancer binding Tractors E12/E47)	TCF3	M31523	0	0.3	6.4
32474_at	paired box gene 7	PAX7	X96744	2.8	0.0	6.4
39415_at	heterogeneous nuclear ribonucleoprotein K	HNRPK	X72727	1.7	0.3	6.4
1756_at			AL049328	2.6	0.5	6.4
36347_f_at	H2B histone family, member D	H2BFD	AA873858	4.4	1.4	6.4
32681_at	/hydrogen exchanger), isoform 1 sensitive)	SLC9A1	568616	0	6.0	6.4
40576 f at		HNRPDL	D89678	0	0	6.4
31628_at	solute carrier family 15 (oligopeptide transporter), member 1	SLC15A1	AB001328	1.5	0.4	6.4

I.

33886_at	spectrin SH3 domain binding protein 1	SSH3BP1	AF006516	124	77	6.1
32776_at	vral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	RALB	M35416	11.3		6.4
41288_at	matrix Gla protein	MGP	AI 036744	1		
35223 at	alpha integrin binding protein 63		VECCOO 4	7.7	0.1	0.4
36008 at	protein tyrosine phosphatase type IVA member 3	CANDIO	AB023234	1 0		6.4
41584 at		1 17 4A3	AF041434	/:/	2.4	6.4
40041 at	highly expressed in capacity rich in language Language	NUDIS	AF062529	4.4	6.0	6.4
1100	and the state of t		AF017790	0	6.0	6.4
27071	nuclear receptor subtarnity 3, group C, member 1	NR3C1	M10901	Ŕ	1.1	6.4
3/9/1_at	promodomain adjacent to zinc finger domain, 1A	BAZ1A	AL050089	6.7	6.9	6.4
156.5 at	G protein-coupled receptor 19	GPR19	U64871	1.9	1.2	6.4
56192_at			H15097		-	27
64/33_r_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9	SERPINB9	AA156247	26	12	6.4
48078 at			140.40.41			
59967 at			W04245	0	0	6.4
59975 24			R37678	1.3	0	6.4
70742 at			AI808778	3.6	2	6.4
10/42 at	•		AI939581	3.4	1.2	6.4
י [ס:	lung type-i cell membrane-associated glycoprotein		AA149854	5.2	3.5	6.4
			AA470798	4.2	3.7	6.4
9050E at			AI024309	6.0	1.8	6.4
60000 at			AI289185	2.9	3.5	6.4
2303/ - at			AI220443	4.1	5.4	6.4
67401 at			AI807856	2.4	3.1	6.4
44734 at			A1434675	16.7	16.1	6.4
67470 at			R60867	8.2	1.2	6.4
88016 24			AI928355	7.8	4.5	6.4
80301 at	المان مانا مانا مانا مانا مانا مانا مانا		AI703450	0	0	6.4
74500 at	אווובאוויוועפ ל	KNSL2	AI953141	4.1	3.8	6.4
74300 at			AW015038	0.4	1.4	6.4
43965 at	That cyloloxic granule-associated KINA-binding protein	TIA1	AL046419	1.3	1.7	6.4
42303 at			AA115111	1.2	1.7	6.4
68369 at			T91110	2.6	2.5	6.4
บบบบบ การการ			T89659	1.5	-1	6.4
9022/_r_at			AI057455	۲.	90	6.0

Figure 13XX

46371_at	hypothetical protein FLJ10895		N36090	1.2	6.4	6.4
/01/3_at			AI808579	2.5		6.4
	hypothetical protein MGC5306		W93232		4 8	6.4
٠٠,۱ ٠			AI422758		0	6.4
52052_t_at			H98105	16.3	22.9	6.4
46845 at			A1027546	0.5	3.1	6.4
23000 at			AA114900	9.9	3.8	6.4
42313 at	ATF	ATP1B3	AA151771	8.1	4.7	6.4
40332 at			AA435933	4.4	4.2	6.4
44301 r at			AI096866	8.9	9.6	6.4
5/190 Lat			AI802804	1.6	9.0	6.4
72406 + 2+			2945576	5.2	2.2	6.4
11020 1 01			AA552962	1	0.4	6.4
41030 at	NIAAU494 gene product		AB007963	6	5.6	6.4
35769 at			AB028965	9	9	6.4
39163_at	likely nomolog of rat kinase D-interacting substance of 220 kDa; KiAA1250 protein		W27233	5.4	0.2	6.4
48860_at	CGI-99 protein		A1342336	7 7	7.0	
59721_at	clone FLB4739		A1973147	, r	7.0	4.0
51002_s_at 	cargo selection protein (mannose 6 phosphate receptor binding protein)		AI380317	2.2	1.2	6.4
52261_at			1005014	-		
	alutaminase		A19/0054	5.6	4.7	6.4
50244 at	inding protein 2 (F coli Min) like)	200	AI982852	0	2.2	6.4
44657 at	ב לביכסון אוווים וואפן	NUBRZ	AA552351	4.8	5.6	6.4
37097 at	Solute carrier family 17 (sodium phosphote)		A1970788	1.2	0.9	6.4
37114 at	crintion factor 1	SLC1/A1	D28532	1.1	0	6.3
34740 at	A.	AIBF1	L32832	6.1	1.1	6.3
39777 at		XO3A	AF032886	6.6	3.5	6.3
41183 at	tion factor 2' and DNA and the training		AF075587	0.4	4.8	6.3
33399 at	ribosomal protein S6	CSTF3	U15782	5.9	4.6	6.3
39124 r at	or notential channel 1	RPS6	AA142942	0	1.1	6.3
39609 21	rocophila) homolog 2	(FCI	99068X	0.3	1.7	6.3
20040 24		M2	U80457	0.4	0.2	6.3
32240 at			AL080094	6.0	0	6.3

Figure 13YY

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18 - O	CUSS antigen (activated B lymphocytes, immunoglobulin (CI superfamily)	CD83	Z11697	10.7	8.3	6.3
1461_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells NFKB!A inhibitor, alpha	IFKBIA	M69043	17	4.9	6.3
51831_s_at			AM/001505	,	(
54914_at			00000000	<u>1</u> C	3.9	6.3
56401 at	zinc finger protein 22 (KOX 15)	ZNEGO	A1740930	C.0	Υ)	6.3
56895 at	ein Fl. 112455	141.22	A1951311	χ.	4.7	6.3
47443 at			AI3/9622	9.0	3.1	6.3
47448 at			AI268054	0.5	0.8	6.3
66749 at			R37637	3.9	0.3	6.3
52068 24			AA970080	1.5	2.2	6.3
55100 at			AI221328	æ	2.1	6.9
33178 at			AI138596	2.4	1.8	6.3
03270 at			AI590337	2.3	1.3	9
02370 at			T54678	8.3	3.3	6.3
20005 4 24			T65381	1.6	0	63
18 1 GOOD			AI817150	-	0.3	6.3
0007 5_41	inconin (conagenzilorinogen domain containing) 3 (Hakata FC antigen)	FCN3	AI652910	3.8	4.7	6.3
63817_at	DKFZP434B203 protein		V 000000 V V		ì	
52634_at			AMOSESSE	0.4	7.0	6.3
45478_at			AW020390	7	2.6	6.3
43931 at	hypothetical protein FI 111269		AW009224	2.5	2.5	6.3
65839 at	PC3.96 protein		AI / 4 1 5 2 4	4.4	1.9	6.3
50122 at			AW022836	3.7	4.4	6.3
59076 at			W87467	3.1	3.7	6.3
46869 at			AI701486	0.2	1.3	6.3
74680 r at	FI N29 gans product		T03685	9.9	1.1	6.3
	ביילה שמים לה מחתרו		AW002527	4.7	7	6.3
46678 at			R42863	1.2	2.7	6.3
51949 at			AI734922	1.7	4.5	6,3
46706 at			AI982758	2.9	3.7	6.3
70198 4 24			AA149518	6.0	4.4	6.3
82253 1 24			AI821980	1.2	0.3	6.3
22233 1 dt			AA663583	1.3	0	6.3
86/60_r at			AI096457	0	0.5	6.3

			A1985333	3.6	-	9
ar	transforming growth factor, beta-induced, 68kD	TGFBI	M77349	200	3 0	0
	uncoupling protein 2 (mitochondrial, proton carrier)	11000	1104502	1 0	0.0	0.3
33777_at t	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)		D34625	6.6	6.5	6.3
at	apoptosis associated speck-like protein containing a CABD		2 4 4			
			A1148558	5.7	5.1	6.3
	poly(rC)-binding protein 3	0000	AI9/2498	6.2	5.5	6.3
39695 at	d factor for complement (Open o	FCBF3	AL046394	2	0.3	6.2
	poola	DAF	M31516	9.9	1.1	6.2
32106_at s	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitryosin), member 4	SERPINA4	128101	0.5	0.5	6.2
		0000				
2039 s at F	ne related to SRC FGR YES	141.09B	042391	1	0.7	6.2
Γ		7. L	M14333	0	1.6	6.2
1		KPNB1	L38951	0	0	6.7
Τ	tigen) I	FOLH1	M99487	2	9.0	6.2
Γ	creative production of subject of the most of the property	DNAJB6	AI540318	5.4	6.0	9
33175 at			AL049378	1.8	0	6.2
			AA156237	6.0	0	6.2
‡	Brace (arminopeptingse (arminopeptingse A)	ENPEP	L12468	2.2	0.5	2,9
7			AI655458	1.9	0.3	9
T	ment protein, gamma	NAPG	U78107	3.4	-	
T	nember 4	IGSF4	AL080181	0.5	0	6.0
Τ	Carried and a Ca	CTSK	X82153	3.2	0	9
55729 at			AA576941	8.8	2.7	6.9
63623 at			AA476783	1.1	1.3	6.2
	Ornithine decarboxylase antimics 1		AI694297	7.7	0	62
	-	OAZ1	D78361	2.8	1.9	9
1	complement component 5		AA926703	3.6	6.0	62
7	Chient	C5	T71645	0.2	0.1	9
46943 at			AA622412	9.0	0.0	6.0
62008 at			AI733124	1.5	0.5	6.2
18061 24			AI935871	0.8	0.0	200
40207			N58188	6.0	0.5	6.2
1000						

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Figure 13AAA

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74033 at turnor necrosis factor, alpha-induced protein 2	TNFAIP2	A1986430	53.5	15.5	9
4227U at		W24320	4.7	1.5	9
		AA827798	8.	2.4	9
76067_at DNA fragmentation factor, 45 kD, alpha polypeptide	DFFA	AI671302	1.7		9
550iO g at		AA451732	0.5	0.2	9
81955 at		H19232		6.0	9
01830_at		AI634650	0.2	0	6.1
3/031_dl		AA167704	10.2	9.4	9
90557_at		AA195804	4.3	6.0	6.1
91434_at		AI221300	6.0	1.2	9
04151_dt		AI808593	0	6.0	9
4,2023 at		AA020957	2.2	3.8	9
00091_at		AI989354	5.3	5.6	9
1 2 2 1 2 2		AI921708	2.4	1.5	9
43104 Lat Collagell, type I, alpha 2	COL1A2	AI610692	2.8	9.0	6.1
54020 34		AA147881	0	1.6	9
30333 at		AA399009	2.9	2.6	9
00000 at		AI973024	1.6	e	9
23001 4		AF150371	1.2		
4		AA195855	0.4	1.6	9
44320_at hypotitetical protein MigC348/		AA905113	4.4	2	9
44502 at		AA417797	4.7	3.8	9
04302 <u>a</u> 1		R42005	1	1.2	9
70000 at 58077 at		H03627	9.0	1.6	9
80613 at		R77480	1.6	9.0	9
53498 at		AI221511	1.4	2.6	9
60571 at		AA464480	9.6	7	6.1
		AI307109	7	2.3	9
38747 at CD34 antigen		AI653240	1.5	2	9
T	CD34	M81945	0.7	0.2	9
55759 at R7.H1 protein		AI652861	0	2.7	9
1		AA292201	25.6	8	6.1
02138 at		R09516	4	0.1	6.1
70033 st		AI345255	0.3	0	6.1
9955 <u>a</u> l		N33374	6.0	2.1	6.1

		BCL7A	X89984	7.4	5.2	9
59766 at			AA904413	5.6		
48769_at	hypothetical protein MGC4368		AI 121013		0.7	0.1
41625_at	thyroid hormone receptor associated protein, 240 kDa subunit		AB011165		2 6:1	9
35402 at	death receptor 6					
41240 at	and the transfer of the transf	0	AF068868	5.9	2.1	9
1367 f at	inhibiting C	PSMA2	AA772359	7	4.5	9
1077 5 24		UBC	M26880	3.2	2.2	9
24007	turrior protein pos (Li-Fraumeni syndrome)	TP53	X02469	0.7	С	
3428/ at	KIAAU958 protein		AB023175	2.3	0	
153_t_at	HZB histone family, member R	H2BFR	X00088	3 5	8.0	
38901_at	specific	USP19	AB020698		0.00	
	plastin 1 (1 isoform)	PLS1	120826	101	5.0	
35341_at	$\neg \tau$	RNF15	1190547	7.0);-	
38059 g at	_	DPT	722865	2: 0	1.1	٥
40699 at	CD8 antigen, alpha polypeptide (p32)	CD8A	M12824	2.0	1.0	
40748_at	carboxypeptidase A2 (pancreatic)	CPA2	1110077	1.7	7.0	١
1254 at	guanylate cyclase activator 1A (retina)	GIICATA	136861	7.00	5.9	9
276_at	DnaJ (Hsp40) homolog, subfamily A. member 1	DAIAIA	100001	6.3	0.7	١
42272 at		TACANO TACANO	L08069	8.2	5.2	
60261 r at			AA/43565	5.5	1.3	Ψ
1			AI627708	1.4	0.7	9
66616 at			AI694231	9.0	0	9
42757 at			AA285069	4.4	2.7	9
77391 at			AA424339	0	9.0	9
ય] *	WIAA0117 motois		AL037805	2.8	2.4	9
88207 at	MANULLY DIOLEM		AI656542	5.4	2.8	
48435 at			AA086015	9.0	1.2	9
55396 at			AI796988	0	8.0	9
48454 at			N55264	5.8	2.5	9
52531 at			AI200546	3.2	2	9
76098 5 35			AA019613	1.5	2.6	9
66724 at	hymothotical protein [111140		AI304317	7.3	10	9
15220 at	Typodietical profess red 1142		A1698705	1.7	6.0	9
#3222 at			AA430014	1.8	1.9	9
3200/_dt			014000	,,,,		

7	CHOIS.	•	***	•	 	٠.,	•	•	٠

150300 g at				ŀ		
			W92947	2.8	1.9	9
4001/ at			AA013349	1.2	7	9
58622_at			AA463374	3.5	27.33	9
65108_at			AI346432	0.0		
43485_s_at	hypothetical protein FLJ21343		A1633875	5.9	A C	9
55353_at			AA760977	33.6		9
48737_at			A1831738	3	000	9
51381_at			A1480091		†	0
36181_at	LIM and SH3 protein 1	LASP1	X82456		5 -	0
36940_at	TGFB1-induced anti-apoptotic factor 1	TIAF1	D86970	1 0	10	0
32562_at	endoglin (Osler-Rendu-Weber syndrome 1)	ENG	X72012	5.1	7 /	5
41619_at		ADORA2BP	AI 022398	0	, U	0 0
31727_at	ectonucleoside triphosphate diphosphohydrolase 2	ENTPD2	U91510	1.5	9.0	0 4
41689_at	plasmolipin		R16035	2.4	1.4	9 4
40487_at			W26634	c		0.0
40862 i_at	creatine kinase, brain	CKB	X15334	11.6	1 6	200
41304_at	- 1	NRP2	AF016098	10.8	5.7	200
	karyopherin alpha 5 (importin alpha 6)	KPNA5	AF005361	1.2	C	5.9
409/1_at	KIAA0229 protein		D86982	2.4	C	5.0
34231_at	=1		AF074606	0	0.7	5.0
- 11	Max-interacting protein		AB011090	1	1.6	500
31961_r_at			AF070579	1.3	0 6	50
39976 at	hypothetical protein from EUROIMAGE 783647		AL050087	9.4	4.1	965
363/1_at	microfibrillar-associated protein 3	MFAP3	L35251	2		5.9
35348 at	protein kinase, AMP activated, beta 1 non catalytic subunit	PRKAB1	AF022116	10.8	m	5.9
38014 at	adenosine deaminase, RNA specific	ADAR	X79448	7.8	7.4	5.9
3/2/0 at	Ψı	PCP4	N22969	0.3	0.4	5.9
906_at	signal transducer and activator of transcription 4	STAT4	L78440	54.6	10.3	5.9
30/39_at			AA481476	9.0	2.8	5.9
4/039 at	splicing factor, arginine/serine-rich 11	SFRS11	AI002238	0	0	5.9
56569 at			AI914124	7.6	12.8	5.9
90638 r 2+			AA873121	1.3	1.4	5.9
775 A7 ct			AI692681	2.5	0.8	5.9
1/Dd/			AA045155	1.4	<	O u

Figure 13EEE

a l	decay accelerating factor for complement (CD55, Cromer blood DA group system)	DAF	AI888485	3	8.0	5.9
91023_f_at			F03144	2.6	1.2	r.
42721_at			AI261490		4	
84053_at			AI419969	4.5		
45522 at			R41958		O	
87285_at			AA679812	3.5	T	5
43588_at			H69543	3.7	0.7	5
69464_at			AI655655	2.1	2.8	
69558 s_at			AA431588	2.1		
71278_at			AI912743	1.7	1.8	
42875 r_at			T97225	2.3	3	
73781_at			A1669763	1.8		5.9
44/82 at			AA258063	8.2	4.3	
45583 at			AA602585	13.1		
68996_f_at			AI681967	6.2		
881// t at			AI492518	0.8		
5//14_at			AA429113	0	0.8	5.9
45612_at			AI744560	4.9	3.7	5.
62165 at	x UCb protein		W72231	4.8	3.2	9
435/6 at	hypothetical protein		AI348427	9.0	5.	5
54463_at			AI356895	1.6		5
46639_at			AA398558	1.5		
64306_at	ıma polypeptide	FGG	AI568934	1.5	1.5	
74932 at	ubiquitin conjugating enzyme E2B (RAD6 homolog)	UBE2B	AW002331	2.3	2.	
8/195_at			AA191742	0.3	2	5
31816_at	nha; acid (Pompe disease, glycogen storage	GAA	X55079	5.2		
39801_at		PLOD3	AF046889	5	2.1	5
1637_at	ated protein kinase 3	MAPKAPK3	009578	5.8		
39105_at	ulated phosphoprotein	VASP	Z46389		26	
34481_at		'AV1	AF030227	4.5	9.5	
49003_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, NDUFB10 PDSW)	VDUFB10	AA195976		5.8	5.9
49389_at			AI262504	4	3	6 5
					-	

Figure 13FFF

mors:

member 8 homolog

38521_at 38561_at

41170_at 33300_at

32172_at 40926_at

34493_at

7451_at

45758 at

41694 at 990_at

41184_s_at

36061_at 1867_at

39993_at

36992 at

57682_at 57273_s_at

55400 at

75996_at

.275_f_at

62851 g at

48565_at

2686_at '9757_at

45247_at 63083_r_at

			196363	2.1	0	5.8
68133 r at			AI817762	1.4	2.2	5.8
44287_at			H61057	1.5	0	5.8
72244 f at			A1299404	1.4	8.0	5.8
74422_at			H05961	1.3	5	5.8
53209_1_at			T91952	0.2	0.1	5.8
86831_at			N24028	0.5	1.8	5.8
64185_at			AA009833	0	0	5.8
86865_at			A1089920	0.4	2.1	5.8
T		FOXC1	AW022802	2.8	2.3	5.8
T	Torknead box C1		R66534	4.8	1.5	5.8
50134_at			AL119305	2.7	2.7	5.8
42982_at			AL 044906	8.5	2.3	5.8
71106_Lat			R60655	1.8	1.6	5.8
50102_at	16		A1680350	41.7	5.3	5.8
42363_r_at	STAT Induced STAT Infrigitor 3		AA191741	3.4	m	5.8
44526_at			AA831034	6	9.0	5.8
52714_at			AA166624	1.7	1.6	5.8
58541 s_at			AI024369	1.5	1.7	5.8
697/4 at			99069N	3.3	3.5	5.8
45071_at			AI671126	1.4	1.6	5.8
45675_at	UKFZP4341216 proteiii		N99610	1.1	1.1	5.8
54039_at			A1572226	3.2	4	5.8
57744 at	HSPC0/2 protein		AW007845	1.5	0	5.8
57396 g at			D16154	0.6	4.0	5.8
1411_at			AA780435	1.7	9.0	5.8
38926_at			AA913861	1.3	1.4	5.8
66655_at			D63481	2.9	3.2	5.8
34/43_at	-	KHSRP	AA628946	ري وي:	2.8	5.8
38828 s at	KH-type splicing regulatory protein (1 ook shamb protein		H17730	4.9	5.9	5.8
56546_at	NIAALU40 plotein		AL044098	6.1	5.1	5.8
53881_s_at		C200RF3	H09341	4.2	2.7	5.8
48829 s at	chromosome 11 open reading frame	C110RF24	AA065185	5.6	2.1	5.8
52164 at			N36986	5.5	4.2	5.8
144693 at	hypothetical protein rejies/		22222			

63971_s_at	63971_s_at sirtuin (silent mating type information regulation 2, S.cerevisiae, المصواري) عند المارية الماري	SIRT2	AI984394	3.6	2.4	5.8
54152 at	leukarvotic translation initiation factor 4E binding protein 1	FIFAFRD1	A1026669	α	5.2	α u
701	T DINGHIE DI OCCIII I	LII 4 LDI 1	A1020003	0.0	3.6	0.0
524_at		PMS1	U13695	0.9	0.7	5.7
39790_at		ATP2A2	M23115	0.1	0.5	5.7
40146_at		RAP1B	AL080212	9.7	4.3	5.7
31921_at		OR2F1	U56421	0	2.8	5.7
1184_at	it 2 (PA28	PSME2	D45248	9.3	10.3	5.7
32364_at	sine oculis homeobox (Drosophila) homolog 6	SIX6	AJ011785	2	0.2	5.7
32850_at		NUP153	Z25535	1.6	2.1	5.7
34172_s_at	DNA segment on chromosome X and Y (unique) 155 expressed	DXYS155E	M99578	1.2	1.4	5.7
	sequence					_
33359_at	KIAA0768 protein		AB018311	0.8	0.1	5.7
34256_at	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-	SIAT9	AB018356	0	7.8	5.7
	sialyttransferase; GM3 synthase)					
32405_at	KIAA0707 protein		AB014607		0	5.7
33684_at	wingless-type MMTV integration site family, member 2B	WNT2B	271621	3.8	0	5.7
35166_at	Down syndrome critical region gene 3	DSCR3	D87343	4.6	7.1	5.7
41329 at	hypothetical protein LOC57147		AI458463	7.6	8.1	5.7
33515_at	t-complex 10 (a murine tcp homolog)	TCP10	003399	0	0	5.7
1856_at	v-rel avian reticuloendotheliosis viral oncogene homolog	REL	X75042	5.6	4.1	5.7
36323_at	gamma aminobutyric acid (GABA) A receptor, alpha 1	GABRA1	X14766	1.1	9.0	5.7
39199_at			W28661	0.1	0	5.7
36536_at	schwannomin interacting protein 1		AF070614	10.9	0.2	5.7
31536_at	reticulon 4	RTN4	AB020693	1.5	2.6	5.7
36175_s_at	36175_s_at human immunodeficiency virus type I enhancer-binding protein 2	HIVEP2	AL023584	24.2	7	5.7
37248_at	2	CPZ	U83411	8	9.0	5.7
37687_i_at	Fc fragment of IgG, low affinity IIa, receptor for (CD32)	FCGR2A	M31932	1.8	9.0	5.7
752_s_at	nolog, subfamily B, member 1	DNAJB1	D85429	0	0.1	5.7
41018_at	DKFZP5640243 protein		AL050015	0.7	0.8	5.7
722_at	rcd1 (required for cell differentiation, S.pombe) homolog 1	RQCD1	D87957	1.2	0	5.7
42301 at			AA44100	0.3	9.0	5.7
66550_at			AA972106	0.2	0	5.7

Figure 13III

E0979 at			AI675751	0.1	1.6	5.7
30070 24			AI002236	8.5	0.1	5.7
00373 at			A1276680	9.0	1	5.7
40944 at			AA903287	14	5	5.7
-1 (AA142842	12	11.9	5.7
0001/ at			AI792916	2	1.1	5.7
01970 at			H00945	2.4	1.2	5.7
03230 dt			A1588981	0.2	1.6	5.7
50950 21	sin 3. associated polypeptide, 18kD	SAP18	AW006285	2.1	1.3	5.7
43865 at			R49396	1	3.1	5.7
45721 at	endothelin converting enzyme 1	ECE1	AL039866	12.6	4.3	5.7
164552 at			H04794	2.3	0.8	5.7
64221 at			H27234	0	0	5.7
70428 at			A1685341	10.9	2.3	5.7
13384 at			AW000990	0	2.6	5.7
56008 at			AA284288	0.3	1.7	5.7
54604 at	hyaluronan synthase 3	HAS3	A1338972	4.2	2.9	5.7
78269 at			AA218544	1.3	0.8	5.7
60981 at			AI554853	6.0	1.7	5.7
56759 at			AI914936	3.7	0.4	5.7
18148 r at			AI168326	4.2	1.9	5.7
52391 f at			AA592983	0	0.3	5.7
51238 at			AA005354	1.2	0.7	5.7
51588 at			2933319	6.4	0.2	5.7
39443 s at	cytochrome c oxidase subunit Vb	COX5B	M19961	4.7	2.3	5.7
40120 at	hydroxyacyl glutathione hydrolase	HAGH	66606X	5.7	2.9	5.7
33833 at	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	SPTAN1	J05243	5.1		5.7
37320 at	phosphatidylserine synthase 1	PTDSS1	D14694	5.3		5.7
45521 s at	KIAA0100 gene p		A1967955	5.4	5.5	5.7
65737 r at			AI701293	5	2.7	5.7
39542 at	ectodermal neural cortex (with BTB-like domain)	ENC1	AF059611	1.5	0.7	5.6
1713_s_at	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	U26727	4.7	0	5.6
33010_at	solute carrier family 5 (neutral amino acid transporters, system A). member 4	SLC5A4	AL008723	0	0.4	5.6

40267_s_at	KIAA1036 protein		A1880840	2.2	C	56
38183_at	forkhead box F1	FOXF1	U13219		0.7	5.6
40411_at	thyroid hormone receptor binding protein		D80003	2.5	1.8	5.6
1448_at	proteasome (prosome, macropain) subunit, alpha type, 3	PSMA3	D00762	4.3	4	5,6
41237_at	major histocompatibility complex, class I, A	HLA-A	D32129	14.9	9.7	5.6
35876_s_at		SGPL1	AI128825	1.5	0.4	5.6
1361_at	telomeric repeat binding factor (NIMA interacting) 1	TERF1	U40705	0	-	5,6
2047_s_at		JUP	M23410	0.1	1.1	5.6
38882 <u>r_at</u>	- 1		AF096870	1.7	4.1	5.6
35214_at	UDP-glucose dehydrogenase	UGDH	AF061016	3.7	2	5.6
35230_at	hypothetical protein, clone 24751		AF070530	17.3	5.7	5.6
34371_at		PPP4R1	U79267	1.5	1.6	5 6
33080_s_at	RAP1, GTPase	RAP1GA1	AB007943	1	0.7	5.6
36785_at	heat shock 27kD protein 1	HSPB1	223090	1.2	0.7	5.6
37603_at	interleukin 1 receptor antagonist	IL1RN	X52015	8.9	5.9	9.5
40724_at	zinc finger protein 200	ZNF200	Y14443	2.5	6.0	5.6
1022_f_at	interferon, alp	IFNA14	V00542	0.1	0	5.6
84981_r_at	collagen, type III, alpha 1 (Ehlers-Danios syndrome type IV, autosomal dominant)	COL3A1	T54146	5.1	8.6	5.6
60835_at			AI831561	30.1	6	5.6
78605_at			A1080388	6	4.4	5.6
61557_at			AI074020	0	3.3	5.6
62371 g at	-		AI221377	6.6	2.9	5.6
578_at	recombination activating gene 2	RAG2	M94633	1.3	0.5	5.6
91669_at			AA491645	8.4	6.2	5.6
60635_at	hypothetical protein FLJ23282		W61076		2.5	5,6
67515_at			AI479011	1.9	2.4	5.6
65360_at			R45940	2.3	2.2	5.6
86405 at			Z38166	0	0.4	5.6
86822_at			AI621229	3.4	2.8	5.6
68047_at			AA936632	10.3	14	5.6
43620_at			AA774785	3.7	2.1	5.6
70814_at			AI833139	9.0	1.7	5.6
4409/ at	UKFZP386C1324 protein		A1928466	0.7	1.3	5.6
42848_at			C20550	9.0	e	5.6

32923_r_at	synapsin I	SYN1	M58378	1.5	0.5	5.6
ø			N78362	0	3.1	5.6
~;			N54910	3.2	2.1	5.6
72961_i_at			AI950023	1.8	1.4	5.6
56028_at			AI768884	0.8	2	5.6
42740_at			AI243610	1.5	1.9	5.6
53655_at			AI300574	9.0	2.1	5.6
57497_at			AA419263	2	1.9	5.6
58944_s_at	ribosomal protein	RPS6KC1	AA670286	30	77	5.6
34572_at	carbonic anhydrase VII	CA7	M76424	1	6.0	5.6
46391 i at			AI761712	0.2	1	5.6
51055_r_at			AA962343	0.7	2.6	5.6
53068_at			AI738621	1.9	2.3	5.6
57660_r_at	┪		R43504	4.1	3.4	5.6
46103_at	MEK partner 1		AI335267	0.2	9.0	5.6
64749 r at	\neg		AA535979	1.8	0	5.6
51854 at	KIAA1128 protein		AA424126	14.4	6.3	5 5
54355_at			AI523391	2.5	12	5.6
32704_at	dedicator of cyto-kinesis 2	DOCK2	D86964	9	2.6	5.6
34864_at	hypothetical protein		AF070638	4.9	0 6	7.6
49390_at			AA999858	5.6	5 6	7
51056_at	hypothetical protein DKFZp434D0412		AW025176	3.6) (m	5.5
61291_at	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	SDHA	AI348006	2.7	1.3	5.6
58945_f_at	hypothetical protein FLJ11773		T55569	4 5	6	7 7
47787_at			AA045461		- 2	7.5
32460_at	gamma aminobutyric acid (GABA) A receptor, beta 2	GABRB2	867368	0	0	5 5
39386_at	gene predicted from cDNA with a complete coding sequence		D14811	4.2	1.7	2 2
31812_at		GMPR	M24470		9.3	ار ار
31586_f_at	\neg	IGKC	X72475	C	000	7. 7.
162_at	ubiquitin specific protease 11	USP11	U44839	2.9	280	7 5
40582_at	protein tyrosine phosphatase, receptor type, J	PTPRJ	AI806482			5.5
32706_at	HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A	HIRA	X89887	0	1.6	5.5
33284_at	myeloperoxidase	MPO	M19507	1.3	0.8	5.5

Figure 13LLL

oligodendrocyte m TNF receptor-asso solute carrier familiant associated family transferase salytransferase thyroid hormone ubiquitin-conjuga	nber 2 beta yeast UBC9)	TRAF1 SLC31A2 RAD9	U19261 U83461 U53174	33.5 10.5 2.8	12.9	5.5
at solute carrier familiate solute carrier familiate solute carrier familiate solute carrier familiate solute carrier familiate solute carrier familiate solute carrier familiate solute carrier familiate solute sialytransferase) at thyroid hormone at phosphatidylinosi at at at at at at at at at at at at at	nber 2 beta yeast UBC9)	SLC31A2 RAD9	U53174	10.5	12.9	5.5
at solute carrier familiaria RAD9 (S. pombe) at HBV associated fariation in a sialytransferase 4 sialytransferase 4 at thyroid hormone at thyroid hormone at at at at at at at at at at at at at	nber 2 beta yeast UBC9)	SLC31A2 RAD9	U83461 U53174	2.8	9 9	
at solute carrier farms at RAD9 (S. pombe) at HBVD 9(S. pombe) at HBVD 9(S. pombe) at HBVD 9(S. pombe) at HBVD 9(S. pombe) at thyroid hormone at phosphatidylinosi at ubiquitin-conjuga at at at at at at at at at at at at at a	beta yeast UBC9)	RAD9	U53174	2.8	<u>-</u>	ď
at RAD9 (S. pombe) at HBV associated fa r_at sialytransferase 4 at thyroid hormone at phosphatidylinosi at phosphatidylinosi at a	beta yeast UBC9)				5	, ,
at HBV associated faraterial sialytransferase 4 sialytransferase 4 at thyroid hormone at at at at at at at at at at at at at	beta yeast UBC9)		AA160708	6.8	8.2	5.5
r at sialytransferase 4 sialytransferase) at thyroid hormone at phosphatidylinosi at ubiquitin-conjuga at at at at at at at at at at at at at	beta yeast UBC9)		1 1 20 7 2	1 4	6.0	5.5
sialytransferase) thyroid hormone iphosphatidylinosi ubiquitin-conjuga	beta yeast UBC9)	SIA14A	123/2	•		
thyroid hormone phosphatidylinosi ubiquitin-conjuga			1107011	1 7	C	5.5
thyroid hormone phosphatidylinosi ubiquitin-conjuga			AFU/U3/1			7
thyroid hormone phosphatidylinosi ubiquitin-conjuga ubiquitin-conjuga transfer to conjuga transfer tra		TRIP13	U96131	0		
phosphatidylinosi ubiquitin-conjuga ubiquitin-conjuga transparine brain no		PIPSKIB	X92493	1.3	0	C
In district Prain III		UBEZI	AL031714	0.1	0.7	5.5
at at at at at at at at at at at at at a			AA165208	2.3	2	5.
at at at at at at at at at at at at at a			144621324	0.7	1.4	5.
at at at at at at at at at at at at at a			AA912180	2.3	1.5	5
at at at at at			A1131053	6.0	9.0	5.
to the prain III			A1796514	2.4	0	5.
to trating brain nu			A1989733	2.3	e	5.5
to heating brain nu			41435504	1.4	1.4	5.5
ot cutative brain nu			AI 043172	0.7	4	5.5
un nitative brain nu			A1792919	4.7	1.3	5.5
SUBUS at putative Significance	n	V 3 > C C	41857509	1.2	0.1	5.5
cytochrome c oxi		XCV00	AA133355	13	0.7	5.5
Γ			00000100		1.5	
			44262084	9.9	2.9	5.5
43793 at			AA992185	4.1	2.4	
48655_r_at			A1862887	21.3	17.7	
44092_at			N34402	1.6	2.2	5.5
53256 at			A1307778	1.7	1.8	5.5
50125_r_at			AA828830	0.1	0.4	5.5
67369 at		+	T81819	0	6.8	5.5
66084_at			A1857594	3.4	3.2	5.5
45769 g at		1.E.C.	A1887641	4.8	2.8	
44066_s_at G protein-coupled receptor kinase-interactor	ractor 1	5	N36861	4.7	2.1	5.5
160174 at			AA461205	7.8	5	

1, 3, 3 at			200000			
	UDP-N-acetyl-alpha-D-galactosamine-polypentide N		AA019836	9.0	0.8	5.5
	acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNII	AW021000	0.2	0.5	5.5
Lat J	retinoic acid receptor responder (tazarotene induced) 1	RARRES1	A1669229	6 9		
	v-ets avian erythroblastosis virus E26 oncogene homolog 2	ETS2	AI870399	7.0	4 0	5.5
			AA286940	4 2	0 0	0.0
	hypothetical protein FLJZ3033		AI653719	3.4	6.0	0.0
	Sec23.interacting protein p126		AA405686	2.4	2.4	7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7
			AI332962	2.7	3.7	5.5
			W29045	5.4	0.5	100
			T92565	0	0	2 2
			AA528592	2.6	1.2	5.5
	dynein cytoplasmic intermediate actual of		AF034176	8.1	8.1	2.5
	Z. a	DNC12	AI986201	1.3	1.4	5.5
			W95017	4.1	5.1	0 4
	KIAA0876 protein		AA009692	2.8	2.6	, r
			AA524529	2.9	2.7	5 4
	Succinate Cod ligase GDP forming after and		W68180	6.3	5.2	7.5
	Times of the source of the sou	SUCLG1	AA826261	4.1	3.3	5.5
	chloride channel nucleotide sensitive 1A		AI280108	5	4.9	2 2
		CLNS1A	N32865	2.2	1.4	5.5
	-1 C	ATP10B	AB018258	0.3	0	5.4
	thyroid hormone recentor heta (avian pathroblostic)	PI3	L10343	12.9	0.4	5.4
	viral (v erb-a) oncogene homolog 2)	HKB	M26747	1.6	0.4	5.4
	Blyceronephosphate O-acyltransferase	GNPAT	AJ002190	0.5	C	5.7
	reticulocalbin 1 FE band calcium binding at		AL049471	10.7	3.2	5.4
	Ubiquitin carrier protein	RCN1	D42073	14.7	9.7	5.0
			M91670	5.9	7.8	5.4
	Vesicle associated membrane protein 1 (consistent		U90426	1.4	1.3	5.4
	Seven in absentia (Drosophila) homolog 2	VAMPI	AF060538	3.4	0.1	5.4
	2 8000000 (builded a)	SIAHZ	U76248	7.7	3.6	5.4
	hydroxysteroid (17.heta) dehydrogenase 3	000	AA161065	1.1	1.1	5.4
	IJ.≒	HSD1/B3	U05659	2.3	1.7	5.4
			D50926	7.2	5.1	5.4

Figure 13NNN

36925_at heat shock 70kD protein 2 1231_at ubiguitin-conjugating enzyme E2B (RAD6 homolog 1) 38300_at frizzled (Drosophila) homolog 1 34041_at small inducible cytokine subfamily A (Cys.Cys), me 46538_at 6625_at chromosome 11 open reading frame 15 6625_at chromosome 11 open reading frame 15 62393_at chromosome 11 open reading frame 15 62425_at 62425_at 91727_at glucose phosphate isomerase 65510_fat chromosomal protein S11 58814_at ribosomal protein S11 54860_at daghtor-related protein complex 1, mu 2 subunit 87801_at daghtor-related protein complex 1, mu 2 subunit 87802_rat daghtor-related protein complex 1, mu 2 subunit 87820_rat daghtor-related protein complex 1, mu 2 subunit 87820_rat daghtor-related protein complex 1, mu 2 subunit	mber 22	HSPA2 UBE2B FZD1	L26336	0 0	0.0	٠.
t ubiquitin-conjugat frizzled (Drosoph at small inducible capt at chromosome 11 at chromosome 11 at chromosome 11 at at glucose phosphate at at ribosomal proteinate at at ribosomal at at at ribosomal at at at ribosomal at at at adaptor-related at at at at at at at at at at at at at	mber 22	JBE2B -ZD1		00		5.4
at frizzled (Drosopi at small inducible of at chromosome 11 at chromosome 11 at at at glucose phospha f at ribosomal protei at ribosomal protei at adaptor-related at rat adaptor-related at rat at adaptor-related at rat at adaptor-related	mber 22	-ZD1	M74525	0.0	1	5.4
at chromosome 11 at chromosome 11 at chromosome 11 at at at ribosomal protei at ribosomal protei at ribosomal protei at adaptor-related at ribosomal protei at ribosomal ribosom	mily A (Cys.Cys), member 22 frame 15	CCVVOC	AB017363	0.1	o	5.4
at chromosome 11 at at at at ribosomal protei at at ribosomal protei at at ribosomal protei at at at adaptor-related at at at at at at at at at at at at at		0C1A22	U83171	6.9	5	5.4
at chromosome 11 at at at glucose phospha at glucose phospha at ribosomal protei at ribosomal protei at adaptor related at at ribosomal protei at ribosomal protei at adaptor related at at adaptor at			AI632740	4.2	0.1	5.4
at at at adaptor related at at at ribosomal protei at at at at at ribosomal protei at at at at at at at at at at at at at		C110RF15	AI188389	8.0	1.4	5.4
at at at at at at reat glucose phospha at glucose phospha at ribosomal protei at ribosomal protei at adaptor-related at fat adaptor-related at at at at at at at at at at at at at			AA890177	2	0	5.4
at glucose phospha glucose phospha at adaptor related at adaptor at adaptor at at adaptor at at adaptor at adaptor ada			AI277415	1.7	1.2	5.4
glucose phospha ribosomal protei ribosomal protei at adaptor-related			AA921956	1.3	1.8	5.4
glucose phospha at ribosomal protei at adaptor-related at			W45259	1.1	1.3	5.4
glucose phospha rit ribosomal prote at adaptor-related at			AI651474	1.5	0.4	5.4
glucose phosphariting in the sound protein at adaptor-related at a adaptor-related at at a second protein at a second protein at a second protein at a second protein at a second protein at a second protein at a second protein at a second protein a second protei			AI743571	1.9	1.2	5.4
ribosomal proteint adaptor-related		GPI	AI248811	2.8	9.0	5.4
ribosomal protei			AA034458	0.4	0.4	5.4
ribosomal protei			AA628524	1.2	2.9	5.4
nt adaptor-related		RPS11	AA603467	2.9	1.9	5.4
adaptor related			AI797678	2.3	2.4	5.4
87801_at 43177_at 88280_r_at 69345_at 71549_r_at	protein complex 1, mu 2 subunit	AP1M2	W92449	1	1.1	5.4
43177_at 88280_r_at 69345_at 71549_r_at			AA604144	4.1	2.4	5.4
88280 <u>r</u> at 69345 <u>at</u> 71549 r at			AI732470	0.3	0.1	5.4
69345_at 71549_r_at			AA703174	3.7	6.0	5.4
71549 r at			N95633	2.2	0	5.4
			AA699538	3.6	2.2	5.4
52384_s_at			AI984780	15.6	1.9	5.4
50266_at			AI741178	7.7	6.5	5.4
49302_at HBV associated factor			AI971817	13.9	9.1	5.4
64183_r_at			R55749	1.1	1.2	5.4
85971_at			N54973	1.7	3.2	5.4
42804_at			W86160	3.7	5.1	5.4
56845_at Ras homolog enriched in brain 2	ı brain 2	RHEB2	AA056145	0	2.3	5.4
44951_r_at			AI732184	2	2.7	5.4
44393_at hypothetical protein			AA604681	1.6	1.4	5.4
44572_g_at			AI765278	1.1	1.4	5.4

61128_at 45787_at			N70394	ر د د	80	7
45787_at			A1338787			1 7
	cyclin L ania 6a		N29695	1		7.0.4
36/0/ s_at	serine/threonine kinase 9	STK9	X89059	180		7 0.4
41895_at			W93764	60		5 C
48859_f_at	HMP19 protein		A1968989	2.2	90	5.4
			N98235	3.7	4	5.4
52731_at	hypothetical protein FLJ20294		AI359466	1.5	2.3	5.4
56755_at			AI802568	1.1	0.5	5.4
41976 at			T11500	1.8	3	5.4
- 11			3145395	1.3	1.7	5.4
82137_f_at			AA876935	2	1.	7 4
91067 i at			AI681736	0.5	0.2	5.4
39738_at	olypeptide 9, non-muscle	МҮН9	282215	0.5		5.4
39774_at	oxidase (cytochrome c) assembly 1-like	OXA1L	X80695	3.2	3.1	5.4
56351_at			AI436023	2.5	2.5	5.4
51089_at	KIAA1140 protein		AL042799	6.5	4.5	5.4
53848_at			AI422099	4.2	3.7	5.4
57079_at			AA503073	3.1	3	5.4
54912_at	translocase of inner mitochondrial membrane 13 (yeast) homolog TIMMI3B	IIMM13B	AL035821	5.2	3.4	5.4
64901_at		ARL1	AI357567	6 1	3.4	7.7
65603_at	epeat-containing 6	BIRC6	AA886981	5,1	5 6 6	7.7
35109_at	KIAA0756 protein		AB018299	0	0.4	5 2
37503_at	KIAA0984 protein		AB023201	1.7	1.1	5 2
31731_at	olog 4 (Drosophila Pc class)	CBX4	AF013956	2.5	0	5.3
40156_at	KIAA0040 gene product		299715	1.6	2.7	5.3
32641_at	androgen-induced prostate proliferative shutoff associated protein	l	AB023196	2.2	2.9	5.3
148_at	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR		U88629	6.4	1.4	5.3
33652_at	loproteinase domain 20	ADAM20	AF029899	1.7	6.0	L.
34178_at	zinc finger protein 297	ZNF297	AI884738	9	3.4	, LC
41559 at			AA434319	7.1	2	5.3
33896_at		EP300	U01877	6.0	0	5.3
38/5/_at	PUGFA associated protein 1	PDAP1	U41745	2.9	1.8	5.3

Figure 13PPP

35227_at	-01	RBBP8	U72066	5 1	0.0	C
1930 K at	Dreast cancer Z, early onset	BRCA2	U43746	2.2	2 4	0 0
40332 at	- 1		AF109134	00		0.0
3//32 at		RYBP	AI DAGGAO	t.0	2.4	5.3
1505_at	thymidylate synthetase	TYMS	D00506	13.1	4.6	5.3
66170_at			066000	1:1	1.5	5.3
76032_at			A1/3233/	1.5	1	5.3
76206 at			AI370844	0.7	1.3	5.3
66402 at			AA731738	1.6	6.0	5.3
66899 at			AA748556	O	1.2	, r.
51079 at	ATP-hinding cassatte sub family, A (ABC1)		AI733062	3.2	0.8	200
59166 at	Commission of the cassociation of (ABCL), member /	ABCA7	AI668632	1.7	0.8	7
58530 r at			AI091214	4	9.0	5.3
61829 at			T66185	3.4	2.5	2 2
47513 at			AA007461	2	1 1	2 2
82053 at			AA679424	9	4.2	0.0
92147 at			AI471845	2.6	10	0.0
50030			N92830		2 6	0.0
10202			AI967991	12	1 1	0.0
100 6 24	ras responsive el	RREB1	A1097330	100	0 0	
109 S at	piasminogen activator, urokinase receptor	PLAUR	1109937	000	7.0	5.3
86470 at			700000	10.0	3.3	5.3
88607_at			AH004513	1.0	0	5.3
64001_s_at	seven in absentia (Drosophila) homolog 2	0 4	A1660692	6.0	0.2	5.3
69842_f_at	95557	SIAHZ	AW008929	11.6	4.2	5.3
89412 at			AI766478	2	0.7	5.3
70151 at			AI804386	8.3	3.5	7
59671 at			AI805522	8.6	6.3	5 2
72686 at			AI798769	0	1.5	53
74218 at			Ai093728	2	0.3	5.3
66144 at			A1990680	9.0	1.5	, C
60527 at	Rho GTPase activating protein E		AA872556	1.1	1.2	77
89121 at	100000000000000000000000000000000000000	ARHGAP5	AI768264	3.2	3.1	7
			AI740879	0	4.3	i r
45159 r at			N74103	2.3	2.1	7
10007	to the second se		H71807	0.3	0.4	, r.
43037_at	dimetnylarginine dimethylaminohydrolase 1	DDAH1	AI309320	2.1	2.1	5 4
				11.1		0.0

Figure 13QQQ

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osoco_at Cuds antigen (activated B lymphocytes, immunoglobulin superfamily)	CD83	AI983994	7.3	7.3	5.3
59068_r_at		70007714	C		
55379_at		A1145307	7 .	6.0	5.3
48313_at		A1140322	2.1	1.4	5.
91678 at CGI-14 protein		AI363/05	0	0	5.
Γ		AI814/61	 	2.6	5.
48749_at		K32893	0.2	0.4	5.3
58827 at		U11630	2	5.7	5.3
54519 r at		A1992368	3.8	4.2	5.
31502 at		AA976211	2.4	2.5	5
31668 f at		W27953	3.5	2.1	5.3
40056 st		W28193	0.8	0.1	5
F0002 f at		AI080164	1.7	0.7	5
51005 - at		AA525753	2.1	6.0	5.2
96188 f 24		AA743794	0.3	2.9	5.3
000000000000000000000000000000000000000		AI733033	0.6	9.0	5.3
40824 at IDAN Finding and 17 LAK lymphocytes		AB002405	4.3	1.1	523
T	RANBP16	AB018288	4.8	2.5	7
A026E at Consider the control of the		AB014520	4.1	4.3	7.2
Good-at gualiline nucleotide binding protein (G protein), alpha 15 (Gq class)	GNA15	M63904	0.3	1.5	5.3
	BI VPB	027142	ľ		
_at	מראונט	032143 AIDE2130	5.5	3.8	5.3
57152 at WAS protein family, member 2	WACES	0.120.129	4.0	5.5	5.3
65501_s_at	7 1004	W/2145	2	0.4	5.3
52012_at		AIS1068/	4.9	2.7	5.3
35066 g at fetal hypothetical protein		AIDSAUZU	5.2	3.5	5.3
svnaptojanin 1		084971	0.7	1.5	5.2
Γ	STINJI	AB020717	0	0	5.2
H2A histone fam		AF055581	0.4	0.3	5.2
t 7	HZAFD	298744	2.4	2.6	5.5
inhibitor of growth family momber 3		AF051321	3.7	2.4	5.2
2' 3'-cyclic nicle	ING3	AC004537	1.1	0.2	5.2
protein tyrogine	CNP	M19650	8.3	3.9	5.2
+ CMT3 (SUDDING	PTPN1	M31724	12.9	5.3	5.2
1100 at Simil 3 (Suppressor of mit two 3, yeast) homolog 2	SMT3H2	A1971724	7 0	7.0	

		A 049951	90	000	1
TIVATING PROTEIN		AL096752	5.6	0.0	3.6
	DNAJ85	AF088982	7.0	2.,	2.0
heterogeneous nuclear protein similar to rat helix destabilizing protein		\$63912	0	0.3	5.2
oorin 62kD	NIIDEO	VEOF21			
synovial sarcoma, X breakpoint 4	SCVA	1728271	8.9	2.5	5.2
9	2074	090841	0	1.1	5.2
		AI184/10	2.1	0.5	5.2
S100 calcium-binding protein A5	1.400	AF063564	1.2	1.5	5.2
n. SCN Circadian Oscillaton, Bratain (SCOD)	STOUAS	218954	1.6	0.7	5.2
kappa light polypeptide gene enhancer in B-cells	NFKB2	AB011178 X61498	29	11.4	5.2
/drogenase 1. soluble					
il sarcoma viral related opcodene homolog	י ארטין	K03000	1.8	Э	5.2
ginina/sarina rich 8 (cuprosses 1 1011010B	LYN	M16038	10.4	7.2	5.2
Similar same inche (suppressor of white. la homolog)	SFRS8	108377	2	6.0	5.2
	MSL3L1	AI 050178		,	L
r (dihydrotestosterone receptor; testicular	AR	M23263	0 0	† L	5.6
			0	<u>ς</u>	5.2
		W72265	2.5	00	C u
		R37682	2.2	5.5	2.0
il. 24 (22 d)		R27299	0	80	10.0
Solute carrier ratinity 34 (soutum phosphate), member 2	SLC34A2	AI587292	0.4	22	5.5
		AI656531	0.7	Ö	5.0
		AI023195	1.9	6.0	5 2
		AA806110	9.0	0.5	5.2
		AA872454	1	2.1	5.2
		AI223339	0	0.7	5.5
		AI655380	1.2	62	L C
		N73778	3.9		5.0
		AA424811	0.7	0	5.2
		AI089319	1.7	1.4	5.2
		CONVCOV			

Figure 13SSS

48164_at			172557	1		ı
68187_at			44632138		4.4	5.5
50275_at	hypothetical protein		A1042154	1 0	0	5.2
44233 i_at			ALU43134		2.5	5.2
49132 at			0.175027	0.3	2.5	5.2
51121 at			AI4589/5	6.5	0.6	5.2
43785 i at			R45590	8.8	4.6	5.2
50069			Z39990	1.6	1.8	5.2
75449 at			A1090586	2.3	3.6	5.2
75737 4 24			R40373	2.4	2.7	5.2
50175 pt			A1239473	3.1	1.5	5.2
71557 24			AA700040	2.1	2.2	5.2
75020 24			H64589	9.5	3.8	5.2
40929 at			N70317	0	C	5.2
00000 at	Carta protein		W07150	3.3	0.6	7 2
000/0 at			AI093876	2.5	0.00	4.5
44908 at			H38046	2.2	5 -	2.6
26200 at			A1363050	V -	7 7	3.6
50392_at			A1792455	t	ţ .	5.6
50930_at			41796010	1.4	1.5	5.2
47425_at	pancreatitis-associated protein	DAD	010010		5	5.2
44507 i at		L.Y.L	AI52101/	2.7	2.3	5.2
53661 at			N26892	1.5	1.1	5.2
46005 at			AL038450	16.2	2	5.2
50147 6 24	and the second second		N81145	m	10	5.2
46580 at	KIAA130E postoja	MAT2B	AI344107	2.1		5 2
43478 at	hynothetical protoin El 190373		AA411382	2.7	0.8	5.5
50186 5 24	ווא אסמונימונים או חו		AW021103	17.4	9.0	5.2
7 4			AA143060	0.7	1.2	2.5
57060 24			W60953	3.9	2	5.5
40651 c 24	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		AI829724	0	60	5.0
40031 S at	col acouppin releasing normone receptor 1	CRHR1	AF039523	2	0.5	5.0
18354 at			AA434246	0.4	0.2	5.2
32650 24			AI929033	3.4	26	100
34030 at	1 1	RING1	AL031228	2.8	1 0) r.
2035 S at	nding protein 1	MPBI	M55914	0) r
41540_at	protein phosphatase 1, regulatory subunit 7	PPP1R7	250749	5.2	2.9	5.5

Figure 13TTT

53708_at	cation chloride cotransporter interacting protein		AI467928	6.1	5.6	5.2
56575_at	CGI-108 protein		AW025521	3.8	1.8	5.2
81045_at	zinc finger protein 24 (KOX 17)	ZNF24	AA134771	2.4	2.7	5.2
59136_at			AA779895	5.2	5.1	5.2
45255_at	CGI-69 protein		AI354351	2	3.5	5.2
45808_at	anaphase-promoting complex subunit 7		AA131793	5	2.4	5.2
55567_at			AA147933	5.3	5.3	5.2
		MEIS2	AF017418	1.3	0	5.1
34467 g at	5-hydroxytryptamine (serotonin) receptor 4	HTR4	Y12505	9.0	0.4	5.1
	sperm associated antigen 9	SPAG9	AB011088	4	1.6	5.1
40187_at			AW016815	0.7	1.4	5.1
31832_at	KIAA0286 protein		AB006624	41.3	5	5.1
40067_at	E74-like factor 1 (ets domain transcription factor)	ELF1	M82882	0.5	0.5	5.1
38181_at	matrix metalloproteinase 11 (stromelysin 3)	MMP11	X57766	2	0.1	5.1
40468_at	KIAA0554 protein		AB011126	8.3	0	5.1
38512_r_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu	ELAVL3	D26158	4	1.5	5.1
35459 at	regulator of G-protein signalling 13	RGS13	AF030107	3	C	4
32165 at	(35kD)	SFRS7	1.41887		0 0	1
	hypothetical protein		782180		2.1	7.1
33447_at	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)		X54304	1.5	2.2	5 1
32980 f.at	H2B histone family, member L	H2BFL	AI688098	1.5	0.7	5
282_at	M-phase phosphoprotein 1	MPHOSPH1	L16782	0.7	0	5.1
33924_at	KiAA1091 protein		AB029014	24.9	10.8	5.1
31386_at	immunoglobulin kappa variable 1/0R15-118	IGKV10R15-118	M20812	1.1	0	5.1
32271_at	FOS-like antigen-1	FOSL1	X16707	0	0	5.1
33842_at	Fanconi anemia, complementation group G	FANCG	AC004472	0	0	5.1
36818_at			AF052100	1.7	0.2	5.1
36937_s_at	${}^{-}$	1	828060	1.6	0.1	5.1
38114_at		RAD21	D38551	7.4	5.2	5.1
37976_at	lg superfamily protein		AL034397	0.7	0.5	5.1
41028 at	ryanodine receptor 3	RYR3	AJ001515	0.5	0.1	5.1
43459 at	KIAA0680 gene product		A1472209	0	5.3	5.1
48034_at	eukaryotic translation initiation factor 2 alpha kinase 3	EIF2AK3	AA534710	3.4	2.6	5.1
42326_at			AW003808	2.7	0.7	5.1

15-10-al			AA608964	0.7	0.6	2.
45502_at			AI990713	1.3	1.5	5.1
55226_at z	zinc-binding protein Rbcc728		D59325	2.5	1.4	5.1
51211_at			AA700460	0.4	2.4	5.1
58246_at h	hypothetical protein FLJ12903		AI807668	5.4		5.1
80689_at			AA922110	4	4.2	5.1
42624_at			H19417	1.9	3.5	5.1
47905_at			AI889332	2.6	2.2	5.1
83568_at			R06436	13	9.0	5.1
			N67792	1.1	1.1	5.1
	HSPC030 protein		AA203505	8.5	2.4	5.1
68450_r_at			AI659354	1.4	0.1	5.1
69778_at			AI972712	0	0.7	5.1
70405_at			AI804384	5.5	2.6	5.1
72307_at			N24412	6.0	1.7	5.1
			AI222957	3.5	8.0	5.1
	KiAA1105 protein		AW003305	1.4	2.5	5.1
	nuclear pore complex protein		AA521256	0.8	1.2	5.1
\neg	hairy/enhancer-of-split related with YRPW motif-like	HEYL	AL040197	4.4	3.2	5.1
43863 i at			AI863402	8.1	1.2	5.1
43868_at			R49368	1.6	2.2	5.1
一			R54026	4.2	4.4	5.1
t l	hypothetical protein FLJ10737		W87554	0.1	0.2	5.1
42937_at			H45282	2.5	1.9	5.1
59792 i at			N30160	1	2.2	5.1
44363_at			AI822115	1.8	2.1	5.1
1	desmin	DES	AA527080	9.0	0	5.1
56685_at			AA603472	2.7	1.3	5.1
51778_at			Н66807	0	2.2	5.1
65351 r at			AA146979	5.9	3.2	5.1
52516_at			R44595	0.2	6.0	5.1
47016 at	***************************************		AA993031	0	2	5.1
58170_at			AA813190	2.5	1.3	5.1
55612_at			AA662107	2.3	2.4	5.1
44981 s at			44115266	502	45	u

Figure 13VVV

60138 24			AI675130	1.2	1.4	r.
T			AI823497	3.3	1.1	ιc
Section of the second s	determining region 1) box 22	S0X22	AA700909	0.2	1.6	باتر
Ť			AI082535	6.0	2.1	1
37007 at solute carrier far	rier ramily 30 (zinc transporter), member 1	SLC30A1	A1553933	4	1.3	ıc
54487 at			W63785	10	9	5 5
58180 at KIAA0042 2242			AA044626	æ	3.1	ıcı
1	: Droteiri		AI073412	17.4	0.2	ic:
T			AI632224	0.7	С) LC
T		CALU	AA234047	0	0	0
T	nypotnetical protein		AW005818	9.0	1.7	2
54535 at			AI762208	6.4	2.2	
78736 r at			AW008207	2.2	2.2	5.1
40409 at aldebyde debydzo	debudromon 10 Martin		AI094933	4.1	3.8	5.1
Π	wolfage denondent anion change?	ALDH10	U46689	5.3	3.9	5.1
Γ	Periode (NIA) II boto (1800)	VDAC3	AF038962	4	0.3	5.1
36601 at vinculin	diase (Divo) ii Deta (100kD)	T0P2B	X68060	3.6	2.7	5.1
	Jantar	VCL	M33308	5.2	4.6	5.1
T	protein 1.7	SLA	D89077	3.5	3.7	5.1
Γ	tein rich in leucinon	RPL17	X53777	2.1	1.8	5.1
Τ	-1		K07969	4.4	2.9	5.1
Τ	and another heat in a constant		T65761	5.3	1.5	5
Т		TGFBI	AI624028	5.1	2.2	5 1
T	ilidase o (alpira polybeptide)	HEXA	M16424	5	1.5	5.1
53857 at			AA773816	5.1	5.1	5.1
84122 at			H09392	1.8	4.9	5.1
49450 at mitogen activated	Ctivated protein kinase kinase kinase 13		A1939453	2.8	4.2	5.1
Γ	The (Drosome macropain) Submit plans 1.3	MAPSKIS	W72274	2.1	3.9	5.1
1	Vacuolar profein corting 11 (vact home les)	PSMA/	AA877820	4.2	3.4	5.1
	vacuolar protein sorting 11 (yeast normalis)	VPS11	AW007365	3.8	1.6	5.1
	thannel 1 hamalan	VPS35	AI961227	2.7	2.9	5.1
1	righted 1, Holliolog		AL048491	5.4		5.1
15 7			AI952279	3.2	23	5 1
040 at Iredu-4-like upidu	e upiquitii-protein ilgase		AI668780	3.9		5 2
33047_at			A1011100	,		

Figure 13WWW

•	inventors:	1.411	nuconen, er ar.	

38241_at			10000	-	70	u
010		BTN3A3	U90548	3.4	V C	שור
10/6_at	interleukin 1, alpha	11.1A	M28983		1.70	
296_at	tubulin, beta polypeptide	TUBB	X79535	91	10.7	ر]،
33716_at			AIOE AAS	0 0	17.7	5
40957_at	KIAA0160 protein	KIAAO160	1,90440		0	5
33804_at	protein tyrosine kinase 2 beta	DTV20	U03881	14.6	17.7	2
39348 at	16	r Inzo	043522	14.6	13.4	5
31935 c at	$\overline{}$	TKW 11 1 1	x99209	2.4	3.5	2
B		DDX11	U75968	8.0	0	5
33480_at	motilin	Z	X15393	7 2		
34562_at	zinc finger protein with interaction domain		V02010	0 0	2.7	5
1030_s_at		TOP1	0102011	7.7	0	5
41601 at		1 0	000/00	6./	2.8	5
41792 at	ATP-binding cassette sub-family C (CETB/MDD) manhar o	0000	AA142964	2.1	3.7	5
36812 at	hreast cancer anti-estrone resistance 3	ABCCS	L78207	0.9	9.0	l.C
40357 at	Inhihin heta A (activin A activin AB alaka	BCAR3	U92715	9.0	3.1	2
37221 at	protein kings AMD dogs activity AB alpha polypeptide)	INHBA	103634	38.6	4.9	1
37552 04	totalis and asset of the comment, regulatory, type II, beta	PRKAR2B	M31158	9	46) [
507 c at		TESK1	D50863	1.7	3.6	ی ایر
30102 34	ers domain	ELF2	U43189	2.5	2.5) 14
39102 dt	epithellai memorane protein 3	EMP3	U87947	4 8	200	7 4
49409 L at			AA910006	0)
63580_at	serologically defined colon cancer antigen 43	SDCCAG43	AIR32477	0 4		0
5382/ at			AA781176	3.7	200	ر ا
/9503_at			AI 036462		700	S
84194 at			T52159	000	0.7	S
84249_at			44503172	1.0	5.1	2
63397_at	Rho associated, coiled coil containing protein kinase 1	DOCK1	2/10000	5.1	1.4	5
48363_at		ועססעו	AI8/2948	2.5	2.6	5
64333 s at	Dyrophosphatase (inorganic)		AA651889	3	3	5
43850 s at	PP1201 protein	ì	AW009649	39.9	10.9	5
75954 at			AA668732	3.4	5.4	5
59745 1 34			AI978606	0		2)
			N99174	2.8	2.2	5
03300 at			AI885627	1.3	2.3	100
4420/_at			AI422986	18.5	7 4	

entors:

73947 at			A1986440	4 1	191	ц
50218_at			AI816806	2.3	1.5	2
78017_at			A1638269	6.0	1.4	5
44839_s_at			AW006891	9	2	5
78252 r_at			AA034137	2.8	1.5	5
75252_at			AI379494	2.5	2.3	5
47773 at			AA836114	1.5	1.5	5
1017_at	mutS (E. coli) homolog 6	MSH6	U73737	0	2	2
43450_at			R50504	1.4	3.4	2
65887_at	transducer of ERBB2, 2	T0B2	A1830948	4	3.4	5
60924_i_at			H63111	0	0	5
33966_at	interleukin 7	الـ7	M29053	8.0	1.7	വ
55988_at	G5b protein		AI446559	7.3	3.5	2
70228 r at	protein kinase, cAl	PRKAR2B	AI792179	5.3	9.7	5
65938_at	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	AL118637	0	0	5
48287_at			AA233912	2.3	1.5	5
48329_at			AA876002	0.7	0.7	S
61433_at			AI887923	5	3.1	5
47644 at			AI963632	2.4	1.3	5
1813_at				1.3	0	5
42295 at			Ai150454	3.1	2.2	5
48889_at			T51931	0	1.1	5
51250 f at			H17134	1.3	1.5	5
53017_at			3144516	0	0	5
74926 <u>r</u> at			AI252805	1	0.5	5
84962 f at			R42423	2.8	9.0	5
86300_at			AA342715	0.1	1.8	2
41603_at	transducin (beta) like 3	TBL3	005609	4.8	3.8	2
1583_at	tumor necrosis factor receptor superfamily, member 18	TNFRSF1B	M32315	0	1.6	5
35170_at	ia, class 2C, member 1	MAN2C1	AF044414	4	2.8	2
35247_at	small nuclear RNA activating complex, polypeptide 5, 19kD		AI557062	5.5	2.9	5
1447_at	proteasome (prosome, macropain) subunit, beta type, 1	PSMB1	D00761	0.2	0.4	S
65130 at			AI749588	4.8	0.5	5
45577_s_at			AI471038	3.4	4.9	5

Inventors:

40011_d(N.acetylglucosamine-1-phosphodiester alpha-N- acetylglucosaminidase		AW007594	5.2	4	C)
49488_at	DKFZP434F1735 protein		AW005775	4.9	3.5	5
45815_at	hypothetical protein		AL048939	4	2.9	2
54479_at			AA214559	5.8	3.9	5
39503 s_at	dihydropyrimidinase-like_4	DPYSL4	AB006713	1.9	0.2	4.9
37140_s_at	ectodermal dysplasia 1, anhidrotic	ED1	AF061193	0.5	0.7	4.9
33011_at	neurotensin receptor 2	NTSR2	Y10148	9.0	0	4.9
37839_at			AL109700	1.6	0	4.9
31861_at	immunoglobulin mu binding protein 2	IGHMBP2	L14754	3.9	1.4	4.9
31890_s_at	zinc finger protein 143 (clone pHZ·1)	ZNF143	AF071771	9.0	0	4.9
38173_at	KIAA1076 protein		AB028999	1.4	1.6	4.9
40141_at	cullin 4B	CUL4B	AB014595	0	1.3	4.9
41208_at	S164 protein		L40392	8.0	1.5	4.9
35438_at	SEX gene		X87852	1.5	6.0	4.9
33360_at	f-box and leucine-rich repeat protein 11	FBXL11	AB023221	9	3.5	4.9
34151_at	DKFZP586M1019 protein		AL050284	1.9	2.5	4.9
41026_f_at	glycophorin E	GYPE	U05255	3.1	1.1	4.9
884_at	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3	ITGA3	M59911	2.1	2.5	4.9
	receptor)					
33555_at	immunoglobulin-like transcript 7		AF041261	1.5	0.2	4.9
39986_at	DKFZP586D0919 protein		AL050100	16.5	4.2	4.9
1584_at	cell division cycle 25C	CDC25C	M34065	3.1	1.8	4.9
36859_at	non-metastatic cells 5, protein expressed in (nucleoside	NMES	AF067724	3.8	0.1	4.9
ø	ATPase, Na+/K+ transporting, beta 2 polypeptide	ATP1B2	AF007876	1.3	0.8	4.9
37746 r at	suppression of tumorigenicity 5	ST5	U15131	0.8	0.1	4.9
37561_at	Inuclear transcription factor Y, alpha	NFYA	AL031778	1.3	1.8	4.9
418_at	antigen identified by monoclonal antibody Ki-67	MKI67	X65550	0.4	0	4.9
320_at	peroxisomal biogenesis factor 6	PEX6	D83703	0	9.0	4.9
38281_at	caspase 7, apoptosis related cysteine protease	CASP7	U67319	22.7	14.4	4.9
38842_at	Leman coiled-coil protein		AB023206	3.1	3.1	4.9
38318_at			AL050128	1.2	1.2	4.9
63309_at	CGI-15 protein		A1241474	4.1	0.4	4.9
10 11000			A1123450	c	0	0 7

Figure 13ZZZ

89795 at			AL040892	3.2	2.1	4.9
65135 at			AI916853	6.9	3.6	4.9
76200 r at			AI095270	2.3	2.4	4.9
57576 r at			AA780978	1.2	1.7	4.9
49536 at			AI733696	2.4	1.8	4.9
90922 at			A1608696	0.5	0.2	4.9
50475 at			AI679625	0	0	4.9
62418 i at			AA908810	0.5	1.2	4.9
56258 f at			AI370094	1	0.2	4.9
54626 at			AI301188	2.2	3.4	4.9
67087 at			AI351909	10.3	6.4	4.9
62174_at	SWI/SNF related, matrix associated, actin dependent regulator of SN chromatin, subfamily b, member 1	SMARCB1	N63449	14.3	1.9	4.9
42773_at			T67520	0.8	1.2	4.9
67336 at			AA525014	2	1.3	4.9
59365 at			D59637	32.9	6.9	4.9
51183 at	transcriptional intermediary factor 1 gamma		85986N	7.5	4.9	4.9
83046_r_at			AI459177	2.7	1.7	4.9
47988_at			AA028166	1.9	1.1	4.9
92163_at			AA504454	8.0	0	4.9
59020_at			AI492162	1.5	0.7	4.9
42690_at			AA034063	3.3	2.3	4.9
64334_at	chromosome 1 open reading frame 2	C10RF2	A1961216	2.6	1.9	4.9
69668_at			A1744371	0.3	0.8	4.9
43050_at			AI613413	2	2.5	4.9
64601_at			AI763164	1.3	1.3	4.9
43065_at	DNA (cytosine-5-)-methyltransferase 3 alpha	DNMT3A	N26002	0.3	1.2	6.4
50376_at	hypothetical protein FLJ11137		A1278629	2.5	3.5	4.9
48205_at			N34861	2	2.8	4.9
65405_at			H67680	0	1	4.9
48867_at			AA527919	8.1	4.4	6.4
60214_at			AA227861	1.8	1.9	4.9
64216_at			H09657	1.3	1.2	4.9
51254 at			A1090139	3.3	3.6	4.9
45975 at			N55070	-	2.3	4.9

53151 at	sex comb on midleg homolog 1		AI660003	12	100	
02/40 at	1100		172588	0.5	0.4	1, 1, 0
40234 at	Cal-146 protein		AA043242			
55959_at			04178020		7 1	4.9
64743_at			07C330	3.7	5./	4.9
64342_at	connective tissue growth factor	1010	1800330		0.5	4.9
46296_at	hypothetical protein FLJ10579	Cler.	AW008273	9.3	2.1	4.9
60968 at			W60903	2.4	8.9	4.9
47134 at			AI990212	25.3	8.3	4.9
1630 s at	Spleen tyrosine kinase		Al935766	0	1.3	4.9
37737 at	protein. Lisoaspartate (Discourtate) Complete It	SYK	729630	5.1	3.9	4.9
38011 at	RPRS, mediating protein	PCMT1	D25547	1.9	0.5	
38789 at	Protection Remarks the second of the second		AB006572	5.3	2	49
57545 at	children of sandil syndrome)	TXT	L12711	4.6	3.3	
48750 at	class I cytokine receptor		AA706499	3.6	1.7	4 9
44705 at			AI983115	5.2	4.6	
64309 4 24	\neg		AA133356	4.7	3.0	
\n	disease)	АРР	AI625555	0.1	8.0	
45276 g at	protein x 0001		0.0001			
51123_at			W30943	3.4	e	4.9
57156_at	HSPC023 protein		H11724	5.2	5	6.4
52044 at	hypothetical protein FI 122649 similar to signal postidio		W92964	3.4	3.2	4.9
1	SPC22/23	FLJ22649	AI801545	0.4	3.8	4.9
44079_at	general transcription factor IIIA	CTESA				
46719_at		20	AA166851	4.5	3.9	4.9
47093_at			A1499694	0.3	0.1	4.9
38659_at	Suppressor of clear. C. elegans, homolog of		AA527178	5.4	4.5	4.9
41662_at			AB020669	3.5	3.3	4.8
39723 at			AL050272	1.4	2.2	4.8
40445 at	e factor 3 (ets domain transcription factor	CUL1	AF062536	16	6.5	4 8
	cets domain transcription factor, epithelial	ELF3	AF017307	8.0	0	4.8
1420 s at	lation initiation factor 4A, isoform 2	EIF4A2	D30655	2.2		
72267 -+	AAT-binding transcription factor)	NFIC	X12492		4:2	200
3338/ at		GAS7	AB007854			φ Σ
420_at	Imelanocortin 2 receptor (adrenocorticotropic hormone)	MC2R	X65633			χ.
			200000	7 - 7	5	4.8

Figure 13BBBB

39616 at			AI 050227	185	C	α V
35824_at	zinc finger protein 238	ZNF238	AJ223321			2 4
430_at	Inucleoside phosphorylase	NP PN	X00737	86	C	4 8
1289_at	glutathione S-transferase M5	GSTM5	L02321	2		4 8
438_at	protein kinase, cAMP-dependent, catalytic, alpha	PRKACA	X07767	1.5	1.2	4 8
37334_at		HNRPA0	U23803	0	0.1	4 8
197_at		NME3	U29656	0.8	0	4.8
40749_at	nning 4-domains, subfamily A, member 2 (Fc	MS4A2	X07203	2.6	0	
	-1					
48782 at	putative nuclear protein		AL040705	0	1.1	4.8
50795_at			A1693592	0.5	0	4.8
67002_at			AI025553	1.9	2	4.8
49415_at			AI027972	0.7	0.8	4.8
78715_at			AI379702	2.3	Œ	4.8
58052_at			W90549	1.3	0.5	4.8
59210_at			T79178	2.7	m	4.8
55556_at			AA968469	1.6	2.8	4.8
62066_at			AI919146	1.4	1.4	4.8
65268_at			AA526937	0.4	9.0	4.8
55194_at			AI638607	7.9	4.1	4.8
58302_at			AA971619	1.4	2.4	
84320_at			AA602573	3.2	3.5	4.8
			AA017033	6.9	m	4.8
88673 f at	hypothetical protein DKFZp434H247		T41344	0.8	1.2	4.8
43225 i at			AA001052	9.5	4	4.8
43231_at			N70008	4.6	2.8	4.8
59054_at			AA489100	4.1	6.6	4.8
55343 at			AI557402	8	3.6	4.8
4434/at			N53347	3.8	1.3	4.8
/2264_at			AI948563	0	9.0	4.8
56319_at	cofactor required for Sp1 transcriptional activation, subunit 6 (77kD)	CRSP6	C05931	4.3	2.7	4.8
59667_at			AW016310	1.6	0 7	4.8
60860_f_at			AI086805	0	1.2	
43103_at			AA394147	0.5	6.0	4.8

			R66718	0.8	6.0	4.8
			W85737	0.5	2.3	4.8
52744_at			T70610	0.5	2.2	4.8
32909_at	aquaporin 5	AQP5	U46569	1.3	0	4.8
59574_at			AI807378	4	1.3	4.8
54198_at			AA262451	0.4	0.7	4.8
45165_at			AI831506	7.8	3.2	4
54296_at			N35708	1.1	2.4	4 8
53156_at			D80679	3.2	1.1	4 8
45004_r_at			N46092	2.1	1.4	4.8
41886 r at			R85286	7.4	1.2	4.8
55309_at			W90521	0.2	1.3	4.8
64795_at			AA127743	1.2	1.4	4.8
/5246_s_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	SLC1A3	W26838	43.1	7.2	4.8
42034_at			AA250845	e -	23	α
43599_at			T62955	8 1	2.5	4 8
70119_at			AI766259	1.4	1.4	4
70656_at			AI827487	0.5	0.8	4
/346/ 1 at			AI799544	9.0	0.7	4
88572_at			AI652684	2.2	2.3	4
40826_at	MAP/microtubul	MARK3	M80359	2.9	1.9	4
32749_s_at	filamin A, alpha (FLNA	AL050396	e	2.8	4 8
56821_at	hypothetical protein FLJ10815		AI963454	3.9	4.1	4.8
65813 at	zinc finger protein homologous to Zfp 36 in mouse	ZFP36	N32721	3.9	2.8	4.8
48568_at			AA305994	2.5	1.3	4.8
63/93_at	UNA polymerase epsilon p12 subunit		AI797479	5.4	3.7	4.8
65/66_at	hypothetical protein LOC58481		AI335452	2.8	2.4	4.8
44823 s at			AA521476	4.7	4.4	4.8
46315 at			AA233808	e	3.5	4.8
44842 at	COP9 complex subunit /a		AI971871	3.4	2.9	4.8
49633_at	hypothetical protein HES6		N21131	4.9	4.9	4 8
399/1_at		LYL1	M22637	4.8	3.5	4.8
53120 at	hypothetical protein FLJ20442		AI681916	5.2	4.3	4.8
54878_at			AL048421	4.9	3.8	4.8

Figure 13DDDD

47077 at			AI697908	1.5	1.9	4.8
38624_at	solute carrier family 12 (potassium/chloride transporters),	SLC12A4	AF054506	1	0	4.7
39559_at	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	KMO	AF056032	4.2	1.3	4.7
38704_at	actin binding protein; macrophin (microfilament and actin		AB007934	3.8	3.6	4.7
	filament cross linker protein)					
41678_at	EphB2	EPHB2	AF025304	0.8	7.5	4.7
34940 at			AL080095	1	0	4.7
39701 at	paternally expressed 3	PEG3	AB006625	1.3	0	4.7
31408 at	retinal pigment epithelium derived rhodopsin homolog	RRH	AF012270	0.4	0	4.7
40454 at	FAT tumor suppressor (Drosophila) homolog	FAT	X87241	0.2	1.3	4.7
40559 at			AL096727	1.2	0	4.7
41126_at	solute carrier family 1 (glutamate/neutral amino acid	SLC1A4	AA978353	5.7	7.9	4.7
	transporter), member 4					
32297_s_at	s_at_killer cell lectin-like receptor subfamily C, member 2	KLRC2	AJ001684	0.2	0	4.7
	gamma tubulin ring complex protein (76p gene)		W28255	6.0	1	4.7
41331 at			R93981	2	1.2	4.7
33463 at	xanthene dehydrogenase	ХDН	U39487	1	9.0	4.7
38986 at	glucose regulated protein, 58kD	GRP58	249835	7.9	16.1	4.7
33493 at	erythroid differentiation and denucleation factor 1		AF048849	1.8	9.0	4.7
38216 at	thyroid hormone receptor interactor 8	TRIP8	L40411	1.1	9.0	4.7
36069 at	KIAA0456 protein		AB007925	0	3.7	4.7
36456_at	DKFZP5641052 protein		AL080063	10.7	6.9	4.7
40322 at	interleukin 1 receptor-like 1	IL1RL1	D12763	1.5	0.2	4.7
37308_at	KIAA1624 protein		AI888084	2.5	3	4.7
35847_at	ubiquitin specific protease 24	USP24	AB028980	3.7	Ř	4.7
121_at	paired box gene 8	PAX8	66969X	2	1.2	4.7
36872_at	cyclic AMP phosphoprotein, 19 kD		AL120559	13.9	12.3	4.7
36122_at	proteasome (prosome, macropain) subunit, alpha type, 6	PSMA6	X59417	7.7	3.3	4.7
36966_at	ankyrin 3, node of Ranvier (ankyrin G)	ANK3	U43965	1.8	0	4.7
37201_at	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive	171H4	D38535	0.6	2.9	4.7
	Sycoprocenty		1	1		
41002_at	solute carrier family 16 (monocarboxylic acid transporters), imember 5	SLC16A5	U59299	9.0	0.3	4./
39158 at	activating transcription factor 5	ATF5	AB021663	6.7	9.9	4.7

41075 at	A kinase (PRKA) anchor protein 3	AKAP3	AF087003	1.9	0.8	4.7
46462_at			AI822047	9.0	0.4	4.7
58008_at			AA521240	0.4	0.5	4.7
48088_at			AI300073	0	3.3	4.7
47174_r_at			AA285149	2.4	1.8	4.7
.66352_at			AI003755	0.2	0.7	4.7
58030_at			AA845345	1.8	6.0	4.7
77208_at			AI732988	1.4	1.9	4.7
77298_at			AI675783	0.2	2.7	4.7
54069 at	hypothetical protein		AI431793	0.1	1.2	4.7
91011_at			A1668698	2.5	0	4.7
53456_at			T61326	1.6	0.2	4.7
55868_at	cadherin-like 24	CDH24	A1820755	1.9	1.7	4.7
44742_s_at	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2		AA205994	10.7	5.1	4.7
42816_at			238762	4.2	1.2	4.7
58366_at			R71447	0	0	4.7
47961_at			AW013851	1.4	1.3	4.7
83066_r_at			AI536659	-	3.4	4.7
48371_at	aldehyde dehydrogenase 12		N70701	9.0	1.7	4.7
51675_at			AI791859	1.6	1.6	4.7
63074_at			AA570454	4	3.7	4.7
69658_at			AI754641	9.0	0.5	4.7
42916_at			H53950	2.5	1.1	4.7
63900_at			R42022	0	1.6	4.7
42866_s_at			AW003230	1.5	4.5	4.7
49165_at	hypothetical protein PR02013		AW024795	0	2	4.7
45434 at			H05785	3.3	1.2	4.7
56681_at			AA628511	0	9.0	4.7
43998_at	hypothetical protein FLJ11159		AI954729	0	9.0	4.7
47805_at			AL046561	1.1	2.3	4.7
60872_at	ribosomal protein S19	RPS19	N91770	1.7	2.8	4.7
54820_at			AA203581	1	1.7	4.7
54933_at			AI356461	11.3	8.8	4.7
45890 at			W21855	· ·	1.3	4.7

Figure 13FFFF

65265_r_at			T90778	0	0.71	4.7
65795_r_at			AL042362	9.4	66	4 7
59474_at			AI924028	0.5		4.7
60143 r at			H71532	2.2	12	4.7
59493_at			AA521317	1 3	2 5	47
45788_i_at	mannosyl (alpha-1,3-) glycoprotein beta-1,4-N. acetylglucosaminyltransferase, isoenzyme B.	MGAT4B	AI741591	2.2	2.6	4.7
46090_at			AARO6216	0 %	0 0	7
261_s_at	apolipoprotein B (including Ag(x) antigen)	APOB	M19828	300	0 6	4.7
63457 f at			AA022988	3 2 5	t 00	4.7
49213 s at	KIAA1557 protein		AI692432	0.7	1.2	4.7
46025 at			AA040740	6.4	3.5	4 7
55829_at			AA058944	3.7	2.9	4 7
53975_at	KIAA1151 protein		Z78399	23.6	3.4	4.7
55869_at			R58910	1.6		4 7
47872 at			AI417194	1.9	1.3	4 7
54985_at			AI346820	2.8		4 7
46997_at	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4		N74643		2.1	4.7
51028_at			A1218306	3 6	6 3	Ţ,
57452_at			AA451798	2.0	0.0	4.
51667_f_at			NESORR	200	6.0	4.7
32166_at	KiAA1027 protein		AB028950	000	0 6	4.7
32229_at	eukaryotic translation initiation factor 4E-like 3	EIF4EL3	AF038957	1.1	0.00	4.7
34368_at	histone deacetylase 2	HDAC2	U31814	4.4	0	4.7
32518_at	zinc finger protein 259	ZNF259	AF019767	0.8	0	4.7
43422 at	CD27-binding (Siva) protein		AW025365	3.9	3.3	4.7
53884 at	7		AA312905	4.9	3.9	4 7
33689 s at	U-dopachrome tautomerase	DDT	AF012434	4.5	1.8	4 7
42831_at			AI201843	4.7	4.2	4 7
45/12 at			Н98166	3.3	2.6	4 7
65620 at			W52855	4.6	4.4	4.7
77017 24		PDK4	AI763378	0.3	3.7	4.7
3/842_at	II-mta domain-containing protein		AF054589	1.5	3.2	4.7

Figure 13GGGG

	 	,,,	CT	u

35434_at	MADS box transcription enhancer factor 2, polypeptide D	MFF2D	1116797	1 1	0 4	-
	(myocyte enhancer factor 2D))	1000	T : T	0.	0.4
39866_at	ubiquitin specific protease 22	USP22	AR028986	90	0 0	0 0
31309_r_at			1150277		o c	1
41695 at	KiAA0414 protein		10	0.4	0.0	0.4
39490 f at	ADP-ribosylation factor GTPase activating protein 1	ADECADI	MOC201	0 0	2.2	4.6
39696 21	16	ד ואס ויוע	WZ0301	7	4.0	4.6
24051 24			AB028974	0.8	0	4.6
34901 at	re receptor; GTP binding protein		D10923	6.3	3.2	4.6
1310_at	proteasome (prosome, macropain) subunit, beta type, 2	PSMB2	D26599	5.5	7	46
40149_at			AL049924	C	C	7 6
	prostaglandin D2 receptor (DP)	PTGDR	U31099	13		0 4
38171_at	WD-repeat protein		1194747	250		7
1969_s_at	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk.	CDK7	X77743		1 2	1
	activating kinase)	:	?		0.1	0.4
31594_at	keratin, hair, acidic, 3A	KR1HA3A	Y16788	1.2	0	91
32868_at	transglutaminase 3 (E polypeptide, protein glutamine gamma.	TGM3	110386	100		7
	Ö)	L10386			4.6
292_s_at	CDC-like kinase1	CLK1	M59287	7		0 4
32250_at	H factor 1 (complement)	HEI	V07522	7 0		0.1
35186 at		7	270,00	4.5	6.7	4.6
10631 24	translation of EDDDo 1		AJ009770	1.7	1	4.6
10001 at	Maisuucei oi Endbz, 1	T0B1	D38305	0	0.3	4.6
34 / / 9_at	IneuAcaipha-z, 3-dal-beta-1, 3-dalNAc-alpha-2, 6-sialyltransferase		R90942	1	0.1	46
1	alpha2,6-sialyltransferase			1		j f
35143_at	KIAA1031 protein		AI138605	50.6	24.11	3 /
37358_at	lubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	UBE2E1	A1039880	4.8	1.7	4.6
37715_at	SKI-INTERACTING PROTEIN		AF0/4518/			
38442_at	microfibrillar associated protein 2	MEAP2	1110719	0.1	0.0	4.0
40718 at	cathebsin W (lymphopain)	TOW.	013/10	4.0		4.6
63307 at	KIAA1184 protein	VIOV.	AFU13511	6.3	2.3	4.6
기-			AL041566	15.3	2.5	4.6
			AI357616	1.6	1.3	46
40790 r at			AA421236	0.4	0.4	46
42399 at	١		AA449090	1.5	00	4.6
43022_at	hypothetical protein FLJ22351		AA196189	4.1	2.1	4 6
52929_at			AL044396	4.8	1 5	4 6
					<u> </u>	,

Figure 13HHHH

		,	

57537_at			AA001250	9.6	8.5	4.6
63399_at	E3 ubiquitin ligase SMURF1		AI126305	1.6	1.7	4.6
73870 at			AI700737	0.5	9.0	4.6
90776_at			AA781939	3.3	1.8	4.6
42564_at			W84667	5.1	2.9	4.6
76920_at			AA745592	4.1	3.6	4.6
35593_at	amine oxidase, copper containing 2 (retina specific)	AOC2	AB012943	0.4	6.0	4.6
61991_at			AI147060	1.4	2.6	4.6
84050_at			AI583750	9.0	1.3	4.6
62314_at			H04394	13.8	3.7	4.6
56433_s_at	56433_s_at KIAA0826 protein		AA463908	6.0	1.3	4.6
45471_s_at	aldehyde oxidase 1	AOX1	AI589531	2.3	2.1	4.6
48569_at	48569_at STRIN protein		AI608790	1.5	2.8	4.6
69448_i_at			AI700454	2.8	4.7	4.6
70246_at			AA630253	1	0.2	4.6
57139_at			AI341271	2.2	2	4.6
44804_s_at	hypothetical protein FLJ21313		AI982913	7.4	2.4	4.6
51131_at			AW007736	6.7	8.3	4.6
51872_r_at			AA890487	2.5	2.3	4.6
55549_s_at	Kruppel-type zinc finger protein		AI783578	4	1.2	4.6
75247_f_at			AA548037	3.4	6.5	4.6
62440_at			A1198946	6.3	3.6	4.6
58254_at	interleukin-1 receptor-associated kinase M		AI018069	1.4	2	4.6
60606_r_at			N68442	9.0	0.5	4.6
63718_at			N63823	0	2.1	4.6
43278_at			AA600721	1.1	1.6	4.6
50694_at	Carbonic anhydrase related protein 10		AI815895	4.2	3	4.6
47571_at	zinc finger protein 236	ZNF236	AA004757	6.0	1.3	4.6
52406_s_at			AI125673	0	1.7	4.6
42184_at			AA430269	4.4	1.4	4.6
43970_at			AA557271	6.0	1.1	4.6
49524_at	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	AMMECR1	AI032981	3.6	2.1	4.6
59468 at	SRY (sex determining region Y)-box 11	S0X11	R44341	0.3	2.4	4.6
64326 r at			A1866358	0	2.7	4.6

45119_at			AI638568	0	0	4.6
60129 f at			R92776	0.1	6.0	4.6
49816_at			H50751	1.5	0	4.6
50968_at			AA053842	1.6	1.5	4.6
81806_at	KIAA1681 protein		AI694702	3.7	4.7	4.6
44499_at			N67390	7.8	3.8	4.6
45590_at			AI673025	0.7	1	4.6
45080_at			103765	9.0	1.3	4.6
45700_at	KIAA1209 protein		AI816833	2.6	1.2	4.6
46183 at			AI810826	7	6.2	4.6
54506_at			AI289311	1.3	1.8	4.6
64883_at			AI744083	6.0	2.9	4.6
56005_at			AA044906	3.8	2.6	4.6
46308_at	a disintegrin-like and metalloprotease (reprolysin type) with	ADAMTS1	AI810627	1	9.0	4.6
47152 at	hypothetical protein FLJ20291		N32572	2.1	0.8	4.6
57347_at			AA725801	0	0.8	4.6
49101_at			AI761058	4.1	1.8	4.6
47641_at			AI732810	1	3.1	4.6
1827_s_at			M13929	6.0	0	4.6
64832_at			AA113447	1	0.7	4.6
63121_at			188970	4.2	1.3	4.6
54096_at			3149758	1.8	0.4	4.6
75380_at			AA099289	2.1	2.9	4.6
85307_at			AI469339	4.1	1.2	4.6
76239 r_at			AA059247	2.6	3.9	4.6
824_at			U90313	0.4	0	4.6
38605_at	NADH dehydrogenase (ubiquinone) $1 {\sf beta} {\sf subcomplex}, 1 (7 {\sf kD}, {\sf MNLL})$	NDUFB1	AI345944	3.5	2.1	4.6
40955_at	prostate tumor over expressed gene 1	PTOV1	U79287	5.2	2.6	4.6
33485_at	ribosomal protein L4	RPL4	D23660	3	1.9	4.6
39672_at	protein tyrosine phosphatase, non-receptor type 7	PTPN7	M64322	3.2	4.4	4.6
34406_at			AB011174	4.9	2.7	4.6
34828_at	polymerase (RNA) II (DNA directed) polypeptide I (14.5kD)	POLR21	AL037557	4	2.9	4.6
36639_at	adenylosuccinate lyase	ADSL	AF067853	4.6	ε	4.6

32550_r_at	CCAAT/enhancer binding protein (C/EBP), alpha	CERPA	V1162E		,	
37029 at	ATD everthage HI transmorting mithable did 1	ל ייי	111223	υ. υ.	4.9	4.6
10 / C	synthase, it it transporting, innoctionarial r1 complex, U subunit (oligomycin sensitivity conferring protein)	Alpo	X83218	4.1	2.2	4.6
48055_at			NEGEAN	<	C	
56906 at			100040	1 1	2.3	4.6
65578 at	cathensin S	COL	AM193410	4.7	4.1	4.6
56225 at		200	AI81/14/	2.4	2.2	4.6
50700			AI744466	5.6	3.3	4.6
28/80 s at	nypotnetical protein FLJ1035/		R42449	5	2.6	46
43053 g at			AW025012	4 9	3.2	97
44085_at			A1 040188			1,
46098_at			AAA02100	1 0	4 0	4.6
46594 at	hypothetical protein FLJ20186		00277000	4 1	1.2	4.6
5/150 24			AW014/80	4.5	4.3	4.6
14100 at			AI453531	4.3	2.8	4.6
52313_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A	HADHA	AI972144	3.9	2.4	4.6
	(trifunctional protein), alpha subunit subunit			-		
41113 at	KIAA0557 protein					
20000			AI871396	1	0.4	4.5
33000_at	NOCE (Lys-Asp-Giu-Leu) endoplasmic reticulum protein retention receptor 2	KDELR2	M88458	0	0.3	4.5
35527_at	lannel, voltage-dependent, alpha 2/delta subunit 1	CACNAPPI	M76560	2		
40204_at		CTRI	X71877	0.0	4.0	4.5
192 at	protein (TBP), associated factor DNA	1,10	// 10/ /	0.1	5.1	4.5
	STATE (15) Passociated factor, KINA	IAFZF	018062	1.4	1.2	4.5
40570_at	forkhead box O1A (rhabdomyosarcoma)	FOX01A	AF032885	6.1	c	
40803_at			AI 050161	0.1	0.1	0.4
41142 at	Se	OXCT	1162961	0.0	3.0	Q. 4
41232_at	DKFZP564D116 protein		AI 050022	1 2	0.0	0.4
32227_at	cretory granule	PRG1	X17042	1.0		4.5
32780_at			1701001		5.4	4.5
32104 i at	in dependent protein kinase (CaM kinase) II	000000	MD0102/1	12.4		4.5
	The second by the second secon	CAMINAG	066063	1.3	0.5	4.5
34149_at	(PRL1, Arabidopsis homolog)	PLRG1	W28558		C	
34299_at		ZNF278	ALOGERRO	1-1-		0 L
38662_at			AI 047596	7:1	2.3	U. 4
35321 at	tousled-like kinase 2	1170	000,000	5 (3.1	4.5
5	7	ILNZ	AB004884	7.8	7.3	4.5

35346 at	FEM. 1 (Clelegans) homolog h	FEMIR	1AB007856	α 0	-	1 5
2000	Later A (Conception) money as a series of the series of th	CACOA	0007000	0.5	1 0	7
195_s_at	caspase 4, apoptosis-related cysteine protease	CASP4	028014	11.6		4.5
1271 g at	wrel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in Bidelle 3 (negs)	RELA	L19067	3.6	2.9	4.5
32439 at	ATPase H+/K+ exchanging beta polypeptide	ATP4R	M75110	7.0	0 7	4 5
38105 at	hypothetical protein FLJ11021 similar to splicing factor.		W26521	100	0.6	
	arginine/serine-rich 4			1))
37645_at	CD69 antigen (p60, early T-cell activation antigen)	69GD	222576	3.9	0.8	4.5
1064_at	protein tyrosine kinase 9	PTK9	002680	2.2	1	4.5
38440 s_at	hypothetical protein		AA015605	0.1	2.8	4.5
49880_at	_		R60061	2	1.6	4.5
56143_at			N32840	1.8	0.7	4.5
48158_at	transforming, acidic coiled-coil containing protein 3	TACC3	AA098825	1.1	1.1	4.5
56806_at			AI809891	1.5	3.3	4.5
50757_at			AA418074	3.3	1.3	4.5
54686_at	thyroid hormone receptor associated protein, 240 kDa subunit		AA122265	m	2.5	4.5
66519 at			44845423	a C		, a
77400			277777	0.0	7 7	† ·
4/460 at			N64/94	9.4	7.7	4.5
48854 i at			AW025683	4	2.1	4.5
51367_at			A1189446	0.2	8.0	4.5
80256_at			AI167159	0	0.2	4.5
62081_at			AI209079	1.4	0	4.5
47144 at	ASB-1 protein		AI018173	5.7	4.1	4.5
61971_at			AI986197	1.5	0.4	4.5
57838_at	hypothetical protein FLJ10111		AA196477	2.3	2.4	4.5
82914_at			AI767564	1.9	2.4	4.5
65814_at			N95618	5.5	5.2	4.5
59566_at			AA705681	5.2	1.5	4.5
62147_at	hypothetical protein FLJ11155		A1265860	4.2	0.5	4.5
43784 r at	tumor necrosis factor receptor superfamily, member 7	TNFRSF7	H83425	0.5	1.7	4.5
60504_at			AI859849	13	3.8	4.5
65670_at			AA489239	1.7	0	4.5
44977 g at			AI972721	0	0.1	4.5

Figure 13LLLL

73725 at			A1991175	1.3	1.8	4.5
65225 r at			R93729	2.8	2.5	4.5
56955 f at			Н95587	1.4	0.4	4.5
T	hypothetical protein FLJ11210		AA056538	0	0	4.5
51680 at		MGP	AW023159	2.1	9.0	4.5
Г			AI741373	8.0	0.4	4.5
69126 at			AA470958	9.0	4.2	4.5
64086 at			AA004211	1.1	0.5	4.5
62712 r at			AI870532	1.8	1.3	4.5
63662 at			A1126468	12.6	6.9	4.5
45167 at	homeo box C9	HOXC9	AI332412	1.6	1.2	4.5
46812 at			N78361	0.1	6.0	4.5
45654 at			AI808746	1.6	1.6	4.5
j të	KIAA1634 protein		AI692181	0	2.6	4.5
at			AA190571	6.0	4.3	4.5
gat	keratin 18	KRT18	AI984261	1.1	2	4.5
at			240682	0.3	6.0	4.5
46663 at			A1147033	2.2	1.7	4.5
at	hypothetical protein FLJ10587		N29706	2.3	1.8	4.5
42247 at			AA460661	2	1.4	4.5
76101 at			AA243778	1.8	0.8	4.5
38990 at	F-box only protein 9	FBX09	AL031178	3.6	1.6	4.5
1228 s at	meningioma expressed antigen 6 (coiled coil proline rich)	MGEA6	U73682	2.6	2.3	4.5
36194_at		LRPAP1	M63959	3.9	0.5	4.5
	Z-macroglobulin receptor-associated protein 1)		LOSOFE	4	00	7 7
aı	EBIAR-Z CO-activator (100AD)		022033		0.0	7 4
38050_at	KIAAU164 gene product		0/9980		/: 1	4
38713_at	septin 3	03-Sep	p 299716	4.9		4.5
53799_at	hypothetical protein similar to mouse Dnajl1		AA628434	0	0.4	4.5
43406_s_at	ZAP3 protein		AA890650	4.4	3.1	4.5
58410_at	cat eye syndrome chromosome region, candidate 1	CECR1	A1572068	3.7	3.4	4.5
49569_at	hypothetical protein FLJ20281		AI690893	5.1	4.2	4.5
63544_at			N33295	3.9	2.7	4.5
66112_at	translocase of inner mitochondrial membrane 17 (yeast) homolog		AA234191	3.3	1.4	4.5
	▼					

Figure 13MMMM

56310_at	hypothetical protein FLJ10893		A1824054	دد	121	
51163_at	hypothetical protein FLJ22405		AA115361	1 0	0.0	
57031_at	ZYG homolog		A1901574	0.0	6.3	
65762 at			4100174	7.0	2.1	4.5
65748 at			AI201/92	3.8	1.2	4.5
52596 4 34			AA531437	2.9	1.6	4.5
54406 at			R52511	2.3	0.8	4 5
044400	hypothetical protein UKFZp/6Zi166		AI341234	4	22	7 2
6448/_at			H16514	8	-	7
45115 at			AA909042	4 3	0 1	7 4
	non-metastatic cells 3, protein expressed in	NME3	AW014797	3.2	3 1	4 L
46311 at	CGi-139 protein		AI525879	4	0	1,5
00120 at			AI769737	0 1	200	4 4
39872_at	cadherin, EGF LAG seven pass G-type receptor 1, flamingo	CELSR1	AL031588	17.5		C. 4
0.0	(Urosopnija) nomolog)	i
41856 at			AL 049370	0	0	
39708_at	signal transducer and activator of transcription 3 (acute-phase	STAT3	1 20277	0,00		4.4
	response factor))	//7677	10.0		4.4
37887_at	protein kinase Chk2		AFOOGOOA	C		
763_at	glia maturation factor, beta	CMED	0000004) «	Э	4.4
33072 at	xin) recentor 2	0 1 1 2 2	45001106	5	1.3	4.4
40257 at		FUNI RZ	AF041245	2.2	0	4.4
1456 c at	100	KP528	A 400011	0	2	4 4
40792 5 24	demois (protein 16	IF116	M63838	0.4	2.3	4 4
407.55 at	uomain (PTPRF interacting)	TRIO	AF091395	1	0.4	AA
٧.	MONTHEIRIEU BEIJE A		D14812	1.9		
35347 at	()		AL049782	0.7	0.0	4 4
32471 a at	אוומון לוסווופ-נוכון לתחוש לה	SPRR2C	M21539	1.5	1.4	4.4
			AF052177	2.1	0	VV
32/39 at	MAATII/ protein		AA001791	0.8	0.7	4.0
71017			AL080114	C.		V V
302/0 at	contactin 2 (axonal)	CNTN2	X67734	C C		
36294_at		STK4	1160207	5 5	1.00	4 4
37828_at			A1 050064		0.0	4.4
35978_at	proline-rich Gla (G-carboxyglutamic acid) polypentide 1	PPPC1	AF00004	C:4	1.2	4.4
1728 at	a viral (hmi-1) nnchaene homolog	DIAKT	AF003242	6.3	1.3	4.4
35317 at	a that Collin 1) offered from the collins of the co	בישוו	113689	4.1	0.4	4.4
3231/ar	interinigionia expressed antigen 5 (hyaluronidase)	MGEA5	AB014579	3	3.3	4 4

Figure 13NNNN

Aventors:	rair Haconen, er at.

27110	- 1		AB014560	1.5	3.5	4 4
30118 at	coactivator 1	NCOA1	AJ000882	m		7
36641_at		CAPZA2	U03851	0.4	20	t v
	v-ets avian erythroblastosis virus E26 oncogene homolog 2	ETS2	304102		3.0	1 4
46774 i at			AI888795			1 3
63056_r_at	prostate cancer associated protein 1	PCANAP1	A1525303		0.0	4.4
76105_at			7070797	2.7	Ø G	4.4
66443 at			440400	0.7	8.	4.4
66523 at			AA//5536	0.3	0	4.4
59148 at			AA829524	3.3	m	4.4
66820 at			AI733002	1.2	0.5	4.4
61002 at			AA987549	1.9	1.8	4.4
5355 at			A1147067	C	0.4	0.0
53880 at			AI285891	2.4	0 1	4.4
40/10 at	endoplasmic reticulum oxidoreductin 1-Lbeta		AA001399	12.2	2	7 7
91304 at			AI928094		2 -	7 7
332/4 at			R66045	11.7	2 9	7 7
02923 at			AI312844	13	1 2	
84235 at	pre-B-cell leukemia transcription factor 1	PBX1	AW005924	9.0	20	10
01100 at			AA005089	2.6	60	4.4
			H12221	1.9		4.4
93077 24			AI768586	1.5	5.1	4.4
55056 at			AI024818	23.9	7.8	4 4
51042 at			AA923551	3.3	2.8	4 4
86613 at			AA142984	3.4	2.6	4 4
87506 at			R01897	2	1.2	4 4
63104 at			N80159	1	1.9	4 4
68969 at			H98113	0	0.8	4 4
80894 at	historia acatultransforms		AI679892	4.2	2	4 4
49168 24	חומכונים מכפולונו מוומופן מספ		AA553554	5.7	1.9	4 4
52522 at			AA151917	3.2	2.2	4.4
79405 at	poly(A) binding protoin orthographic 1 191		H06408	3.6	1.3	4.4
50100 at	Population process, cytopiasissic 1-like		AA740146	1.5	1.1	4.4
87/185 r at			AA845353	1.2	1.8	4.4
68299 34			T78883	2.5	2.5	4.4
2017			******	1		

IN HITEGRACION SILE JAMINY, MEMBER 4
synthase (cytochrome c heme-lyase)

Figure 13PPPP

34826_at	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	SDHA	L21936	3.6	0.8	4.4
39086_g_at	single-stranded DNA-binding protein	SSBP	AA768912	2.6	1.2	4.4
75026_s_at	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	MTHFD2	AI990317	0	9.0	4.4
54869_at			AA287799	3.9	3.7	4.4
63840_r_at	hypothetical protein FLJ22318		AA151600	2.1	2.4	4.4
51149_at			AA421991	6.0	3.8	4.4
45339_at	CGI-39 protein; cell death-regulatory protein GRIM19		AA181145	3.3	3.7	4.4
45335_at	CGI-28 protein		AI037884	4.1	2.7	4.4
44654_at			A1669655	3.4	4	4.4
51239_at	hypothetical protein FLJ23239		W67828	4.9	3.8	4.4
52159_at	HEMK homolog 7kb		W93807	2.4	1.7	4.4
50071_at			AL042592	3.3	3.1	4.4
65930_at	30S ribosomal protein S7 homolog		N78337	4.3	2.5	4.4
48731_at			AI948491	4.1	1.6	4.4
38973_at	KIAA1020 protein		AB028943	-	8.0	4.3
38149_at	KIAA0053 gene product		D29642	9.1	8.7	4.3
32673_at	butyrophilin, subfamily 2, member A1	BTN2A1	U90543	6.5	2.5	4.3
	kallikrein 3, (prostate specific antigen)	KLK3	X07730	1	0.7	4.3
	peroxiredoxin 1	PRDX1	X67951	0.4	1.9	4.3
ᆈ	KIAA0737 gene product		AB018280	1.5	1.5	4.3
- 1	interferon, alpha 2	IFNA2	1000207	6.0	0	4.3
	KIAA0197 protein		D83781	2.9	5.2	4.3
39508_at	N-myc downstream-regulated gene 2	NDRG2	AI201607	2.9	1.8	4.3
36256_at	limbic system associated membrane protein	LSAMP	U41901	1.7	1.5	4.3
38982_at	TRF2-interacting telomeric RAP1 protein		W28865	4.4	1.6	4.3
37383_f_at	major histocompatibility complex, class I, B	HLA.B	X58536	4	2.7	4.3
32140_at	sortilin related receptor, L(DLR class) A repeats containing	SORL1	Y08110	1.1	7.0	4.3
35228_at	carnitine palmitoyltransferase I, muscle	CPT1B	Y08682	2.5	4.5	4.3
34575_f_at		MAGEA5	U10689	m	0.4	4.3
35726_at	5100 calcium-bin	S100A2	A1539439	2.7	9.0	4.3
35987_g_at	member of MYST family histone acetyl transferases, homolog of Drosophila MOF		AL050395	0	0	4.3
40005_at	alkylation repair; alkB homolog		X91992	2.4	1.7	4.3

1.8	30/32 s at	Interleukin 5 recep	IL5RA	M75914	0.6	0.5	4.3
decoxycytidine kinase DCK M60527 0.3 at ining finger protein 3 DCK M60524 3.6 at ining finger protein 3 DCK M60524 3.6 at ining finger protein 3 DCK M70533 0.9 at ining finger protein 3 DCK DCK DCK DCK at ining finger protein MGC2628 DCK DCK DCK DCK at ining finger protein MGC2628 DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK DCK at DCK DCK DCK DCK DCK DCK DCK DCK at DCK	4033/_at	ě č	FUT1	M35531	1.8		4.3
at protein predicted by clone 23882 DUCK WB0327 0.3 at protein predicted by clone 23882 MAT2A WB0327 0.3 at ring finger protein 3 AK53465 0.9 0.9 at ring finger protein 3 AK23465 0.9 0.9 at at ribulose-5-phosphate-3-epimerase RPE AK52893 3.7 at at ribulose-5-phosphate-3-epimerase RPE AK628983 3.7 at their/venhancer-of-split related with YRPW motif 2 HEY2 NA628980 0.3 at their/venhancer of-split related with YRPW motif 2 HEY2 AK62890 0.5 at the protein MGC2628 AK462890 0.5 4.0 at the protein MGC2628 AK48897 1.1 4.0 at the protein MGC2628 AK48897 1.2 4.0 at the protein MGC2628 AK48897 1.2	886 at	deoxycytidine kinase	700				
MATCA M27954 3.8	37340 24		Y)	M60527			4.3
Arching finger protein 3	37.340_81	osyltransterase II,	MAT2A	W27954		1.1	4.3
Act Fing linger protein 3 Act Act	406// at	줐		AF054984	2.1	8 1	43
Abcompanies	3/964_at		RNF3	W25793	60		0. 6
Algorithm Algo	55747_at			AA534565	23		t C
g at at at at at at at at at at at at at				N39954	8.4	280	t c
at ribulose-5-phosphate-3-epimerase RPE AA6272519 3.7 at ribulose-5-phosphate-3-epimerase RPE AA677561 1.3 at ribulose-5-phosphate-3-epimerase RPE AA677561 1.3 at hairy/enhancer-of-split related with YRPw motif 2 HEY2 R03374 0.3 at hairy/enhancer-of-split related with YRPw motif 2 HEY2 R03374 0.3 at hairy/enhancer-of-split related with YRPw motif 2 HEY2 R03374 0.3 at at hairy/enhancer-of-split related with YRPw motif 2 HEY2 R03374 0.3 at at hairy/enhancer-of-split related with YRPw motif 2 HEY2 R03374 0.3 at at hairy/enhancer-of-split related with YRPw motif 2 HEY2 R03374 0.3 at at hairy/enhancer-of-split related with YRPw motif 2 HA621047 4.1 at AA278620 0 AA631047 4.1 at AA631047 0.3 at AA676235 0.4 at AA632505 0.4 at AA632505 0.3 at HIA4389 protein R03262505 4 at AA632505 0.3 at HIA4389 protein R032635 0.4 at AA632505 0.3 at HIA4389 protein R032635 0.4 at R0438387 0.3 at HIA4389 protein R032635 0.4 at R0438387 0.3 at HIA4389 protein R032635 0.4 at R032637 0.3 at R032637				AI963304	4 4	3.6	1.5
AA628983 3.7 AA677561 13 AA677561 13 AA677561 13 AA677561 13 AA677561 13 AA677561 13 AA677561 19 AA67761 19	50/8/_at			AA527219	3.7	α κ	5
Additional and part of the protein both both both both both both both both	42502_at			AA628983	37.	0.00	0.4
at ribulose-5-phosphate-3-epimerase RPE AA252480 0.8 at hairy/enhancer.of-split related with YRPW motif 2 HEY2 R93374 0.3 at at hairy/enhancer.of-split related with YRPW motif 2 HEY2 NA6845 0.7 at at at hypothetical protein MGC2628 AA948597 1.9 4.1 at at hypothetical protein MGC2628 AA018217 2.8 4.1 at at pregulated by 1,25-dihydroxyvitamin D-3 AA018217 2.8 4.9 at at KIAA1389 protein AA13812 1.5 4.1 4.1 at at by at at at by at at at at at at at at at at at at at	47188_at			AA677561	, i.	2.0	4.4
at AG262400 US at AG262400 US at AG26338 US at AG26337 US at AG2630 US at AG2850 US at AG28507 US at AG28507 US at AG28507 AJ at AG28507 AJ at AG28507 AJ at AG21047 AJ b. at AM018217 AJ at AM018217 AJ at AM13872 A b. at AM13872 A at AM13872 AJ at AM83387 AM83387 AM265505 at AM83387 AM555505 AM565505 at AM555505 AM555505 AM555505	61114_at		APF	AA252460	2 0	4.7	4.3
at AIGAZ4538 1.9 at hairy/enhancer of split related with YRPW motif 2 HEY2 N46845 0.3 at AIGA3374 0.7 1.8 at AIGA845 0.7 1.8 at AIGA845 0.7 1.8 at AIGA88597 1.9 4 at ARA218670 0.5 4 at AAC1827 0.5 4 at AVO182672 0.6 4 at AVO18217 2.8 4 at AVA13875 0.4 4 at AAI36735 0.4 4 at AAI36735 0.4 AAI36735 0.4 at AA883387 3 AA883387 3 at Putative G protein-coupled receptor 92 AA864327 0.9 at Putative G protein-coupled receptor 92 AA864327 1.9			1	MAC3C400	0.8	6.1	4.3
at hairy/enhancer-of-split related with YRPW motif 2 HEY2 R93374 0.3 at at at at at at at at at at at at at a	51243 at			AI024938	1.9	2.7	4.3
According to the protein motification with TkPW motification with		The Control of the Co		R93374	0.3	1.4	4.3
Ali 1932/7 1.8 Ali 1932/7 0.5 Ali 1932/5 0.5 0.5 Ali 1932/5 0.5 0.5 Ali 1932/5 0.5		I Split related with YRPW motif	HEY2	N46845	0.7	1.2	4.3
Ali	73502 at			AI793177	1.8	0.8	43
AA948597 1.9 AA948597 1.9 AA948597 1.9 AA948597 1.9 AA948597 1.9 AA948597 1.9 AA948597 1.9 AA948597 1.9 AA948597 1.9 AA948597 1.9 AA948597 1.9 AA9483987 1.9 AA9483987 1.9 AA9483987 1.9 AA9483987 1.9 AA9483987 1.9 AA9483987 1.9 AA9483987 1.9 AA883987 1.9 AA883387 1.9 AA8833777 1.9 AA883377 1.	01000 at			AI193207	0.5	1.4	43
Alignospie Ali	03100 at			AA948597	1.9	2	4 3
AAC 21047 4.1 1 1 1 1 1 1 1 1 1	83904 at			AI985614	4	200	1 5
AA278620 0	55253 at			AA621047		38	5.5
hypothetical protein MGC2628	84746_at			AA278620		9 4	4.0
hypothetical protein MGC2628 AA018217 7.8 upregulated by 1,25-dihydroxyvitamin D·3 AW026672 0 KIAA1389 protein AI718112 1 KIAA1389 protein AA136735 0.4 AA136735 0.4 AA136720 1.5 AA833987 3 H94876 2.8 AA862505 0.9 AA864327 1.9	84588_at			A1691077	0 0	0.00	4.0
upregulated by 1,25-dihydroxyvitamin D-3 AW026672 C-0 KIAA1389 protein AI718112 1 KIAA1389 protein R67641 2.4 AA136735 0.4 AA194720 1.5 AA194720 1.5 AA183387 3 AA883987 3 H94876 2.8 AA1652505 0.9 AA864327 1.9	42884_r_at	hypothetical prot		AA018217	000	1.3	0.4
Alignostic Ali	64281_s_at	upregulated by 1,		AW026672	0.7	1.0	4.3
KIAA1389 protein R67641 2.4 KIAA1389 protein AI436735 0.4 AA194720 1.5 AA194720 1.5 AA883987 3 H94876 2.8 AA652505 0.9 AA864327 1.9	86380_at			AI718112		0 0	2.4
KIAA1389 protein A136731 2.4 AA194720 0.4 AA194720 1.5 AA883987 3 H94876 2.8 AA883987 2.8 AA883987 3 AA883987 3 AA883987 3 AA883987 2.8 AA883987 2.8 AA88476 2.8 AA864327 1.9	63279_at			D67641	1	0.0	4.3
AA194720 0.4 3 AA194720 1.5 1. AA883987 3 0 H94876 2.8 2 H94876 2.8 2 H94876 2.8 2 AA864327 1.9 1.9	49234_s_at	KIAA1389 protein		140,041	4.7	3.8	4.3
AA194720 1.5	43754 at			AI435/35	0.4		4.3
Al200514 8.5 2. AA883987 3 0 H94876 2.8 2 Al552505 0.9 1.0 AA864327 1.0 2.0 AA864327 1.0 2	79392 at			AA194720	1.5	1.4	4.3
AA883987 3 0 H94876 2.8 2 Al652505 0.9 1.	58697 at			AI200514			4.3
H94876 2.8 2.8 2.8	13628 21			AA883987	e		4.3
Al652505 0.9 1.	00700			H94876			4.3
putative G protein-coupled receptor 92	00409 at			AI652505		1.6	4.3
	29629_at	Iputative G protein coupled receptor 92		AA864327	0	a c	0 7

45296_at	KIAA1631 protein		A1986035	12	13	4.3
63481_at			AA059478	1.3		
52204_at			AA894564	4 7	2	
54675_at	inhibitor of kappa light polypeptide gene enhancer in B-cells, IKB kinase heta	KBKB	AA521493	2.2	1.6	t 4
63729 f at			N60103	-		
65403 at			N09123	1.	0.7	4.3
67687 at	high-mobility group (nonhistone chromosomal) protein 1	100	7001011	7 0	7.7	4.3
55372_at	otein DKFZp762L1710		A1831481	5 6	5	4.3
52576_s_at	spondin 2, extracellular matrix protein	SPON2	AW007426		1 0	4.3
53161_r_at			AI826333	1.9	3.1	4.3
52790_at			A1150158	2.8	3.1	4 3
44213_at			AI559696	2.6	3.9	4.3
			AI191040	1.8	1.3	4.3
630// at			AI733697	0.3	2.4	4.3
446/3 at			N53555	9.5	13.7	4.3
60/12 at			AA394100	2	0.7	4.3
/1544 at	KIAAU3/9 protein		AA852371	3.3	0	4.3
46366 at			179183	0.7	6.0	4.3
49598 at			H79046	4.2	2.1	4.3
52832 at			AA012862	1.8	3.5	4.3
24324 at			AA662774	0	1.3	4.3
46885 at			AI822096	0.3	0.4	4.3
4/5/0 at			AI741392	2.1	0.3	4.3
48243 at			AI857897	0.4	2.2	4.3
91324 at			AA149539	4.6	1	4.3
48300 at			AA713522	6.2	2.4	4.3
02992_at			AI214996	25.6	10	4.3
57.285 at			AA933717	1.9	2.2	4.3
51553 at			T90529	4.9		4.3
51613 1 at			AI336271	2.9	3.1	4.3
493/8 r at			AI041389	9.7	2.8	4.3
52909_at			3096417	3.2	2.1	4.3
/3258_at			AI675987	1.3	1	4.3
87058_at			190289	0	6.0	4.3

39043_at	actin related protein 2/3 complex, subunit 1A (41 kD)	ARPC1B	AF006084	2.7	1.3	4.3
41865_at			AF052185	4.4	3.3	4.3
	KIAA1036 protein		AB028959	3.9	3.7	4.3
32622_at	dynamin 2	DNM2	L36983	4.5	0.1	4.3
40568_at	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta ATP6B2 polypeptide, 56/58kD, isoform 2	ATP6B2	L35249	3.2	1.8	4.3
32824_at	sis, neuronal 2, late infantile (Jansky. ase)	CLN2	AF039704	3.8	0.8	4.3
35238_at	TNF receptor-associated factor 5	TRAF5	AB000509	3.5	1.5	4.3
35688 g at	mature T-cell proliferation 1	MTCP1	224459	5.3	2.6	4.3
36628_at	ralA binding protein 1	RALBP1	L42542	4.9	2	4.3
36635_at	ATPase, Class VI, type 11B	ATP11B	AB023173	3.8	1.2	4.3
38733_at	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	XRCC5	M30938	4.8	1	4.3
37966_at	beta-parvin		AA187563	2.9	9.0	4.3
39135_at	KIAA0767 protein		AB018310	4.5	3.7	4.3
39173_at	fibrillarin	FBL	X56597	e	3.1	4.3
56362_at	hypothetical protein FLJ20585		AA121624	1.1	1	4.3
56520_at	nudix (nucleoside diphosphate linked moiety X) type motif 5	NUDTS	AI188576	4.8	3.3	4.3
90610_at	leucine-rich neuronal protein	LRN	AI654857	3.3	2.5	4.3
53906_at	differentially expressed in FDCP (mouse homolog) 6	DEF6	AA523303	4.3	4.3	4.3
61668_at			A1963090	5	2.9	4.3
43798_s_at			AI347938	3.5	2.1	4.3
60863_s_at	hypothetical protein from EUROIMAGE 2021883		AA526910	3.9	2.8	4.3
58595 f at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	AA551303	2.6	3	4.3
49110_s_at			T48132	3.8	2.6	4.3
58528_s_at			AI760772	0	6.0	4.3
53354_at			AI668938	4.1	2.2	4.3
51984_at			AA148813	9.0	1.8	4.3
49210 s at	_		AW023011	4.2	3.2	4.3
49914_at	hypothetical protein dJ511E16.2		AA147044	2.7	2.3	4.3
560_s_at			M63589	4.3	4.3	4.3
38970_s_at	Nef-associated factor 1		AJ011896	26.4	7.6	4.2
41457_at	KIAA0423 protein		AB007883	1.5	3.9	4.2

34955 at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	ABCC4	AF071202	1	2.1	4.2
	HMBA-inducible		AI796944	5.5		0 /
36334_at	lymphocyte antigen 9	6Å7	142621	200	0	4.6
1134_at	activated p21cdc42Hs kinase		113738	0.00		7.4
31888 s at	_	10003	AF001004	6.3	4.9	4.2
'n		2000	Ar 001234	5.6	5.6	4.2
40 VOV	dooth offenter domoin in the state in in in		AL049423	1.4	0.5	4.2
10101	מממוו בוובכוסו מ	DEDD	AF043733	2.2	2.5	4.2
	myosin-binding	MYBPC1	X73114	2	0	4.2
40/91 at	polymerase (RNA) II (DNA directed) polypeptide A (220kD)	POLR2A	X63564	5.6	3.1	4.2
40831_at			AL050190	2.8	0	00
33/08_at	overexpressed gene 1	POV1	AF045584	2.3	90	4.2
35940_at	POU domain, class 4, transcription factor 1	POU4F1	X64624	000	0.4	C
33840_at	52	TPD52	U18914	1.7	0.7	0 0
338/0_at	$\neg \tau$		AB029005	2.4	1 4	100
31669_s_at	homeo box A11	HOXA11	AF039307	27	c	100
38138_at	nding protein A11 (calgizzarin)	S100A11	D38583	3.5	0 %	2.4
41532 at		ZNF151	Y09723	13.8		1 0
	Itosa 2 (X-linked recessive)	RP2	AJ007590	3.4		7.7
	ctor, arginine/serine-rich 4	SFRS4	14076	5.4	7 4	7 6
37391_at	cathepsin L	CTSI	X12451	100		4.4
37273 at			AE0021E2	0.0	ν. 	7.4
38405 at	fragile X mental retardation, autosomal homolog 1	EVD1	Ar00/133		2.5	4.2
38441 s at	membrane cofactor protein (CD46 trophoblast lymphocyte areas	T VV I	025165	0.7	6.0	4.2
1		<u> </u>	X59408	2.9	4.1	4.2
55376_at	MIL1 protein		N66625	2.3	00	
91780_at			AI798874	3.5	6.3	4.6
75863_at			AL042660	0 0	000	7.4
89920_at			AI738556	15	5 0	4.2
77070_at			A1949912	ο α	0 0	77
60402_at			41124014	000	2.5	7.4
61255_at			N36277	0, 0	1./	4.2
47221 at			//2021	O.I.	0.7	4.2
47898 at			20000	20	3.9	4.2
53896 at			A1556854		4	4.2
77100 24	M montain (aimilian to the first of the firs		AA147213	2.7	1.3	4.2
4/100 at	LLIM protein (similar to rat protein kinase C-binding enigma)		AA196325	0	Э	4.2

Figure 13UUUU

2.5 6.6 1.4 6.4 1.4 6.4 1.4 6.4 1.4 6.4 1.4 6.4 1.4 6.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1	1	EH domain containing 1	EHD1	A1986040	53.8	2.9	4.2
Machine Mach	82064_at			AA552150	3.8	2.5	4.2
at Implication of parameter in the control of a parameter in the control	at			AI829707	8		2.7
HIV TAI Specific factor 1	at			N32669	5 0		1.0
Ruanine nucleotide binding protein beta subunit 4 17,000 10,		factor 1	TATOE1	201010			4.2
A A A A A A A A A A		de hinding protein both gubusit 4	1000	A4301303			4.2
Registration Regi	+	a constant brown beta subuill 4		Ai85/603	1	4.5	4.2
Relation Relation	00/00 00/00			AI680362	9.0	0.8	4.2
RBM3 N92444 2.3 2.4 2.5 2.4 2.5 2.4 2.5 2.4 2.5 2.4 2.5	00002 at			R91428	0	1.6	4.2
Activate printing month protein 3 Activate prot	_			N92444	2.3	2.4	4.2
AMOSA014 1.2 2.1 1.2 2.1 1.2 2.1 1.2 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6 1.3 3.6	_	tif protein 3	RM3	AI953114	3.6	1.4	4.2
Alignature Ali	62683_at			AA034014	1.2	2 1	C N
Advisor	48597_at			A1871648	10	2.5	4.7
Alexandromain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3E	65676_at			AA115819	0.5	0.5	4.6
Sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, sema domain, sema date domain, sema	67713_r_at			A1006100			4.2
Ale598291	48172 at			261000192			4.2
Al653829 0 0 0	79179 at			K843/6	0	0.8	4.2
Sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain, sema domain, immunoglobulin domain (lg), short basic domain (lg), short bas	88505 24			A1659829	0	0	4.2
Secreted, (semaphorin) 3E	50416 at			AI653291		0.8	4.2
at serna domain, immunoglobulin domain (lg), short basic domain, serna domain, immunoglobulin domain (lg), short basic domain, SEMA3E AL050043 0.4 3.1 at secreted, (semaphorin) 3E at secreted, (semaphorin) 3E 10.5 3.6 at tat GRB2-associated binding protein 1 GAB1 AW002256 0.7 0.9 r_at class at class or an incidence binding protein NUDE1, rat homolog AR827685 3.9 4.3 at LIS1-interacting protein NUDE1, rat homolog AR827685 3.9 4.3 at vanilloid receptor-related osmotically activated channel; OTRPC4 AR458742 1.9 0.4 protein AR458742 3.7 0.4 at rat AR458742 1.9 0.6 at rat AR674479 0.7 0.6 at rat AR796264 1.8 1.3 at rat AR796264 1.8 1.3 at rat AR79627 0.3 2.4	T			AI693716	0.8	0.0	4.2
at H16779 10.5 3.6 at AW005199 1.6 4 r_at GRB2-associated binding protein 1 GAB1 AW022256 0.7 0.9 r_at GRB2-associated binding protein 1 GAB1 AW022256 0.8 1.6 4 r_at LIS1-interacting protein NUDE1, rat homolog AR85768 2.5 0.9 4.3 at LIS1-interacting protein NUDE1, rat homolog AR85768 3.9 4.3 4.3 r_at vanilloid receptor-related osmotically activated channel; OTRPC4 AR458742 1.9 0.4 at protein NG2096 0.7 0.4 at AI796264 1.8 1.3 AI796264 1.8 1.3 AIR AIR996495 0.3 2.4 AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR AIR		Imunoglobulin domain (lg), short basic domain, ihorin) 3E	SEMA3E	AL050043	0.4	3.1	4.2
at AW005199 10.5 3.0 at GRB2-associated binding protein 1 GAB1 AW022256 0.8 1.6 1 at LIS1-interacting protein NUDE1, rat homolog N75945 3.9 1.8 1 at LIS1-interacting protein NUDE1, rat homolog AR857685 2.5 0.9 2 at LIS1-interacting protein NUDE1, rat homolog AR458742 1.9 0.9 2 at List AR458742 1.9 0.4 2 at Protein AR458742 1.9 0.4 3 at AR458742 1.9 0.4 AR458742 1.9 0.4 AR458742 1.9 0.4 AR458742 1.9 0.6 AR458742 1.9 0.6 AR458742 1.9 0.7 AR458742 1.9 0.6 AR458742 1.9 0.7 AR458742 1.9 0.7 AR45874 1.8 1.3 AR45874 1.8 1.3 <t< td=""><td>52226_at</td><td></td><td></td><td>H16779</td><td>3 01</td><td>000</td><td></td></t<>	52226_at			H16779	3 01	000	
at GRB2-associated binding protein 1 GAB1 AW022159 1.0 4 Lat GRB2-associated binding protein 1 GAB1 AW02226 0.8 1.6 Lat LIS1-interacting protein NUDE1, rat homolog AM857685 2.5 0.9 4.3 at LIS1-interacting protein NUDE1, rat homolog AM857685 3.9 1.8 4.3 I at vanilloid receptor-related osmotically activated channel; OTRPC4 AR458742 1.9 0.4 at protein NG2096 0.7 0.6 at AR796264 1.8 1.7 AR796264 1.8 1.3 AR796264 1.8 2.4	74282_at			00/100/100	10.0	0.0	4.2
r_at GRB2-associated binding protein 1 GAB1 #164435 0.7 0.9 r_at interacting protein NUDE1, rat homolog AM5945 3.9 1.6 r_at vanilloid receptor-related osmotically activated channel; OTRPC4 AM458742 1.9 0.4 at at at at at at at at at at at at at a	80476_at			T10442	0.1	4	4.2
at AWUZZZ55 0.8 1.6 rat N5558 2.5 0.9 at LIS1-interacting protein NUDE1, rat homolog AA458742 1.9 0.4 at vanilloid receptor-related osmotically activated channel; OTRPC4 AI674479 0.7 0.6 at AA45875 3.9 4.3 AA458742 1.9 0.4 AI355014 3.7 0.4 AI355014 3.7 0.6 AI355014 3.7 0.6 at AI796264 1.8 1.3 AI796264 1.8 1.3 AI796264 1.8 1.3 AI796245 3.6 2.4 AI796245 0.3 0.3 AI796245 0.3 AI79	Т	binding protein 1	1001	110443	0.7	6.0	4.2
r_at N /5945 3.9 1.8 at LIS1-interacting protein NUDE1, rat homolog ARESTGRS 2.5 0.9 at ARA557873 3.9 4.3 ARA57685 3.9 4.3 ARA57687 1.9 0.0 ARA58742 1.9 0.4 ARA58742 3.7 0.4 ARA58742 0.7 0.6 at N62096 0.7 0.6 ARA58747 1.7 0.6 ARA58747 1.7 0.6 ARA58747 1.8 1.7 ARA58747 1.8 1.3 ARA58747 1.8 1.3 ARA5875 1.8 1.3 ARA5875 1.8 1.3 ARA5875 1.3 2.4 ARA5875 1.3 2.4 ARA5875 1.3 2.4	Т		MD1	AW022256	0.8	1.6	4.2
at vanilloid receptor-related osmotically activated channel; OTRPC4 N62096 0.9 at cat And 587485 3.9 4.3 And 58742 1.9 0 And 58742 1.9 0 And 58742 1.9 0 And 58742 1.9 0 And 587479 0.7 0.6 And 587479 0.7 0.7 And 587479 0.5 1.7 And 587479 0.3 1.3 And 587479 0.3 1.3 And 587479 0.3 1.3 And 587479 0.3 1.3	51481 r at			N/5945	3.9	1.8	4.2
at AA458742 3.9 4.3 f_at AA458742 1.9 0.4 at protein AI355014 3.7 0.4 at N62096 0.5 1.7 r_at AI795264 1.8 1.3 r_at AI796264		protein NIIDE1		85555N	2.5	6.0	4.2
r_at AA458742 1.9 0 at vanilloid receptor-related osmotically activated channel; OTRPC4 AI355014 3.7 0.4 at N62096 0.5 1.7 r_at AI796264 1.8 1.3 r_at R98495 3.6 2.4 wynF8475 0.3 1.3 wynF8475 0.3 1.3	T	1		AI85/685	3.9	4.3	4.2
Al355014 3.7 0.4	75644 r at			AA458742	1.9	0	4.2
Alignation receptor related osmotically activated channel; OTRPC4 Alignation of the protein Alignation of the protein Alignation of the protein Alignation of the protein Alignation of the protein Alignation of the protein Alignation of the protein Alignation of the protein Alignation of the protein Alignation of the protein of	;	The state of the s		AI355014	3.7	0.4	4.2
at N62096 0.5 1.7 at A1796264 1.8 1.3 r_at R98495 3.6 2.4 at WNF842 0.3 1.3		nd receptor-related osmotically activated channel; OTRPC4		AI674479	0.7	9.0	4.2
at Al796264 1.3 rat R98495 3.6 2.4 at WNG842 0.3 1.3	51502_at			N62096		7 1	
Cat R98495 3.6 2.4 ANDER42 0.3 1.3	50997_at			A1796264		7.7	4.7
at WOF842 0.3 1.2	80285 r at			R98495	3.6	D C	2.4
	56441_at			WOSBAD		F C -	4.6

1000						
9			H29258	3.2	2.1	4.2
-1			H41107	6.5	100	4.2
58397_r_at			AA976373	0	0.5	C /
63916_r_at			T50788	0		7.4
55443_at			AA631027	5 5	1 -	4.6
52655_at			A1703170	0,00	/:-	7.4
44392 at			2770201	6.3	1.1	4.2
65043 2+			HU/855	2.4	2.4	4.2
52446 at			AI857698	0	1.8	4.2
32440 at			AI281933	9.0	9.0	4.2
01/04 at	nypotnetical protein FLJZ0036		AW006276	0.7	0.3	4.2
44620 at			H97503	0.3	2	4.2
46444_at			AI288239	0.7	3.4	4.2
50581_at			AA100715	0.5	0.8	4.2
51595_at	protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein	!	W26575	1.5	9.0	4.2
47053_at			A1768650	C		
55359_at			AA23382A	-	5	7.4
55384 g_at			44454036	0.1	1 0	7 4 7
47527 at			A4434030	n (3.2	4.2
63013 at			A1032488	4.6	m	4.2
56735 at			AL120446	6.2	7.7	4.2
51510 7.04			AA262730	0.5	0.6	4.2
55150 + ot			192882	18.1	10.1	4.2
22100 at			AW024222	1.9	1.5	4.2
34302 at			AI765546	2.3	0.7	4.2
838/8 at			AI027677	6.7	2.2	4.2
77330 r at	00000		A1760700	8.6	2.2	4.2
41224 at	П		AB018331	3.5	1.1	4.2
32//4_at	NADH denydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, NASHI)	NDUFB8	AI541050	2.9	1.3	4.2
37581_at	sphatase 6, catalytic subunit	PPP6C	X92972	6	1 4	0.7
36637_at		ANXA11	L19605	e e	1/1	4.2
3/306_at	KIAA0068 protein		D38549		α.	2.7
38810_at	histone deacetylase 5	HDAC5	AF039241	42	3.5	4.2
48014_at			N54957	0	180	4.2
44549_at			AI708776	3.5		100

Figure 13WWWW

11000 at	in document in the second contract in the sec		A1244335	2.9	000	<
15517 5 24	VIAA1007 mist	IDE	AA573292	5.2	26	
110017 S dt	NIAA1UZ/ protein		AI658962	0.0	0 0	,
51906_at			1000014	6.7	2.3	4
51713_at			A1368015	[]	3.3	4
81574 at	Caspase recruitment domain protein 9		A1660536	4.2	3.8	4
51128 at	ain		AI307612	4.2	3.6	4
48042 at			AA166881	3.6	3.6	4
49071 at			AL119388	2.1	8:0	4
51188 at			AI541411	4.2	1.4	4
54765 at	xeroderma nigmentosum complementation		AA454038	4.2	3.6	4
57828 at		XPC	AL042673	3.8	2.8	4
57201 at		UBASZ	AI857945	2.5	2.5	4
46572_at			A/870481	4	2.5	4
65923_at			A1924230	4.3	2.3	4
55695_at	glycine cleavage system protein H (aminomethyl carrier)	1.000	Al344311	3.7	3.2	4
55009_at		500H	AI890917	5.1	4.5	4
38694 at	KIAA0738 gene product		AI359000	2.4	1.7	4
32484 at	ing protein 2		AB018281	0	0.6	4
32029 at	ide denendent protein Kingen 1	CCBP2	N94888	9.0	1.1	4
1711_at	53.binding protein 1	PDPK1	AF017995	1	1.2	4
31528 f at	nilv. member F	I PS3BP1	009477	4.8	3.1	4
33740_at		nzere Olivo	783/38	1.7	1.4	4
38918_at).hox 13	CLNZ	AF023268	1.1	1.3	4
34264_at		SUXIS	AF083105	3	8.0	4.
33868_at	CGI-96 protein		AB026894	1.6	1.4	4.
40937_at	KIAA1454 protein		293241	2.8	1.2	4
33556_at	Huntingtin interacting protein E		AA160056	3.3	2.3	4
33353_at	E3 ubiquitin ligase SMURF2		AF049611		3.7	4
34362_at	mily 2 (facilitated glucose transporter)	2.00	W26466	1.9	2.1	4
	Ω	SLCZA5	M55531	3.5	2.6	4.1
35699_at	budding uninhibited by benzimidazoles 1 (yeast homolog), beta	BUB1B	AF053306	2.1		4
36075 at	putative GTP-binding protein similar to RAY/RAB1C		AL037167	0.3		
10 dl	Cathelician antimicronial pentide	0.160				ť

Figure 13XXXX

25001	Jegor - Jague A Helital Jetaludilli Z	FMKZ	L76569	0.4	-	_
35301_at			AL049941	1 4	1 2	r
3/234_at	kininogen	KNG	KOSERE	F =	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	1
37403_at	annexin A1	ANXA1	X05908	7.7	5 0	4.1
37264_at	zinc finger protein 131 (clone pHZ 10)	7NF131	0170011		6.0	4
37718_at	KIAA0096 protein		003410	F. 1	1.3	4
32792 at	GCIP-interacting profeso n29		U43636	2.2	4.1	4.]
37629 at	Casein kinase 2 alaba prima polymontida		AL031432	5.1	3.2	4.1
1116 at	Onto antigon	CSNK2A2	M55268	1.6	0.5	4.1
20174 at	L	CD19	M28170	2.5	2.9	4
351/4 at	fluctear receptor coactivator 4	NCOA4	X77548	3.2	0.0	4
70037 at			AA058578	0.5	C	7
40/93 at			AA421625	100	202	1
00115 at	nypotnetical protein FLJ20533		H23252	0.4	0.0	
49991_d(AI872374	С	1 7	
30943 at			AL043737	1 5	0	
45332 r at	aspartate beta-hydroxylase	ASPH	AA156838		ο α	
4/409 at			A1290653	4.4	000	
56578 at			AI732852	3.5	0.2	4.1
7007 at			AA884474	2.1		1
40910 at	- 17		A1028262	1.4	000	1
51007 at	Serine protease I ADG12		AA534591	6.0	4.7	
Ţ		CLCN2	AW003232		7 7	
Ţ	regulator of differentiation (in S. pombe) 1	ROD1	AA788925	0.0	0.0	4.1
91176_at			A1792991	0.9	4 1	4 1
79949_at			A170053E	0.0	CO	4.1
53330_at			A100000	7.7	1.6	4.1
81074 at			A1222203	3.3	0.8	4.1
59328 at			AA169554	9.0	0	4.1
65300 at			AI198875	2.3	1.4	4.1
82312 at			AI656358	1	1.1	4.1
59408 at			AI434767	2.9	1.2	4
84869 at			AA857437	1.4	1.8	4 1
47668 at			AI123917	2.9	1.9	1 4
			H94605	1.1	8	4.1
ч			R70662	6.0	6.0	4.1
10 01101						

Figure 13YYYY

60933 at			W90100	0.4	0.1	4.1
48601 at			AI225105	1.4	1.9	4.1
86447 at			AI525627	0.9	6.0	4.1
67812 at			AA504895	1.1	1.3	4 1
56835 at			A/018657	0.7	0.8	4.1
43708 at			T66877	1.3	3.1	4 1
58452 + 24			R10307	4.3	0	4 1
43566 at			W87376	1.9	1.5	4 1
86737 at			AI674899	4.1	1.3	4 1
70089 24			H88330	10.2	9	4 1
70352 at			AI765926	0.5	0.3	4 1
70831 at			AI803691	0	6.0	4 1
63471 24			AI797620	0.3	0.0	4.1
71008 21			N92630	4.8	1	4 1
77275 2+			AI863088	1.9	4.6	4.1
01162 24			H23230	1.3	80	4 1
51076 of			AI989878	1.5	19	11.0
74040 at			N49842	0.1	3.4	1
12256 2t	nuclear pore complex interacting protein	NPIP	A1991242	6.0	Ĉ	1 7
77228 24			R87972	1.2	0	117
66178 at			AI300953	0	0	4.1
55572 at			AA410395	0.5	9.0	4 1
88143 24			AA938267	2.2	3.4	4 1
65566 at	etoposide induced mBNA		AI253134	3.1	m	4 1
51226 at			AI741005	0	9.0	4.1
45141 at			N53536	0.8	1.5	4.1
52072 at	hypothetical protein El 110719		N51102	2.1	1.4	4.1
53197 g at	Suppression of humoriaenicity 16 (molecules 4:44		AA873182	5.1	8.0	4.1
55409 at	and the control of th	ST16	AI084226	3.2	2.6	4
51133 i at			AI128820	1.6	0.4	4.1
61005 at			AI334373	6.0	2.8	4.1
71884 fat			AA009648	4.5	m	4.1
91156 at			AI028732	1.4	0.5	4.1
78191 + 2+			AI219949	0.2	0.4	4.1
יסיטים מו			AI468969	1.6	6.0	4 1

Figure 13ZZZZ

79940 r at						
283 at	inhiquipol outochromo o controlled		T96976	2.6	1.3	4.1
2017	acidanio ey tochionia e reduciase core protein i	UQCRC1	L16842	8 %	171	/ J
40176 at		RFP	103407) 14	/ -	4.1
41749_at	ES1 (zebrafish) protein, human homolog of	C210BE33	1152002		C. 1	4.1
32317_s_at	sulfotransferase		U34804	4.5	3.1	4.1
41504 c at	V.mof miscarles					
41004_s_al	villal illusculoaponeurotic fibrosarcoma (avian) oncogene homolog	MAF	AF055376	3.9	3.2	4.1
35331_at	catenin (cadherin associated protein), alpha like 1	CTMMAI 1	700001			
36537_at	Rho-specific guanine nucleotide exchange factor pt 1.4	TIVILI	/90/60	4.1	3.3	4.1
32510 at	aldo keto reductase family 7 member A2 (asteria alaria)		AB011093	3.3	1.7	4.1
	reductase)	AKR7A2	AF026947	3.5	2.1	4.1
32528_at	ClpP (caseinolytic protease, ATP-dependent, proteolytic subunit,	CLPP	750853	6		
	E. coli) homolog		2) †	7.7	4.1
48833_at			AI749098	4	2.0	
32011_at		ARNT	AI768497	3	2.5	4.1
43456 at	Serine/threonine protein kinase MASK		A12000E2		7.7	1.4
52248_s_at			20666310) r	0.5	4.1
56404_at	CGI-109 protein		U07565	3,7	3.1	4.1
46242_at			000760	7.7		4.1
50996_s_at	HSCARG protein		AA215/96	4.1	2.8	4.1
48094 at			AI080/01	2.1	0.7	4.1
50172 at			AA531025	4.4	3.8	4.1
43795 s at	NADH dehydrogenase (ribigininge) 1 slabs subsection of 2000		AI377006	2.2	3.1	4.1
		NDUFA8	AW005361	3.5	2.6	4.1
52908_at	hypothetical protein FLJ21324		AAGECTO			
54950_at			1000019 1100001	4.6	3.9	4.1
42633_r_at			AI / BUBUI	3.5	3.2	4.1
45716 at	RAN, member RAS oncogene family		153591	0.5	2.1	4
39016 r at	keratin 6A	KAN	W81244	9.0	2.1	4
1292 at	dial specificity obserbation 2	KRT6A	L42611	0.1	0.1	4
31993 f at	ממנו באבניוניול איוסיאוומומספ כ	DUSP2	L11329	18.4	2.6	4
30016 7 24			U80764	1.00	1 7	
31507 f at	iluosoitiai protein 515	RPS15	J02984	α.	V	1
3100/ I at	nemoglobin, beta	HBB	M25079	2	T C	4
32068_at	complement component 3a receptor 1	C3AR1	1162027	0 4	t, c	1
			(1)	,	_	-

Figure 13AAAAA

32120_at	small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated	SCYA18	Y13710	7.8	7.9	4
38535_at	distal·less homeobox 4	DI X4	1173308	0		
41169_at	plasminogen activator, urokinase receptor	PLALIR	V74020	0 0	×.0	4
1696_at	polymerase (DNA directed), beta	a 10a	774039	8.4	4.2	4
33668 at	ribosomal protein 1.12	20.0	023013	1.3	1.8	4
497 at	o in a linear section of the section	KPL12	AF037643	2.1	1.2	4
	Vogt disease)	CLN3	U32680	2.1	1.4	4
38928_r_at		TYR	M27150	-	,	
32834_r_at	sudD (suppressor of bimD6, Aspergillus nidulans) homolog	COURS	AE013501	4 0	0.4	4
34216_at		222	160000		0.6	4
41247_at			MM4/8904	12.3	0.3	4
38617_at	LIM domain kinase 2	07,641	H12054	1.5	1	4
41488 at	hypothetical protein 4.21106 1	LIMINZ	D45906	27.3	4.4	4
38676 at			AC002394	8.2	4.9	4
35221 at	er de la company	STCH	AA059408	7.6	3.8	4
32222 at	1 P8 protein		X91648	2.3	0	4
36295 at			AA152202	18.5	14.2	4
35762 at	KINANA92 cratein	ZNF134	U09412	1		
35,02 at			AB007952	Ċ	250	
53003 at	CDC like kings 3	ARHE	S82240	6.0	- 2	1
36155 24	SCOOTING WINDS 2	CLK2	129218	2.7	7 0	
30133 at	NAMOZ/3 gene product		D87465	0-		1
36208 at		BRD2	D42040	7:1	1.1	4
38363 at	sine kinase binding protein	TYRORP	WIGOGA	0.1	0.0	4
2005_s_at	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	IAK3	131313	7.7	2.3	4
63867_at		200	03131/		1.2	4
56847_at		LOA	A19/1/09	2.4	2.1	4
58206 at			AI911070	0	0	4
75747 at			W63702	0	0.3	4
56460 at			AA626334	2.3	2	4
76055 at			AA809379	0	0	V
76905 at			AA707217	0.8		A
77142 at			A1674760	3.4	0.7	4
76710 at	Cardiotrophia like outoking: policytonskie 178		AI640484	3.4	1.8	4
\$ - - - -	factor-3		AI040033	92.7	4.7	4
			_	_		

Figure 13BBBBB

59179 at			189693	10	0	
59200 at			178626	1.4	2.8	4
52137_at			AI140767	1.3		4
52805_at			AI024348	0.8	0.7	4
53873_at			R67688	1.9	2.1	4
80872_at			AA533574	0	0.2	4
54757_at			N51283	1.5	2.7	4
63205_at			AA770196	2.9	3.4	4
67051_r_at			AI345851	1.4	2.6	4
81565_at			W85907	0.7	0.4	4
50631_at			AA843724	8.0	1.7	4
59000_at	x 010 protein	010	AA629304	9.9	4.8	4
51623_at	DKFZP434116 protein		AA203689	1.9	1.6	4
55656_at			AI651905	1.3	1.6	4
60502_at			AI743953	0	0	4
43115_at			A1686303	1.5	2.8	4
42669_at	KIAA1304 protein		R00834	2.9	1.8	4
43573_at			AA251274	1.1	2	4
68403_at			AA781446	1.3	0	4
43646_at	zinc finger protein 14 (KOX 6)	ZNF14	AA599140	1.6	9.0	4
42475_at			194540	2	m	4
69432_at			AI655716	1.2	-1	4
79912_at			AA642419	1	2.2	4
43673_at			AI056293	1.5	2.3	4
89479_at			AI810541	0.5	1.5	4
45308_at			AA114834	2.5	3.7	4
77927_i_at			AI743151	2	9.0	4
71619_at			A1936553	6.0	6.0	4
84510 at	interleukin 20 receptor, alpha	IL20RA	A1800588	5.2	0.4	4
65541_at			AA628960	3.2	1.9	4
43038_r_at	KIAA1363 protein		AI769531	0	8.1	4
74131_at			AI989784	5.1	2	4
50354_at	FK506 binding protein precursor		N36303	2.5	3.9	4
77105_at	Fzr1 protein		AI732960	0.7	2.2	4
65416_i_at			R91398	2.2	1.2	4

Figure 13CCCCC

787292 at 1 AL036075 AL036075 90332_at 1 190310 at 1 AL777061 90332_at 2912_at 3 AL777061 AL777061 90332_at 4 AL777061 AL827603 96258_at 4 AL827603 AL827603 45624_at 5 Core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-bigalactosyltransferase AL827603 45624_at 6 Core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-bigalactosyltransferase AL827609 45624_at 7 Core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-bigalactosaminase. AL827609 45624_at 7 Core 2 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-bigalactosaminase. AL967868 45624_at 8 DEAD/H (Asp-Glu-Ala-Asp-His) box polypeptide 17 (72kD) DDX17 AA461244 45624_at 1 DEAD/H (Asp-Glu-Ala-Asp-Cilic AL967821 AA888172 59798_r at 1 Imping translocation breakpoint JTB AA4888172 59798_r at 2 Ald-Asp-Grade AA888172 AA888172 59079_at 3 Alternophilin, subfamily 3, member 4 AA888172 AA888172 5560_at 4 Amoramine oxidase A AAA888172	0.4 0.6 0.7 0.7 1.6 0.7 1.7 1.7 1.7 1.7	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
KIAA0493 protein	0.6 0.7 0.7 1.6 1.7 1.7 1.7 5.2	0.3 1.9 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0
KIAA0493 protein Ala	2.2 2.2 1.7 2.1 5.2 5.2	1.0 6.0 6.0 7.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1
Alichard 293 protein Alichard 293 protein 2	22.2	0.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00
tat core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3- galactosyltransferase galactosyltransferase at niban protein DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD) at lumping translocation breakpoint adenosiine deaminase, RNA-specific butyrophilin, subfamily 3, member A2 at monoamine oxidase A thyroid hormone receptor interactor 6 thyroid pormone receptor interactor 6 at KIAA0750 gene product lactate dehydrogenase B macrophage lectin 2 (calcium dependent) UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase at regulator of G-protein signalling 10 KIAA0747 protein ARIAA0747 protein	2.2	6 0 0 1 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0
tore1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3- galactosyltransferase at niban protein DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 17 (72kD) DDX17 AA adenosine deaminase, RNA-specific butyrophilin, subfamily 3, member A2 at monoamine oxidase A thyroid hormone receptor interactor 6 TRIP6 AA AA AA AA AA AA AA AA AA AA AA AA	5.2	2.8 6.9 5.9 1.6 1.6 1.6 1.6 1.6 1.6 1.6
corel UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3- galactosyltransferase galactosyltransferase galactosyltransferase at niban protein DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD) at jumping translocation breakpoint adenosine deaminase, RNA-specific adenosine deaminase, RNA-specific adenosine deaminase, RNA-specific adenosine deaminase, RNA-specific adenosine deaminase, RNA-specific adenosine deaminase, RNA-specific at monoamine oxidase A AAA AAA AAA AAA AAA AAA AAA	5.2	6.9 6.9 7.0 1.6 1.0 1.0 1.0 1.0
at inban protein signaling 10 BTN3A2 AAA thyroid hormone receptor interactor 6 macrophage lectin 2 (calcium dependent) thyroid bornosamine 2-epimerase/N-acetylimannosamine kinase galactosyltransferase NESTAGE AAA AAA AAA AAA AAA AAA AAA	5.2	6.9 2.4 0.1 0.1 0.1 0.1 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
NEBAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 17 (72kD) DDX17 AAA DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 17 (72kD) DDX17 AAA at jumping translocation breakpoint ATB ADAR ADAR butyrophilin, subfamily 3, member A2 ADAR ATB at adenosine deaminase, RNA-specific ADAR ADAR at monoamine oxidase A AAA thyroid hormone receptor interactor 6 TRIP6 ADAR at KIAA0750 gene product AAA at AAA AAA at KIAA0750 gene product ADAR at Calcium dependent) ADAR AAA AAA at KIAA0750 gene broduct ADAR at Calcium dependent) ADAR AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA	4 1	2.4 5.9 1.6 0.1 1.2 9.5 9.5
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD) DDX17 AAaat jumping translocation breakpoint ADAR		0.1.0
at Equitor of G-protein signalling 10 DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 17 (72kD) DDX17 AAA adenosine deaminase, RNA-specific butyrophilin, subfamily 3. member A2 BTN3A2 AAA AAA AAA TRIPE AAA AAA AAA AAA AAA AAA AAA	16.7	0.1.0
at impoing translocation breakpoint adenosing translocation breakpoint adenosing translocation breakpoint adenosing translocation breakpoint adenosing translocation breakpoint adenosing translocation breakpoint adenosing translocation breakpoint and adenosing at at monoamine exidase A at monoamine exidase B at INAAO750 gene product at INAAO750 gene product at INAAO760 gene product at Inactate dehydrogenase B anacrophage lectin 2 (calcium dependent) and Inactate dehydrogenase B anacrophage lectin 2 (calcium dependent) at INAAO760 gene product at Inactate dehydrogenase B anacrophage lectin 2 (calcium dependent) at INAAO760 gene product at Inactate dehydrogenase B anacrophage lectin 2 (calcium dependent) and INAAO760 gene product at INAAO7	20.7	01 01 1.2
at lumping translocation breakpoint at lumping translocation breakpoint adenosine dearminase, RNA-specific ADAR BTN3A2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	7.5	1.2
adenosine dearminase, RNA-specific ADAR BTN3A2 AAA at thyroid hormone receptor interactor 6 at monoamine oxidase A AAA at KIAAA0747 protein adenosine dearmine 2-epimerase/N-acetylmannosamine ADS kinase at regulator of G-protein signalling 10 KIAA0747 protein ADARAACAA PROTEIN STANDARD ADS ADARAACAAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAA ADARAACAAA ADARAACAA ADARAACAAA ADARAACAAACAAA ADARAACAAAA ADARAACAAAAAAAAAA	0 0	9.5
BTN3A2 AAR	7.6	0,00
AAA	2.5	7.5
thyroid hormone receptor interactor 6 thyroid hormone receptor interactor 6 at monoamine oxidase A at KIAA0750 gene product lactate dehydrogenase B macrophage lectin 2 (calcium dependent) UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase at regulator of G-protein signalling 10 KIAA0747 protein KIAA0747 protein AA2 AA2 AA3 AA4 AA4 AA4 AA5 AA5 AA5 AA5	2.6	6.8
thyroid hormone receptor interactor 6 at monoamine oxidase A at KIAA0750 gene product lactate dehydrogenase B macrophage lectin 2 (calcium dependent) UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase at regulator of G-protein signalling 10 KIAA0747 protein thyroid hormone receptor interactor 6 ADE ADE ADE ADE ADE ADE ADE ADE ADE ADE	4.8	3
thyroid hormone receptor interactor 6 at monoamine oxidase A at KIAA0750 gene product lactate dehydrogenase B macrophage lectin 2 (calcium dependent) UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase at regulator of G-protein signalling 10 KIAA0747 protein KIAA0747 protein	1.2	1.1
thyroid hormone receptor interactor 6 at monoamine oxidase A at KIAA0750 gene product lactate dehydrogenase B macrophage lectin 2 (calcium dependent) UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase at regulator of G-protein signalling 10 KIAA0747 protein	1	6.1
at monoamine oxidase A at KIAA0750 gene product lactate dehydrogenase B macrophage lectin 2 (calcium dependent) UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase at regulator of G-protein signalling 10 KIAA0747 protein	0.2	0.5
at KIAA0750 gene product lactate dehydrogenase B macrophage lectin 2 (calcium dependent) UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase at regulator of G-protein signalling 10 KIAA0747 protein	5.4	0.2
lactate dehydrogenase B	1.4	1.9
macrophage lectin 2 (calcium dependent) UDAN-Nacetylglucosamine-2-epimerase/N-acetylmannosamine kinase at regulator of G-protein signalling 10 KIAA0747 protein	4.3	4.2
UPP-0-1970 Control of the control of	3.2	2.4
kinase at regulator of G-protein signalling 10 KIAA0747 protein	4	4
at regulator of G-protein signalling 10 KIAA0747 protein	2.9	1.6
KIAA0747 protein	2.0	
	t ::	
W31943	0.7	2.5
	7.0	
HSPC009 protein	0. t	n -
56235 at MAD2 (mitotic arrest deficient, yeast, homolog) like 2		. I

Figure 13DDDDD

50926_s_at	fatty acid hydroxylase		K54585	4	4	7
56875_at	tRNA selenocysteine associated protein		AA082704	1.1	0.7	4
48670_at	CGI-119 protein		AI189791	1.6	1.2	4
52090_at			AI198126	1.1	9.0	4
57210_at			AI862775	3.9	3.3	4
54061_at	hypothetical protein FLJ10595		AA088424	1.7	2	4
52841_at			AA731740	4.1	4	4
47057_at			D20714	3.5	3.4	4
47104_at			AI760368	4.5	3.4	4
47922_at			AA423837	2.6	0	4
38981_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex. 3 (12kD, B12)	NDUFB3	AA203354	1.1	2.4	9.8
279_at	ar receptor subfamily 4, group A, member 1	NR4A1	L13740	0.8	1.9	3.9
37491_at	TATA box binding protein (TBP) associated factor, RNA polymerase II, A, 250kD	TAF2A	D90359	3.5	1.6	3.9
34539_at	olfactory receptor, family 7, subfamily E, member 12 pseudogene	OR7E12P	AF065854	8.0	0.5	3.9
39897_at	DEAD/H (Asp.Glu-Ala-Asp/His) box polypeptide 16	DDX16	N36997	3.2	2.1	3.9
41852 at		RLF	U22377	2.3	0.7	3.9
34544_at	zinc finger protein 267	ZNF267	X78925	4.3	2.9	3.9
39784_at			U26032	0	0.4	3.6
40098 at	EH domain containing 1	EHD1	AF001434	28.1	9.0	3.9
40121_at	huntingtin interacting protein 2	HIP2	U58522	0.8	1.5	3.9
	S13	RPS13	W28765	6.0	1	3.9
39290_f_at	PAI-1 mRNA-binding protein		W28257	6.0	0	3.9
31342_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N- acetylgalactosaminyltransferase 2 (GalNAc.T2)	GALNT2	X85019	4.4	1.3	3.9
32711_g_at	potassium voltage gated channel, shaker related subfamily, beta member 1	KCNAB1	X83127	1.6	8.0	3.9
33234_at	KIAA0117 protein		AA887480	2.7	3	3.9
41193_at	dual specificity phosphatase 6	DUSP6	AB013382	11.5	2.5	3.9
33267_at			AF035315	4	1.5	3.9
33327_at		C110RF9	AB023171	0.1	0.7	3.9
40960_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide B4GALT:	B4GALT1	D29805	16.7	4.9	3.9
	1					

Figure 13EEEEE

40988_at	YME1 (S.cerevisiae) like 1	YME1L1	A 11 32637	1 5	C	C
40997_at	mitogen activated protein kinase kinase kinase 12	MAP3K12	AIGEOGRA	517	2.3	20,00
41279 f at	mitogen-activated protein kinase 8 interacting protein 1	MAPKRIP1	AF007134	200	0.0	3.9
31671_at	RNA binding motif, single stranded interacting protein 1,	RBMS1P	D82351	3.7	4.6	9.8
33479 g at	7	C C				
36270 at	+-	ZANI	X63759	1.4	1.2	3.9
37438 at	KIAA0419 gene product	CD86	U04343	4.9	13.2	3.9
33835 at	KIAA0721 protein		AB007879	1.5	2.1	3,9
36298 at	Derinherin		AB018264	3.4	9.0	3.9
41595 at	oroto	PRPH	L14565	1.2	ō	3.9
36821 at	ווייים ליני ליני ליני ליני ליני ליני ליני		AB023164	1.6	2.1	3.9
36753 24	الماماسوا		AL050367	0	Ó	3.0
8 000	and ITIM domains), member 4	LILRB4	AF072099	8.1	8.9	9.6
35799 at	DnaJ (Hsp40) homolog, subfamily B, member 9	DNAJB9	AI 080081	1 2		
36754_at		ADCYAP1	X60435	0.40	J C	w c
36110_at	RABSA, member RAS oncogene family	RABSA	M28215	2.4	5 6	5.0
36203_at		ODC1	X16277		0.0	2.0
37212_at		SP2	028588	700	50 -	3.9
508_at	suppressor of Ty (S.cerevisiae) 4 homolog 1	SUPT4H1	1143923		1 0	3.9
37915_at	bromodomain adjacent to zinc finger domain, 2B	BA72B	41 080173		500	3.9
61865_at			A1423165	0.7	3.4	3.9
56434_at			AA579598	0.7	4 0	3.9
90278_at			AA709455	200	200	3.9
50842_at			WOODO	0 0	7.0	3.9
76533_at			V1660694	7.7	3.7	3.9
58132_at			A A SO 7 2 E S	4.0		3.9
66742_at			A400/238	۹.۲	3.3	3.9
77647 at			A/681652	1.1	0.5	3.9
61771 at			AI131078	1.8	4	3.9
			AA886300	3.2	0.3	3.9
79240 at			AI425073	1.1	1.1	3.9
61543 at			AI435163	3	0	3.9
51343 r at			AI184720	3.6	1.6	3.9
52067 at			R62551	2.9	-	3.9
			AI220827	1.7	0.5	30

Figure 13FFFFF

52664_at			AI263842	1.1	1.2	3.9
80265 at	1000		AI420422	3.7	1.2	3.9
ro.	KIAAUSSS protein		AW008847	1.5	1.3	3.9
60906 r at	hypothetical protein FLJ10773		AA044181	4.4	4.8	3.9
80908 at			AA884148	1.9	2.2	3.9
03022_at			A1809213	1.2	0.1	3.9
54777 at			N58166	5.7	2.8	3.9
7030F at			H61899	0.1	0	3.9
79350 at			AA706315	0	0	3.9
79350 at			AI479376	5.3	1.1	3.9
79300 at			AA555312	3.2	5.5	3.9
70700 24			AI608810	0.2	1.3	3.9
F1644 24			AI690729	0.5	2.8	3.9
77035 24	nolog, subtamily A, member 2	DNAJA2	AI560867	1.2	1.3	3.9
// 3338 at			AI939620	4.6	2.5	3.9
40034 at			R44338	0	0.4	3.9
43034 at	Cal-og protein		AW008524	2.8	3	30
32422 al			AI741514	2.8	1.2	3.9
31000 r at			AA829939	0	0.3	0 8
71122 at	hypothetical protein FLJ10052		AI689756	4.4	2	3.9
43437 at			R60981	0.2	0.1	o m
F7111 of			R85261	2.5	3.2	0 8
Ę :			W87368	0.2		300
1	INT-KEIV-18 antigen		AI425002	13.9	8.8	8
77557 2t			W44959	1	0.5	3.9
81066 : 24			AA226241	9.9	2.8	3.9
77520 - at	himothodiscoloristics in the contraction of the con		AI285898	9.9	2.3	3.9
57960 at	III potinetical protein PLJZ0094		Al480121	0.7	0.7	6 %
3/000 at			AL037445	1.3	60	300
33183_at	collabsin response mediator protein-5; CRMP3 associated molecule		AI879238	6.0	0.7	3.9
			A1192897	0	1 2	C
44547_at			A1971552	17	2.1	9.0
51798_at	hypothetical protein FLJ11000		AW006887	14	1.3	3.9
49787_s_at	49787_s_at KIAA1547 protein		A1291302	1,10	C1	3.9

Figure 13GGGGG

hypothetical protein FLJ12484 M45523 6.2 Abpothetical protein FLJ12484 AA655463 1.8 Absorbed AA655463 1.8 Absorbed AA655463 1.8 Absorbed AA6557191 2.6 Absorbed AA657191 2.6 Absorbed AA70267 1.7.9 Absorbed AA80633 1.7 Absorbed AA16856 1.6 RAD230 AA16856 1.6 RAD231 AA16856 1.6 RAD23 (S. cerevisiae) homolog A AA016550 3.3 RAD23 (S. cerevisiae) homolog A AA016650 3.4 Acetylglucosamineidase AA037529 6.8 Acetylglucosamineidase AA037520 0.4 Acetylglucosamineidase AA037520 0.4 Acetylglucosamineidase AA037520
AA459463
AI768349 N49233 N49233 N49233 N49233 N74444 N74444 AA573272 N700572 N700572 N7005724 AI807693 AI2041224 AW021681 AA860344 AA960356 AA16856 AA16856 AA16853 AA515640 AA515640 AC033007 AA515640 AC033007 AA515640 AC03307 AA515687 AF052111 AA515687 AF052111 AA515687 AA516687 AI246687 AI2467 AI246687 AI246687 AI246687 AI246687 AI2467 AI2467 AI2467 AI
N49233 N74444 N74444 N74444 A4573272 A1807524 A180753 A1807633 A2037529 A416856 A416856 A4416856 A4416856 A4416856 A4515640 AC003007 UQCKC2 J04973 A4515640 AC003007 ACD33A AC03252 AA515640 ACD33A AA515640 ACD33C23 AA515640 ACD33C3C3 AA515640 ACD33C3C3 AA515640 ACD33C3C3 AA515640 ACD33C3C3 AA515640 ACD33C3C3 AA515640 ACD37529 AA515640 ACD37529 AA515640 ACD37529 AA515640 ACD3752 AA515640 ACD3752 AA515640 ACD3752 AA515640 ACD3752 AA515640 ACD3752 AA515640 ACD3752 AA515640 ACD3752 AA515640 ACD3752 AA515640 ACD3752 AA515640
N74444 A4557191
AA557191 AA573272 W70067 W70067 AI807693 AI807693 AI807693 AI80724 AW021681 AA860344 F64805 AA416856 AA416856 AA037529 R79063 AC003007 AC003007 AC01307 AC01
AA573272
W70067 1 W70067 1 Al807693 1 Al041224 Al041224 1 AA860344 1 AA860344 1 AA416856 AA416856 AA416856 1 AA037529 AA037529 1 AA037529 AA037529 1 AA037529 AA037529 1 AA037529 AA037529 1 AA037529 AA037529 1 AA037529 AA037529 1 AA037529 AA037529 1 AA037529 AA03752 AA03752 1 AA03752 AA03752 AA03752 1 AA03752 AA03752 AA03752 AA03752 1 AA03752 AA037
AIR07693 AL041224 AL041224 AW021681 AA860344 T64805 AA416856 AA416856 AA037529 R79063 AA037529 R79063 AA037529 R79063 AA515640 AC03007 AC03007 ALDH9 U34252 ALDH9 U34252 ALDH9 U34252 ALDH9 U34252 ALDH9 U342687
ALO41224
olog 4 MADH4 AW021681 AA860344 AA860344 F64805 AA416856 AA416856 AA416856 AA037529 R79063 R79063 AA515640 AA515640 AC003007 AC003007 AC003007 ALDH9 U34252 ALDH9 U34252 M68864 Y18007 CTSC A1246687
AA860344 T64805 EMP3 AA416856 AA416856 AA037529 R79063 AA5156400 AA515640 AA515640 AA515640 AA515640 AA515640 AA515640 AA51564000 AA51564000 AA515640000 AA5156400000000000000000000000000000000000
T64805 AA416856 AA416856 AA05790 AA037529 R79063 R79063 AA515640 AC003007 UQCRC2 J04973 RAD23A D21235 ALDH9 U34252 ALDH9 U34252 ALDH9 U34262 CTSC A1246687
AA416856
EMP3 AW005790 AA037529 R79063 R79063 AA515640 AA615640 AC003007 UQCRC2 J04973 RAD23A D21235 AF052111 ALDH9 U34252 ALDH9 U34252 CTSC A1246687
AA037529 R79063 R79063 R79063 AA515640 AC03007 UQCRC2 104973 RAD23A D21235 ALDH9 U34252 ALDH9 TY18007 CTSC A1246687
R79063 AA515640 AA515640 AC03007 UQCFC2 104973 AF052111 ALDH9 U34252 M68864 Y18007 CTSC A1246687
AA515640 AC003007 UQCRC2 J04973 RAD23A D21235 AF052111 ALDH9 U34252 M68864 Y18007 CTSC A1246687
AC003007 UQCRC2 J04973 RAD23A D21235 AF052111 ALDH9 U34252 M68864 Y18007 CTSC A1246687
UQCRC2 J04973 RAD23A D21235 AF052111 ALDH9 U34252 M68864 Y18007 CTSC AI246687
RAD23A D21235 AF052111 AF052111 ALDH9 U34252 M68864 Y18007 CTSC A1246687
AF052111 ALDH9 U34252 M68864 Y18007 CTSC A1246687
ALDH9 U34252 M68864 Y18007 CTSC A1246687
M68864 Y18007 A1246687
Y18007 A1246687
A1246687
N22262 3.8
3
on initiation factor 2, subunit 3 (gamma, EIF2S3 N38902 3.7